(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification[7]: **C12N 15/12**, C07K 14/47, 16/30, G01N 33/68, C12Q 1/68, A61K 31/7088 // A61P 35/00

(21) International Application Number: PCT/US00/33312

(22) International Filing Date: 8 December 2000 (08.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/169,681	8 December 1999 (08.12.1999)	US
60/171,350	21 December 1999 (21.12.1999)	US
60/189,315	14 March 2000 (14.03.2000)	US
60/203,791	12 May 2000 (12.05.2000)	US
60/210,600	9 June 2000 (09.06.2000)	US
60/220,114	21 July 2000 (21.07.2000)	US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

(57) Abstract: The invention relates to compositions, kits, and methods for detecting, characterizing, preventing, and treating human cervical cancers. A variety of novel markers are provided, wherein changes in the levels of expression of one or more of the markers is correlated with the presence of cervical cancer.

NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION,
AND THERAPY OF CERVICAL CANCER

RELATED APPLICATIONS

5   The present application claims priority to U.S. provisional application serial no.
60/169,681, filed on December 8, 1999, U.S. provisional application serial no.
60/171,350, filed on December 21, 1999, U.S. provisional application serial no.
60/189,315, filed on March 14, 2000, U.S. provisional application serial no. 60/203,791,
10   filed on May 12, 2000, and U.S. provisional application serial no. 60/210,600, filed on
June 9, 2000, all of which are expressly incorporated by reference.

FIELD OF THE INVENTION

        The field of the invention is cervical cancer, including diagnosis,
15   characterization, management, and therapy of cervical cancer.

BACKGROUND OF THE INVENTION

        The increased number of cancer cases reported in the United States, and, indeed,
around the world, is a major concern. Currently there are only a handful of treatments
20   available for specific types of cancer, and these provide no absolute guarantee of
success. In order to be most effective, these treatments require not only an early
detection of the malignancy, but a reliable assessment of the severity of the malignancy.
        Cancer of the cervix is one of the most common malignancies in women and
remains a significant public health problem throughout the world. In the United States
25   alone, invasive cervical cancer accounts for approximately 19% of all gynecological
cancers. In 1996, it is estimated that there will be 14,700 newly diagnosed cases and
4900 deaths attributed to this disease (American Cancer Society, Cancer Facts & Figures
1996, Atlanta, Ga.: American Cancer Society, 1996). In many developing countries,
where mass screening programs are not widely available, the clinical problem is more
30   serious. Worldwide, the number of new cases is estimated to be 471,000 with a four-
year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer* In:
"Human Papillomavirus", New York, Oxford Press, pp 9-39; National Institutes of

- 2 -

Health, Consensus Development Conference Statement on Cervical Cancer, Apr.1-3, 1996).

The precursor to cervical cancer is dysplasia, also known in the art as cervical intraepithelial neoplasia (CIN) or squamous intraepithelial lesions (SIL). While it is not

5   understood how normal cells become transformed, the concept of a continuous spectrum of histopathological change from normal, stratified epithelium through CIN to invasive cancer has been widely accepted for many years. A large body of epidemiological and molecular biological evidence has established human papillomavirus (HPV) infection as a causative factor in cervical cancer. HPV is found in 85% or more of squamous cell

10   invasive lesions, which represent the most common histologic type seen in cervical carcinoma. Additional cofactors have also been identified, including oncogenes that have been activated by point mutations and chromosomal translocations or deletions.

In light of this, cervical cancer remains a highly preventable form of cancer when pre-invasive lesions are detected early. Cytological examination of Papanicolaou-

15   stained cervical smears (also referred to as Pap smears) is currently the principle method for detecting cervical cancer. Not surprisingly, the effectiveness of Pap smear screening varies depending not only upon the quality of the sample being used, but also upon subjective parameters that are inherent to the analysis. In addition, despite the historical success of the test, concerns have arisen regarding its ability to reliably predict the

20   behavior of some pre-invasive lesions (Ostor *et al.*, 1993, *Int. J. Gynecol. Pathol.* 12: 186-192; and Genest *et al.*, 1993, *Human Pathol.* 24: 730-736).

It would be therefore be desirable to provide specific methods and reagents for the diagnosis, staging, prognosis, monitoring, and treatment of diseases associated with cervical cancer, or to indicate a predisposition to such for preventative measures.

25

SUMMARY OF THE INVENTION

The invention relates to novel genes associated with cervical cancer as well as methods of assessing whether a patient is afflicted with cervical cancer. "Cervical cancer " as used herein includes pre-malignant conditions, *e.g.*, CIN and SIL. The

30   methods of the present invention comprise the step of comparing the level of expression of a novel marker in a patient sample, wherein the marker is listed within Tables 1-4, and the normal level of expression of the marker in a control, *e.g.*, a sample from a

patient without cervical cancer. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer or has a pre-malignant condition (*e.g.*, CIN and/or SIL).

In one method, the marker(s) are preferably selected such that the positive

5   predictive value of the method is at least about 10%. Also preferred are embodiments of the method wherein the marker is differentially-expressed by at least two-fold in at least about 20% of any of the following conditions: stage 0 cervical cancer patients, stage I cervical cancer patients, stage II cervical cancer patients, stage III cervical cancer patients, stage IV cervical cancer patients, grade I cervical cancer patients, grade II

10   cervical cancer patients, grade III cervical cancer patients, squamous cell (epidermoid) cervical cancer patients, cervical adenocarcinoma patients, cervical adenosquamous carcinoma patients, small-cell cervical carcinoma patients, malignant cervical cancer patients, patients with primary carcinomas of the cervix, patients with primary malignant lymphomas of the cervix and patients with secondary malignant lymphomas of the

15   cervix, and all other types of cancers, malignancies and transformations associated with the cervix.

In one embodiment of the methods of the present invention, the sample comprises cells obtained from the patient. The cells may be found in a cervical smear collected, for example, by a cervical brush. In another embodiment, the patient sample

20   is a cervical-associated body fluid. Such fluids include, for example, blood fluids, lymph, ascitic fluids, gynecological fluids, urine, and fluids collected by peritoneal rinsing.

In accordance with the methods of the present invention, the presence and/or level of expression of the marker in a sample can be assessed, for example, by detecting

25   the presence in the sample of :

- a protein corresponding to the marker or a fragment of the protein (*e.g.* using a reagent, such as an antibody, an antibody derivative, or an antibody fragment, which binds specifically with the protein or a fragment of the protein)

30   - a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by a protein corresponding to the marker

- 4 -

- a transcribed polynucleotide (*e.g.* an mRNA or a cDNA), or fragment thereof, having at least a portion with which the marker is substantially homologous (*e.g.* by contacting a mixture of transcribed polynucleotides obtained from the sample with a substrate having one or more of the markers listed within Tables 1-4 fixed thereto at selected positions)

- a transcribed polynucleotide or fragment thereof, wherein the polynucleotide anneals with the marker under stringent hybridization conditions.

The methods of the present invention are particularly useful for identifying patients with a pre-malignant condition such as CIN and/or SIL. The methods are also useful for further diagnosing patients having an identified cervical mass or symptoms associated with cervical cancer. The methods of the present invention can further be of particular use with patients having an enhanced risk of developing cervical cancer (*e.g.*, patients having a familial history of cervical cancer and patients identified as having a mutant oncogene). The methods of the present invention may further be of particular use in monitoring the efficacy of treatment of a cervical cancer patient (*e.g.* the efficacy of chemotherapy).

The methods of the present invention may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of markers. According to a method involving a plurality of markers, the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-4 is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer. A significantly enhanced level of expression in the sample of one or more of the markers listed in Tables 1-4, or some combination thereof, relative to that marker's corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. The markers of Tables 1-4 may also be used in combination with known cervical cancer markers in the methods of the present invention.

In a preferred method of assessing whether a patient is afflicted with cervical cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

a) the level of expression of a marker in a patient sample, wherein at least

one marker is selected from the markers of Tables 1-4, and

b) the normal level of expression of the marker in a control non-cervical

cancer sample.

5   A significant difference between the level of expression of the marker in the patient

sample and the normal level is an indication that the patient is afflicted with cervical

cancer.

The invention further relates to a method of assessing the efficacy of a therapy

10   for inhibiting cervical cancer in a patient. This method comprises comparing:

a) expression of a marker in a first sample obtained from the patient prior

to providing at least a portion of the therapy to the patient, wherein the

marker is selected from the group consisting of the markers listed within

Tables 1-4, and

15   b) expression of the marker in a second sample obtained from the patient

following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample, relative to

the first sample, is an indication that the therapy is efficacious for inhibiting cervical

cancer in the patient.

20   It will be appreciated that in this method the "therapy" may be any therapy for

treating cervical cancer including, but not limited to, chemotherapy, radiation therapy

and surgical removal of tissue, e.g., a cervical tumor. Thus, the methods of the

invention may be used to evaluate a patient before, during and after therapy, for

example, to evaluate the reduction in tumor burden.

25   The present invention therefore further comprises a method for monitoring the

progression of cervical cancer in a patient, the method comprising:

a) detecting in a patient sample at a first time point, the expression of a marker,

wherein the marker is selected from the group consisting of the markers listed in Tables

1-4;

30   b) repeating step a) at a subsequent time point in time; and

c) comparing the level of expression detected in steps a) and b), and therefrom

monitoring the progression of cervical cancer in the patient.

The invention also includes a method of selecting a composition for inhibiting cervical cancer in a patient. This method comprises the steps of:

a) obtaining a sample comprising cancer cells from the patient;

b) separately maintaining aliquots of the sample in the presence of a
5   plurality of test compositions;

c) comparing expression of a marker listed within Tables 1-4 in each of the aliquots; and

d) selecting one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition,
10   relative to other test compositions.

In addition, the invention includes a method of inhibiting cervical cancer in a patient. This method comprises the steps of:

a) obtaining a sample comprising cancer cells from the patient;

b) separately maintaining aliquots of the sample in the presence of a
15   plurality of test compositions;

c) comparing expression of a marker listed within Tables 1-4 in each of the aliquots; and

d) administering to the patient at least one of the test compositions which induces a lower level of expression of the marker in the aliquot
20   containing that test composition, relative to other test compositions.

The invention also includes a kit for assessing whether a patient is afflicted with cervical cancer. This kit comprises reagents for assessing expression of a marker listed within Tables 1-4.

In another aspect, the invention relates to a kit for assessing the suitability of
25   each of a plurality of compounds for inhibiting a cervical cancer in a patient. The kit comprises a reagent for assessing expression of a marker listed within Tables 1-4, and may also comprise a plurality of compounds.

In another aspect, the invention relates to a kit for assessing the presence of cervical cancer cells. This kit comprises an antibody, wherein the antibody binds
30   specifically with a protein corresponding to a marker listed within Tables 1-4. The kit may also comprise a plurality of antibodies, wherein the plurality binds specifically with a protein corresponding to a different marker listed within Tables 1-4.

- 7 -

The invention also includes a kit for assessing the presence of cervical cancer cells, wherein the kit comprises a nucleic acid probe. The probe binds specifically with a transcribed polynucleotide corresponding to a marker listed within Tables 1-4. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically

5   with a transcribed polynucleotide corresponding to a different marker listed within Tables 1-4.

The invention further relates to a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer. The method comprises isolating a protein or protein fragment corresponding to

10 a marker listed within Tables 1-4, immunizing a mammal using the isolated protein or protein fragment, isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for production of an antibody which specifically binds with the protein or protein fragment to isolate the hybridoma. The invention also includes an antibody

15 produced by this method.

The invention further includes a method of assessing the cervical carcinogenic potential of a test compound. This method comprises the steps of:

> a) maintaining separate aliquots of cervical cells in the presence and absence of the test compound; and

20   b) comparing expression of a marker in each of the aliquots.

The marker is selected from those listed within Tables 1-4. A significantly enhanced level of expression of the marker in the aliquot maintained in the presence of (or exposed to) the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses cervical

25 carcinogenic potential.

Additionally, the invention includes a kit for assessing the cervical carcinogenic potential of a test compound. The kit comprises cervical cells and a reagent for assessing expression of a marker in each of the aliquots. The marker is selected from those listed within Tables 1-4.

- 8 -

The invention further relates to a method of treating a patient afflicted with cervical cancer. This method comprises providing to cells of the patient an antisense oligonucleotide complementary to a polynucleotide corresponding to a marker listed within Tables 1-4.

5   The invention includes a method of inhibiting cervical cancer in a patient at risk for developing cervical cancer. This method comprises inhibiting expression or overexpression of a gene corresponding to a marker listed within Tables 1-4.

It will be appreciated that the methods and kits of the present invention may also include known cancer markers including known cervical cancer markers. It will further

10   be appreciated that the methods and kits may be used to identify cancers other than cervical cancer.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to newly discovered genes associated with the cancerous

15   state of cervical cells. It has been discovered that the level of expression of these individual genes, also referred to as markers, and combinations of these genes correlates with the presence of cervical cancer or a pre-malignant condition in a patient. Methods are provided for detecting the presence of cervical cancer in a sample, the absence of cervical cancer in a sample, the stage of cervical cancer, and with other characteristics of

20   cervical cancer that are relevant to prevention, diagnosis, characterization and therapy of cervical cancer in a patient. As used herein, "cervical cancer" includes pre-malignant conditions including CIN and SIL.

Definitions

25   As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

30   A "marker" is a naturally-occurring polymer corresponding to at least one of the novel nucleic acids listed within Tables 1-4. For example, markers include, without limitation, sense and anti-sense strands of genomic DNA (*i.e.* including any introns

occurring therein), RNA generated by transcription of genomic DNA (*i.e.* prior to splicing), RNA generated by splicing of RNA transcribed from genomic DNA, and proteins generated by translation of spliced RNA (*i.e.* including proteins both before and after cleavage of normally cleaved regions such as transmembrane signal sequences).

As used herein, "marker" may also include a cDNA made by reverse transcription of an RNA generated by transcription of genomic DNA (including spliced RNA).

As used herein a "polynucleotide corresponds to" another (a first) polynucleotide if it is related to the first polynucleotide by any of the following relationships: The second polynucleotide comprises the first polynucleotide and the second polynucleotide encodes a gene product; 2) The second polynucleotide is 5' or 3' to the first polynucleotide in cDNA, RNA, genomic DNA, or fragment of any of these polynucleotides. For example, a second polynucleotide may be a fragment of a gene that includes the first and second polynucleotides. The first and second polynucleotides are related in that they are components of the gene coding for a gene product, such as a protein or antibody. However, it is not necessary that the second polynucleotide comprises or overlaps with the first polynucleotide to be encompassed within the definition of "corresponding to" as used herein. For example, the first polynucleotide may be a fragment of a 3' untranslated region of the second polynucleotide. The first and second polynucleotide may be fragments of a gene coding for a gene product. The second polynucleotide may be an exon of the gene while the first polynucleotide may be an intron of the gene; 3) The second polynucleotide is the complement of the first polynucleotide.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example a marker of the invention. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic monomers.

A "cervical-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through cervical cells or into which cells or proteins shed from cervical cells are capable of passing. Exemplary cervical-associated body fluids

include blood fluids, lymph, ascites, gynecological fluids, cystic fluid, urine, and fluids collected by peritoneal rinsing.

The "normal" level of expression of a marker is the level of expression of the marker in cervical cells of a patient, *e.g.* a human, not afflicted with cervical cancer.

5 "Over-expression" and "under-expression" of a marker refer to expression of the marker of a patient at a greater or lesser level, respectively, than normal level of expression of the marker (*e.g.* at least two-fold greater or lesser level).

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the

10 promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue-specific manner.

15 A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably linked

20 with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene

25 product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

A "transcribed polynucleotide" is a polynucleotide (*e.g.* an RNA, a cDNA, or an analog of one of an RNA or cDNA) which is complementary to or homologous with all or a portion of a mature RNA made by transcription of a genomic DNA corresponding

30 to a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the transcript.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic

5   acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are

10   arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the

15   nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic

20   acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are

25   occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide

30   residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

- 12 -

A marker is "fixed" to a substrate if it is covalently or non-covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.* standard saline citrate, pH 7.4) without a substantial fraction of the marker dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.* encodes a natural protein).

Expression of a marker in a patient is "significantly" higher than the normal level of expression of a marker if the level of expression of the marker is greater than the normal level by an amount greater than the standard error of the assay employed to assess expression, and preferably at least twice, and more preferably three, four, five or ten times that amount. Alternately, expression of the marker in the patient can be considered "significantly" higher or lower than the normal level of expression if the level of expression is at least about two, and preferably at least about three, four, or five times, higher or lower, respectively, than the normal level of expression of the marker.

Cervical cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, cervical cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (*e.g.* a package or container) comprising at least one reagent, *e.g.* a probe, for specifically detecting a marker of the invention, the manufacture being promoted, distributed, or sold as a unit for performing the methods of the present invention.

Description

The present invention is based, in part, on identification of novel markers which are expressed at a higher level in cervical cancer cells than they are in normal (*i.e.* non-cancerous) cervical cells. The markers of the invention correspond to nucleic acid and polypeptide molecules which can be detected in one or both of normal and cancerous cervical cells. The presence, absence, or level of expression of one or more of these markers in cervical cells is herein correlated with the cancerous state of the tissue. The invention thus includes compositions, kits, and methods for assessing the cancerous state

- 13 -

of cervical cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells).

The compositions, kits, and methods of the invention have the following uses, among others:

5   1)   assessing whether a patient is afflicted with cervical cancer, including assessing whether the patient has a pre-malignant condition, *e.g.,* CIN and/or SIL;

        2)   assessing the stage of cervical cancer in a human patient;

        3)   assessing the grade of cervical cancer in a patient;

        4)   assessing the benign or malignant nature of cervical cancer in a patient;

10   5)   assessing the histological type of neoplasm (*e.g.* squamous cell, small cell, etc.) associated with cervical cancer in a patient;

        6)   making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer;

        7)   assessing the presence of cervical cancer cells;

15   8)   assessing the efficacy of one or more test compounds for inhibiting cervical cancer in a patient;

        9)   assessing the efficacy of a therapy for inhibiting cervical cancer in a patient;

        10)   monitoring the progression of cervical cancer in a patient;

20   11)   selecting a composition or therapy for inhibiting cervical cancer in a patient;

        12)   treating a patient afflicted with cervical cancer;

        13)   inhibiting cervical cancer in a patient;

        14)   assessing the cervical carcinogenic potential of a test compound;

25   and

        15)   inhibiting cervical cancer in a patient at risk for developing cervical cancer.

The invention thus includes a method of assessing whether a patient is afflicted

30   with cervical cancer which includes assessing whether the patient has a pre-malignant condition. This method comprises comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control, *e.g.,* a non-

- 14 -

cervical cancer sample. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer. The marker is selected from the group consisting of the markers listed within Tables 1-4.

5   The polynucleotides set forth in Tables 1-4 represent previously unidentified nucleotide sequences. These nucleotide sequences were identified through subtracted library experiments described herein. Also provided by this invention are polynucleotides that correspond to the polynucleotides of Tables 1-4. In one embodiment, these polynucleotides are obtained by identification of a larger fragment or

10   full-length coding sequence of these polynucleotides. Gene delivery vehicles, host cells, compositions and databases (all describe herein) containing these polynucleotides are also provided by this invention.

The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but which produce the same phenotypic effect, such as

15   an allelic variant. These altered, but phenotypically equivalent polynucleotides are referred to as "equivalent nucleic acids." This invention also encompasses polynucleotides characterized by changes in non-coding regions that do not alter the polypeptide produced therefrom when compared to the polynucleotide herein. This invention further encompasses polynucleotides, which hybridize to the polynucleotides

20   of the subject invention under conditions of moderate or high stringency. Alternatively, the polynucleotides are at least 85%, or at least 90%, or more preferably, greater or equal to 95% identical as determined by a sequence alignment program when run under default parameters.

Any marker or combination of markers listed within Tables 1-4, as well as any

25   known markers in combination with the markers set forth within Tables 1-4, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in cervical cancer cells and the level of expression of the same marker in normal cervical cells is as great as possible. Although this difference can be as small as the

30   limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method,

- 15 -

and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater.

It will be appreciated that patient samples containing cervical cells may be used in the methods of the present invention. In these embodiments, the level of expression
5   of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker in a cervical cell sample, *e.g.,* cervical smear, obtained from a patient. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.* storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the
10   marker in the sample. Likewise cervical smears may also be subjected to post-collection preparative and storage techniques, *e.g.,* fixation.

It will also be appreciated that certain markers correspond to proteins or fragments thereof, which are secreted from cervical cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are
15   preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the protein or fragment thereof, corresponding to each of these markers can be detected in a cervical-associated body fluid sample. In addition, preferred *in vivo* techniques for detection of a protein or fragment thereof, corresponding to a marker of the invention include introducing into a subject a labeled antibody
20   directed against the protein or fragment of the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

Although not every marker corresponding to a secreted protein is indicated as such herein, it is a simple matter for the skilled artisan to determine whether any
25   particular marker corresponds to a secreted protein. In order to make this determination, the protein corresponding to a marker is expressed in a test cell (*e.g.* a cell of a cervical cell line), extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

- 16 -

The following is an example of a method which can be used to detect secretion of a protein corresponding to a marker of the invention. About 8×10^5 293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5%

5   (v/v) CO_2, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium

10 and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424-54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-^{35}S™ reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO_2 atmosphere described above and incubated at 37°C for a selected period.

15 Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris. The presence of the protein in the supernatant is an indication that the protein is secreted.

Examples of cervical-associated body fluids include blood fluids (*e.g.* whole blood, blood serum, blood having platelets removed therefrom, etc.), lymph, ascitic

20 fluids, gynecological fluids (*e.g.* cervix, fallopian, and uterine secretions, menses, vaginal douching fluids, fluids used to rinse cervical cell samples, etc.), cystic fluid, urine, and fluids collected by peritoneal rinsing (*e.g.* fluids applied and collected during laparoscopy or fluids instilled into and withdrawn from the peritoneal cavity of a human patient).

25 Many cervical-associated body fluids can have cervical cells therein, particularly when the cervical cells are cancerous, and, more particularly, when the cervical cancer is metastasizing. Cell-containing fluids which can contain cervical cancer cells include, but are not limited to, peritoneal ascites, fluids collected by peritoneal rinsing, fluids collected by uterine rinsing, uterine fluids such as uterine exudate and menses, pleural

30 fluid, and cervical exudates. Thus, the compositions, kits, and methods of the invention can be used to detect expression of markers corresponding to proteins or fragments thereof, having at least one portion which is displayed on the surface of cells which

- 17 -

express it. Although the proteins having at least one cell-surface portion are not set forth herein, it is a simple matter for the skilled artisan to determine whether the protein corresponding to any particular marker comprises a cell-surface protein. For example, immunological methods may be used to detect such proteins on whole cells, or well

5   known computer-based sequence analysis methods (*e.g.* the SIGNALP program; Nielsen *et al.*, 1997, *Protein Engineering* 10:1-6) may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker corresponding to a protein or fragment thereof, having at least one portion which is displayed on the surface of a cell

10   which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed molecule or protein. Non-limiting examples of such methods include immunological methods for

15   detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods. *In situ* hybridization (ISH) and immunohistochemistry (IHC) methods are preferred.

In another preferred embodiment, expression of a marker is assessed using an

20   antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin}), or an antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a protein or fragment thereof, corresponding

25   to the marker, such as the protein encoded by the open reading frame corresponding to the marker or such a protein which has undergone all or a portion of its normal post-translational modification.

In yet another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient

30   sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a polynucleotide comprising the marker, and fragments thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction

- 18 -

methods prior to hybridization with the reference polynucleotide. Expression of one or
more markers can likewise be detected using quantitative PCR to assess the level of
expression of the marker(s). Alternatively, any of the many known methods of detecting
mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker

5   of the invention may be used to detect occurrence of a marker in a patient.

In a related embodiment, a mixture of transcribed polynucleotides obtained from
the sample is contacted with a substrate having fixed thereto a polynucleotide
complementary to or homologous with at least a portion (*e.g.* at least 7, 10, 15, 20, 25,
30, 40, 50, 100, 500, or more nucleotide residues) of a marker of the invention. If

10   polynucleotides complementary to or homologous with are differentially detectable on
the substrate (*e.g.* detectable using different chromophores or fluorophores, or fixed to
different selected positions), then the levels of expression of a plurality of markers can
be assessed simultaneously using a single substrate (*e.g.* a "gene chip" microarray of
polynucleotides fixed at selected positions). When a method of assessing marker

15   expression is used which involves hybridization of one nucleic acid with another, it is
preferred that the hybridization be performed under stringent hybridization conditions.

Because the compositions, kits, and methods of the invention rely on detection of
a difference in expression levels of one or more markers of the invention, it is preferable
that the level of expression of the marker is significantly greater than the minimum

20   detection limit of the method used to assess expression in at least one of normal cervical
cells and cancerous cervical cells.

It is understood that by routine screening of additional patient samples using one
or more of the markers of the invention, it will be realized that certain of the markers are
over- (or under-)expressed in cancers of various types, including specific cervical

25   cancers, as well as other cancers such as ovarian cancer, breast cancer, etc. For
example, it will be confirmed that some of the markers of the invention are over-
expressed in most (*i.e.* 50% or more) or substantially all (*i.e.* 80% or more) of cervical
cancer. Furthermore, it will be confirmed that certain of the markers of the invention are
associated with cervical cancer of various stages (*i.e.* stage 0, I, II, III, and IV cervical

30   cancers, as well as subclassifications IA1, IA2, IB, IB1, IB2, IIA, IIB, IIIA, IIIB, IVA,
and IVB, using the FIGO Stage Grouping system for primary carcinoma of the cervix
(see Gynecologic Oncology, 1991, 41:199 and Cancer, 1992, 69:482)), of various

- 19 -

histologic subtypes (*e.g.* squamous cell carcinomas and squamous cell carcinoma variants such as verrucous carcinoma, lymphoepithelioma-like carcinoma, papillary squamous neoplasm and spindle cell squamous cell carcinoma (see Cervical Cancer and Preinvasive Neoplasia, 1996, pp. 90-91), serous, mucinous, endometroid, and clear cell

5   subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal {Müllerian} mixed tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated

10   carcinoma, using the WHO/FIGO system for classification of malignant cervical tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue}). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention

15   and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one

20   or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in patients.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in a patient, it is preferred that the marker or panel of markers

25   of the invention is selected such that a positive result is obtained in at least about 20%, and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with a cervical cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a positive predictive value (PPV) of greater than about

30   10% is obtained for the general population (more preferably coupled with an assay specificity greater than 99.5%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly enhanced level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. When a plurality of markers is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-cervical origin in a patient sample), it is preferable that the marker of the invention used therein be a marker which has a restricted tissue distribution, *e.g.*, normally not expressed in non-cervical tissue.

Only a small number of markers are known to be associated with cervical cancers (*e.g.* bcl-2, 15A8 antigen, cdc6, Mcm5, and EGFR). These markers are not, of course, included among the markers of the invention, although they may be used together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

Known oncogenes and tumor suppressor genes include, for example, *abl, abr, akt2, apc, bcl2α, bcl2β, bcl3, bcr, brca1, brca2, cbl, ccnd1, cdc42, cdk4, crk- II, csf1r/fms, dbl, dcc, dpc4/smad4, e-cad, e2f1/rbap, egfr/erbb-1, elk1, elk3, eph, erg, ets1, ets2, fer, fgr/src2, fli1/ergb2, fos, fps/fes, fra1, fra2, fyn, hck, hek, her2/erbb- 2/neu, her3/erbb-3, her4/erbb-4, hras1, hst2, hstf1, igfbp2, ink4a, ink4b, int2/fgf3, jun, junb, jund, kip2, kit, kras2a, kras2b, lck, lyn, mas, max, mcc, mdm2, met, mlh1, mmp10, mos, msh2, msh3, msh6, myb, myba, mybb, myc, mycl1, mycn, nf1, nf2, nme2, nras, p53,*

- 21 -

pdgfb, phb, pim1, pms1, pms2, ptc, pten, raf1, rap1a, rb1, rel, ret, ros1, ski, src1, tal1, tgfbr2, tgfb3, tgfbr3, thra1, thrb, tiam1, timp3, tjp1, tp53, trk, vav, vhl, vil2, waf1, wnt1, wnt2, wt1, and *yes1* (Hesketh, 1997, In: *The Oncogene and Tumour Suppressor Gene Facts Book,* 2nd Ed., Academic Press; Fishel *et al.,* 1994, *Science* 266:1403-1405).

5   Known growth factors include platelet-derived growth factor alpha, platelet-derived growth factor beta (simian sarcoma viral {v-sis} oncogene homolog), thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor), erythropoietin, B cell growth factor, macrophage stimulating factor 1 (hepatocyte growth factor-like protein), hepatocyte growth factor

10   (hepapoietin A), insulin-like growth factor 1 (somatomedia C), hepatoma-derived growth factor, amphiregulin (schwannoma-derived growth factor), bone morphogenetic proteins 1, 2, 3, 3 beta, and 4, bone morphogenetic protein 7 (osteogenic protein 1), bone morphogenetic protein 8 (osteogenic protein 2), connective tissue growth factor, connective tissue activation peptide 3, epidermal growth factor (EGF), teratocarcinoma-

15   derived growth factor 1, endothelin, endothelin 2, endothelin 3, stromal cell-derived factor 1, vascular endothelial growth factor (VEGF), VEGF-B, VEGF-C, placental growth factor (vascular endothelial growth factor-related protein), transforming growth factor alpha, transforming growth factor beta 1 and its precursors, transforming growth factor beta 2 and its precursors, fibroblast growth factor 1 (acidic), fibroblast growth

20   factor 2 (basic), fibroblast growth factor 5 and its precursors, fibroblast growth factor 6 and its precursors, fibroblast growth factor 7 (keratinocyte growth factor), fibroblast growth factor 8 (androgen-induced), fibroblast growth factor 9 (glia-activating factor), pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1), brain-derived neurotrophic factor, and recombinant glial growth factor 2.

25   Known proteases include interleukin-1 beta convertase and its precursors, Mch6 and its precursors, Mch2 isoform alpha, Mch4, Cpp32 isoform alpha, Lice2 gamma cysteine protease, Ich-1S, Ich-1L, Ich-2 and its precursors, TY protease, matrix metalloproteinase 1 (interstitial collagenase), matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase), matrix metalloproteinase 7 (matrilysin),

30   matrix metalloproteinase 8 (neutrophil collagenase), matrix metalloproteinase 12 (macrophage elastase), matrix metalloproteinase 13 (collagenase 3), metallopeptidase 1, cysteine-rich metalloprotease (disintegrin) and its precursors, subtilisin-like protease Pc8

- 22 -

and its precursors, chymotrypsin, snake venom-like protease, cathepsin 1, cathepsin D
(lysosomal aspartyl protease), stromelysin, aminopeptidase N, plasminogen, tissue
plasminogen activator, plasminogen activator inhibitor type II, and urokinase-type
plasminogen activator.

5   Known protein kinases include DAP kinase, serine/threonine protein kinases
NIK, PK428, Krs-2, SAK, and EMK, interferon-inducible double stranded RNA
dependent protein kinase, FAST kinase, AIM1, IPL1-like midbody-associated protein
kinase-1, NIMA-like protein kinase 1 (NLK1), the cyclin-dependent kinases (cdk1-10),
checkpoint kinase Chk1, Nek3 protein kinase, BMK1 beta kinase, Clk1, Clk2, Clk3,
10   extracellular signal-regulated kinases 1, 3, and 6, cdc28 protein kinase 1, cdc28 protein
kinase 2, pLK, Myt1, c-Jun N-terminal kinase 2, Cam kinase 1, the MAP kinases,
insulin-stimulated protein kinase 1, beta-adrenergic receptor kinase 2, ribosomal protein
S6 kinase, kinase suppressor of ras-1 (KSR1), putative serine/threonine protein kinase
Prk, PkB kinase, cAMP-dependent protein kinase, cGMP-dependent protein kinase, type
15   II cGMP-dependent protein kinase, protein kinases Dyrk2, Dyrk3, and Dyrk4, Rho-
associated coiled-coil containing protein kinase p160ROCK, protein tyrosine kinase t-
Ror1, Ste20-related kinases, cell adhesion kinase beta, protein kinase 3, stress-activated
protein kinase 4, protein kinase Zpk, serine kinase hPAK65, dual specificity mitogen-
activated protein kinases 1 and 2, casein kinase I gamma 2, p21-activated protein kinase
20   Pak1, lipid-activated protein kinase PRK2, focal adhesion kinase, dual-specificity
tyrosine-phosphorylation regulated kinase, myosin light chain kinase, serine kinases
SRPK2, TESK1, and VRK2, B lymphocyte serine/threonine protein kinase, stress-
activated protein kinases JNK1 and JNK2, phosphorylase kinase, protein tyrosine kinase
Tec, Jak2 kinase, protein kinase Ndr, MEK kinase 3, SHB adaptor protein (a Src
25   homology 2 protein), agammaglobulinaemia protein-tyrosine kinase (Atk), protein
kinase ATR, guanylate kinase 1, thrombopoeitin receptor and its precursors, DAG
kinase epsilon, and kinases encoded by oncogenes or viral oncogenes such as v-fgr
(Gardner-Rasheed), v-abl (Abelson murine leukemia viral oncogene homolog 1), v-arg
(Abelson murine leukemia viral oncogene homolog, Abelson-related gene), v-fes and v-
30   fps (feline sarcoma viral oncogene and Fujinami avian sarcoma viral oncogene
homologs), proto-oncogene c-cot, oncogene pim-1, and oncogene mas1.

- 23 -

It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing cervical cancer and their medical advisors. Patients recognized as having an enhanced risk of developing cervical cancer include, for example, patients having a familial history of

5   cervical cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients determined through any other established medical criteria to be at risk for cancer or other malignancy.

The level of expression of a marker in normal (*i.e.* non-cancerous) human cervical tissue can be assessed in a variety of ways. In one embodiment, this normal

10   level of expression is assessed by assessing the level of expression of the marker in a portion of cervical cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the cervical cells which is suspected of being cancerous. For example, the normal level of expression of a marker may be assessed using a non-affected portion of the cervix and this normal level

15   of expression may be compared with the level of expression of the same marker in an affected portion of the cervix. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be

20   determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cervical cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the

25   presence of cervical cancer cells in a sample (*e.g.* an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a parafinized, archived human tissue sample, it can be

30   necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the

sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of cervical cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents,

5   each of which is capable of binding specifically with a nucleic acid or polypeptide corresponding to a marker of the invention. Suitable reagents for binding with a polypeptide corresponding to a marker of the invention include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like)

10   include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful

15   for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal cervical cells, a sample of cervical cancer cells, and the

20   like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer. In this method, a protein corresponding to a marker of the invention is isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and

25   translation of a nucleic acid encoding the protein *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the vertebrate exhibits a robust immune response to

30   the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened

- 25 -

using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the protein or protein fragment. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test

5   compound for inhibiting cervical cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of cervical cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of cervical cells, it is likewise recognized that changes in the levels of expression of other of the

10   markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit cervical cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous cervical cells).

15   This method thus comprises comparing expression of a marker in a first cervical cell sample and maintained in the presence of the test compound and expression of the marker in a second cervical cell sample and maintained in the absence of the test compound. A significant decrease in the level of expression of a marker listed within Tables 1-4 is an indication that the test compound inhibits cervical cancer. The cervical

20   cell samples may, for example, be aliquots of a single sample of normal cervical cells obtained from a patient, pooled samples of normal cervical cells obtained from a patient, cells of a normal cervical cell line, aliquots of a single sample of cervical cancer cells obtained from a patient, pooled samples of cervical cancer cells obtained from a patient, cells of a cervical cancer cell line, or the like. In one embodiment, the samples are

25   cervical cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various cervical cancers are tested in order to identify the compound which is likely to best inhibit the cervical cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting cervical cancer in a patient. In this method, the level of expression of one or

30   more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significant decrease in the level of

- 26 -

expression of a marker listed within Tables 1-4, or blocks induction of a marker listed within Tables 1-4, then the therapy is efficacious for inhibiting cervical cancer. As above, if samples from a selected patient are used in this method, then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be

5   efficacious for inhibiting cervical cancer in the patient.

As described herein, cervical cancer in patients is associated with an increase in the level of expression of one or more markers listed within Tables 1-4. While, as discussed above, some of these changes in expression level result from occurrence of the cervical cancer, others of these changes induce, maintain, and promote the cancerous

10 state of cervical cancer cells. Thus, cervical cancer characterized by an increase in the level of expression of one or more markers listed within Tables 1-4 can be controlled or suppressed by inhibiting expression of those markers.

Expression of a marker listed within Tables 1-4 can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be

15 provided to the cervical cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein corresponding to the

20 marker(s). Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of the marker(s). The compound so identified can be provided to the patient in order to inhibit expression of the marker(s) in the cervical cancer cells of the patient.

25   As described above, the cancerous state of human cervical cells is correlated with changes in the levels of expression of the markers of the invention. Thus, compounds which induce increased expression of one or more of the markers listed within Tables 1-4 can induce cervical cell carcinogenesis. The invention thus includes a method for assessing the human cervical cell carcinogenic potential of a test compound.

30 This method comprises maintaining separate aliquots of human cervical cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significant increase in the level of expression of a

- 27 -

marker listed within Tables 1-4 in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human cervical cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by

5   comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

10

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to novel isolated nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention or a portion of such a

15   polypeptide. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention, and fragments of such nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or

20   mutation of nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

25   An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the

30   nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA

- 28 -

of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

5   A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid encoding a protein corresponding to a marker listed in Tables 1-4, can be isolated using standard molecular biology techniques and the sequence information described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in

10   Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual, 2nd ed.,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A process for identifying a larger fragment or the full-length coding sequence of a marker of the present invention is thus also provided. Any conventional recombinant DNA techniques applicable for isolating polynucleotides may be employed. One such

15   method involves the 5'-RACE-PCR technique, in which the poly-A mRNA that contains the coding sequence of particular interest is first reverse transcribed with a 3'-primer comprising a sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer with a known sequence, which preferably contains a convenient cloning restriction site attached at the 5'end. The tagged cDNA is then

20   amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, *e.g.*, BRL Life Technologies Inc., Clotech) according to the

25   manufacturer's instructions.

Isolating the complete coding sequence of a gene can also be carried out in a hybridization assay using a suitable probe. The probe preferably comprises at least 10 nucleotides, and more preferably exhibits sequence homology to the polynucleotides of the markers of the present invention. Other high throughput screens for cDNAs, such as

30   those involving gene chip technology, can also be employed in obtaining the complete cDNA sequence.

In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a database called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone.

5   Software programs exist (TIGR assembler and TIGEM EST assembly machine and contig assembly program (see Huang, X ., 1996, *Genomes* 33:21-23)) that allow for assembling ESTs into contiguous sequences from any organism.

Alternatively, mRNA from a sample preparation is used to construct cDNA library in the ZAP Express vector following the procedure described in Velculescu *et*

10   *al.*, 1997, *Science* 270:484. The ZAP Express cDNA synthesis kit (Stratagene) is used accordingly to the manufacturer's protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert *et al.*, 1988, *Mol. Cell. Bio.* 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes except that the hybridization temperature is reduced to a room temperature. Washes are performed in

15   6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with ^{32}P-ATP trough use of T4 polynucleotide kinase.

A partial cDNA (3' fragment) can be isolated by 3' directed PCR reaction. This procedure is a modification of the protocol described in Polyak *et al.*, 1997, *Nature* 389:300. Briefly, the procedure uses SAGE tags in PCR reaction such that the resultant

20   PCR product contains the SAGE tag of interest as well as additional cDNA, the length of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source to express the cDNA corresponding to a given tag is first

25   converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)-3', contains a poly-T stretch at the 3' end for hybridization and

30   priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads.

- 30 -

Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

cDNA constructed utilizing this or similar modified oligo-dT primer is then processed as described in U.S. Patent No. 5,695,937 up until adapter ligation where only one adapter is ligated to the cDNA pool. After adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Gene trapper technology can also be used. The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithsburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the ^{32}P-labeled oligonucleotide, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

- 31 -

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore,

5   oligonucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence

10   complementary to the nucleotide sequence of a nucleic acid corresponding to a marker of the invention or to the nucleotide sequence of a nucleic acid encoding a protein which corresponds to a marker of the invention. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given

15   nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker of the invention or which encodes a polypeptide corresponding to a marker of the invention. Such nucleic acids can be used, for example, as a probe or primer. The

20   probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

25   Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, e.g., a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which mis-

30   express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, e.g., detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

- 32 -

The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a protein which corresponds to a marker of the invention, and thus encode the same protein.

5   In addition to the nucleotide sequences described in the Tables, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which

10 occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

15   As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 0.1-0.5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be

20 readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

In another embodiment, an isolated nucleic acid molecule of the invention is at

25 least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a nucleic acid corresponding to a marker of the invention or to a nucleic acid encoding a protein corresponding to a marker of the invention. As used herein, the term "hybridizes

30 under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 75% (80%, 85%, preferably 90%) identical to each other typically remain hybridized to each other. Such stringent

- 33 -

conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions for annealing two single-stranded DNA each of which is at least about 100 bases in length and/or for

5   annealing a single-stranded DNA and a single-stranded RNA each of which is at least about 100 bases in length, are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C. Further preferred hybridization conditions are taught in Lockhart, *et al.*, Nature Biotechnology, Volume 14, 1996 August:1675-1680; Breslauer, *et al.*, Proc. Natl. Acad.

10 Sci. USA, Volume 83, 1986 June: 3746-3750; Van Ness, *et al.*, Nucleic Acids Research, Volume 19, No. 19, 1991 September: 5143-5151; McGraw, *et al.*, BioTechniques, Volume 8, No. 6 1990: 674-678; and Milner, *et al.*, Nature Biotechnology, Volume 15, 1997 June: 537-541, all expressly incorporated by reference.

In addition to naturally-occurring allelic variants of a nucleic acid molecule of

15 the invention that can exist in the population, the skilled artisan will further appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-

20 essential" amino acid residue is a residue that can be altered from the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino

25 acid residues that are conserved among the homologs of various species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a polypeptide of the invention that contain changes in amino acid residues that

30 are not essential for activity. Such polypeptides differ in amino acid sequence from the naturally-occurring proteins which correspond to the markers of the invention, yet retain biological activity. In one embodiment, such a protein has an amino acid sequence that

is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of one of the proteins which correspond to the markers of the invention.

5   An isolated nucleic acid molecule encoding a variant protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of nucleic acids of the invention, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are

10   made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic

15   acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced

20   randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*,

25   molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule corresponding to a marker of the invention or complementary to an mRNA sequence corresponding to a marker of the invention. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the

30   invention. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-

- 35 -

coding region of the coding strand of a nucleotide sequence encoding a polypeptide of the invention. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polypeptide corresponding to a selected marker of the

- 36 -

invention to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the

5   major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into a cervix-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense

10   molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector

15   constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α-units, the

20   strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA

25   molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity

30   for a nucleic acid molecule encoding a polypeptide corresponding to a marker of the invention can be designed based upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS

- 37 -

RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742). Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a

5   specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a polypeptide of the invention can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene

10   encoding the polypeptide (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

In various embodiments, the nucleic acid molecules of the invention can be

15   modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*,

20   DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup

25   *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting

30   replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup (1996), *supra*; or as

- 38 -

probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-
O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or
cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation

5   of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery
known in the art. For example, PNA-DNA chimeras can be generated which can
combine the advantageous properties of PNA and DNA. Such chimeras allow DNA
recognition enzymes, *e.g.*, RNASE H and DNA polymerases, to interact with the DNA
portion while the PNA portion would provide high binding affinity and specificity.

10   PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms
of base stacking, number of bonds between the nucleobases, and orientation (Hyrup,
1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in
Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For
example, a DNA chain can be synthesized on a solid support using standard

15   phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds
such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a
link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.*
17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a
chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996,

20   *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be
synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975,
Bioorganic Med. Chem. Lett. 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups
such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating

25   transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad.
Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:648-652;
PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT
Publication No. WO 89/10134). In addition, oligonucleotides can be modified with
hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques*

30   6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To
this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide,

hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the

5   molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions

10   are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

15   II. Isolated Proteins and Antibodies

One aspect of the invention pertains to novel isolated proteins which correspond to individual markers of the invention, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a polypeptide corresponding to a marker of the invention. In one embodiment,

20   the native polypeptide corresponding to a marker can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, polypeptides corresponding to a marker of the invention are produced by recombinant DNA techniques. Alternative to recombinant expression, a polypeptide corresponding to a marker of the invention can be synthesized

25   chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language

30   "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material

includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a polypeptide corresponding to a marker of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the protein corresponding to the marker (*e.g.*, the amino acid sequence listed in the GenBank and IMAGE Consortium database records described herein), which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

Preferred polypeptides are encoded by the nucleotide sequences in Tables 1-4. Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the protein of the corresponding naturally-occurring protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then

compared. When a position in the first sequence is occupied by the same amino acid

residue or nucleotide as the corresponding position in the second sequence, then the

molecules are identical at that position. The percent identity between the two sequences

is a function of the number of identical positions shared by the sequences (*i.e.*, %

5   identity = # of identical positions/total # of positions (*e.g.*, overlapping positions) x100).

In one embodiment the two sequences are the same length.

 The determination of percent identity between two sequences can be

accomplished using a mathematical algorithm. A preferred, non-limiting example of a

mathematical algorithm utilized for the comparison of two sequences is the algorithm of

10   Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in

Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an

algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, *et al.*

(1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with

the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences

15   homologous to a nucleic acid molecules of the invention. BLAST protein searches can

be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino

acid sequences homologous to a protein molecules of the invention. To obtain gapped

alignments for comparison purposes, Gapped BLAST can be utilized as described in

Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402. Alternatively, PSI-Blast can be

20   used to perform an iterated search which detects distant relationships between

molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the

default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be

used. See http://www.ncbi.nlm.nih.gov. Another preferred, non-limiting example of a

mathematical algorithm utilized for the comparison of sequences is the algorithm of

25   Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the

ALIGN program (version 2.0) which is part of the GCG sequence alignment software

package. When utilizing the ALIGN program for comparing amino acid sequences, a

PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be

used. Yet another useful algorithm for identifying regions of local sequence similarity

30   and alignment is the FASTA algorithm as described in Pearson and Lipman (1988)

Proc. Natl. Acad. Sci. USA 85:2444-2448. When using the FASTA algorithm for

- 42 -

comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent

5   identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins corresponding to a marker of the invention. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a polypeptide corresponding to a marker of the invention operably linked to a heterologous

10   polypeptide (*i.e.*, a polypeptide other than the polypeptide corresponding to the marker). Within the fusion protein, the term "operably linked" is intended to indicate that the polypeptide of the invention and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the polypeptide of the invention.

15   One useful fusion protein is a GST fusion protein in which a polypeptide corresponding to a marker of the invention is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal

20   sequence at its amino terminus. For example, the native signal sequence of a polypeptide corresponding to a marker of the invention can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY,

25   1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook *et al., supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

30   In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a polypeptide corresponding to a marker of the invention is fused to sequences derived from a member of the immunoglobulin protein family.

The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion

5   protein can be used to affect the bioavailability of a cognate ligand of a polypeptide of the invention. Inhibition of ligand/receptor interaction can be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a

10   polypeptide of the invention in a subject, to purify ligands and in screening assays to identify molecules which inhibit the interaction of receptors with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

15   Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, *e.g.*, Ausubel *et al., supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide).

20   A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of the secreted protein or other proteins of interest. Signal sequences are typically characterized by a

25   core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to the described polypeptides having a signal sequence, as well as to polypeptides from which the signal

30   sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a protein which is ordinarily not

- 44 -

secreted or is otherwise difficult to isolate. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods.

5   Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the polypeptides corresponding to individual markers of the invention. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants

10   can be generated by mutagenesis, e.g., discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which

15   includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

20   Variants of a protein of the invention which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene

25   library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the

30   polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, 1983,

- 45 -

Tetrahedron 39:3; Itakura *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the coding sequence of a polypeptide corresponding to a marker of the invention can be used to generate a variegated

5   population of polypeptides for screening and subsequent selection of variants. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include

10   sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

15   Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

20   transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify

25   variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

An isolated polypeptide corresponding to a marker of the invention, or a fragment thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. The full-length

30   polypeptide or protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues

- 46 -

of the amino acid sequence of one of the polypeptides of the invention, and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with a marker of the invention to which the protein corresponds. Preferred epitopes encompassed by the antigenic peptide are regions that are located on

5   the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or

10   vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent.

Accordingly, another aspect of the invention pertains to antibodies directed

15   against a polypeptide of the invention. The terms "antibody" and "antibody substance" as used interchangeably herein refer to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site which specifically binds an antigen, such as a polypeptide of the invention, e.g., an epitope of a polypeptide of the invention. A molecule which specifically binds

20   to a given polypeptide of the invention is a molecule which binds the polypeptide, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')$_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides

25   polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope.

Polyclonal antibodies can be prepared as described above by immunizing a

30   suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred

polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression

5   of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA)

10   using immobilized polypeptide. If desired, the antibody molecules can be harvested or isolated from the subject (e.g., from the blood or serum of the subject) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected or (e.g., partially purified) or purified by, e.g., affinity chromatography.

15   For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes,

20   thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein or polypeptide of the invention, and preferably at most 20%,

25   yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers

30   are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B

- 48 -

cell hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology*, Coligan *et*

5   *al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

     Alternative to preparing monoclonal antibody-secreting hybridomas, a

10   monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene

15   *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288;

20   PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

     Additionally, recombinant antibodies, such as chimeric and humanized

25   monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly et al.,

30   U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining

regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the

5   art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041- 1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J.*

10   *Immunol.* 139:3521- 3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446- 449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and

15   Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

Antibodies of the invention may be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having cervical cancer. Such antibodies can be produced, for example, using transgenic mice

20   which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The

25   human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion

30   of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*, U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent

- 50 -

5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be
5   generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

An antibody directed against a polypeptide corresponding to a marker of the
10   invention (*e.g.*, a monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or
15   body fluids (*e.g.* in an ovary-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive
20   materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an
25   example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

Further, an antibody (or fragment thereof) can be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin
30   or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy

- 51 -

anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil

5   decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics *(e.g.*, dactinomycin (formerly actinomycin), bleomycin,

10   mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide

15   possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"),

20   interleukin-6 ("IL-6"), granulocyte macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al.

25   (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future

30   Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp.

- 52 -

303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

5   Accordingly, in one aspect, the invention provides substantially purified antibodies or fragments thereof, and non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a

10   fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is

15   encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. In various embodiments, the substantially purified antibodies of the invention, or fragments thereof, can be human, non-human, chimeric and/or

20   humanized antibodies.

In another aspect, the invention provides non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of: the amino acid sequence of the present invention, an amino acid sequence encoded by the cDNA of the present

25   invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence

30   which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing

in 0.2 X SSC, 0.1% SDS at 65°C. Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal

5   antibodies.

In still a further aspect, the invention provides monoclonal antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the

10   present invention, a fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to an amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an

15   amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

20   The substantially purified antibodies or fragments thereof may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a polypeptide of the invention. In a particularly preferred embodiment, the substantially purified antibodies or fragments thereof, the non-human antibodies or fragments thereof, and/or the monoclonal

25   antibodies or fragments thereof, of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of the present invention.

Any of the antibodies of the invention can be conjugated to a therapeutic moiety or to a detectable substance. Non-limiting examples of detectable substances that can be conjugated to the antibodies of the invention are an enzyme, a prosthetic group, a

30   fluorescent material, a luminescent material, a bioluminescent material, and a radioactive material.

- 54 -

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the invention is a pharmaceutical composition comprising an antibody of the invention and a pharmaceutically acceptable carrier. In preferred embodiments, the pharmaceutical composition contains an antibody of the invention, a therapeutic moiety, and a pharmaceutically acceptable carrier.

Still another aspect of the invention is a method of making an antibody that specifically recognizes a polypeptide of the present invention, the method comprising immunizing a mammal with a polypeptide. The polypeptide used as an immungen comprises an amino acid sequence selected from the group consisting of the amino acid sequence of the present invention, an amino acid sequence encoded by the cDNA of the nucleic acid molecules of the present invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. After immunization, a sample is collected from the mammal that contains an antibody that specifically recognizes the polypeptide. Preferably, the polypeptide is recombinantly produced using a non-human host cell. Optionally, the antibodies can be further purified from the sample using techniques well known to those of skill in the art. The method can further comprise producing a monoclonal antibody- producing cell from the cells of the mammal. Optionally, antibodies are collected from the antibody-producing cell.

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a polypeptide corresponding to a marker of the invention (or a portion of such a polypeptide). As used herein, the term "vector"

refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral

5   genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely

10   expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which

15   serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is

20   operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

25   sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, Methods in Enzymology: Gene Expression Technology vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and

30   those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the

- 56 -

host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

5   The recombinant expression vectors of the invention can be designed for expression of a polypeptide corresponding to a marker of the invention in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed

10   and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein

15   encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion

20   moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and

25   pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San

30   Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter

- 57 -

mediated by a co-expressed viral RNA polymerase (T7 gnl). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage harboring a T7 gnl gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.,* 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.,* 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.,* 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.,* Sf 9 cells) include the pAc series (Smith *et al.,* 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.,* 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al., supra.*

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.,* tissue-specific regulatory elements are used to express the nucleic acid). Tissue-

- 58 -

specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and

5 Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No.

10 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss, 1990, *Science* 249:374-379) and the α-fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a

15 DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense

20 orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic

25 acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant

30 expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny

- 59 -

of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

5   A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*, insect cells, yeast or mammalian cells).

        Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized

10   techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

        For stable transfection of mammalian cells, it is known that, depending upon the

15   expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418,

20   hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

        A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a polypeptide corresponding to a marker of the

25   invention. Accordingly, the invention further provides methods for producing a polypeptide corresponding to a marker of the invention using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the marker is produced.

30   In another embodiment, the method further comprises isolating the marker polypeptide from the medium or the host cell.

- 60 -

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a polypeptide corresponding to a marker of the invention have been introduced. Such host cells can

5 then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a polypeptide corresponding to a marker of the invention sequences have been altered. Such animals are useful for studying the function and/or activity of the polypeptide corresponding to

10 the marker and for identifying and/or evaluating modulators of polypeptide activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous

15 DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous

20 gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a nucleic acid encoding a polypeptide corresponding to a marker of the invention into the male

25 pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the polypeptide of the invention to

30 particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S.

- 61 -

Patent No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring

Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for

production of other transgenic animals. A transgenic founder animal can be identified

based upon the presence of the transgene in its genome and/or expression of mRNA

5   encoding the transgene in tissues or cells of the animals. A transgenic founder animal

can then be used to breed additional animals carrying the transgene. Moreover,

transgenic animals carrying the transgene can further be bred to other transgenic animals

carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which

10   contains at least a portion of a gene encoding a polypeptide corresponding to a marker of

the invention into which a deletion, addition or substitution has been introduced to

thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector

is designed such that, upon homologous recombination, the endogenous gene is

functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a

15   "knock out" vector). Alternatively, the vector can be designed such that, upon

homologous recombination, the endogenous gene is mutated or otherwise altered but

still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to

thereby alter the expression of the endogenous protein). In the homologous

recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by

20   additional nucleic acid of the gene to allow for homologous recombination to occur

between the exogenous gene carried by the vector and an endogenous gene in an

embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient

length for successful homologous recombination with the endogenous gene. Typically,

several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector

25   (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a description of homologous

recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*,

by electroporation) and cells in which the introduced gene has homologously

recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell*

69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a

30   mouse) to form aggregation chimeras (see, *e.g.*, Bradley, *Teratocarcinomas and*

Embryonic Stem Cells: A Practical Approach, Robertson, Ed., IRL, Oxford, 1987, pp.

113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant

- 62 -

female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination

5   vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One

10   example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, *e.g.*, Lakso *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the

15   transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

20   Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

IV. Pharmaceutical Compositions

25   The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") corresponding to a marker of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically

30   acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and

- 63 -

agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

5   The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such compositions can

10   further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention and one or more additional active compounds.

15   The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (e.g., stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the

20   interactions of the marker with one or more of its natural substrates (e.g., peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the

25   marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries

30   (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, e.g., Zuckermann et al., 1994, J. Med. Chem. 37:2678-85);

- 64 -

spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other

5   four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med.*

10   *Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.,* Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor,

15   1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al,* 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al,* 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

20   In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a marker can be accomplished, for

25   example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (*e.g.,* marker substrates) can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively,

30   assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

- 65 -

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the activity of a marker or a biologically active portion thereof. In all likelihood, the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of the marker to identify its natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.,* U.S. Patent No. 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al* ,1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker or downstream elements of a marker-mediated signaling pathway. Alternatively, such marker binding partners may also be found to be inhibitors of the marker.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.,* GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.,* LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

- 66 -

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.,* affect either positively or negatively) interactions between a marker and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies,

5   peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an cervical cancer marker identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be

10 supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker and its binding partner involves preparing a reaction mixture containing the marker and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus

15 forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between

20 the marker and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker and its binding partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance

25 interaction of the marker and its binding partner.

The assay for compounds that interfere with the interaction of the marker with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the

30 reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that

interfere with the interaction between the markers and the binding partners (*e.g.,* by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.,* by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test

5   compounds that disrupt preformed complexes, *e.g.,* compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker or its binding partner is

10   anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating

15   the solid surface with a solution of the marker or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For

20   example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to

25   complex formation (*e.g.,* physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

30   Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker or a marker binding partner can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated

- 68 -

marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.,* biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the protein-immobilized surfaces can be prepared in

5   advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (*e.g.,* by washing) and any complexes formed will remain immobilized on the solid surface. The detection

10   of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.,* using a labeled antibody specific for the

15   initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.,* a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may be used.

20   This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test compounds

25   modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and

30   immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and

- 69 -

densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993
Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate
complexed molecules from uncomplexed ones. For example, gel filtration
chromatography separates molecules based on size, and through the utilization of an

5   appropriate gel filtration resin in a column format, for example, the relatively larger
complex may be separated from the relatively smaller uncomplexed components.
Similarly, the relatively different charge properties of the complex as compared to the
uncomplexed molecules may be exploited to differentially separate the complex from
the remaining individual reactants, for example through the use of ion-exchange

10   chromatography resins. Such resins and chromatographic techniques are well known to
one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and
Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis
may also be employed to separate complexed molecules from unbound species (see,
e.g., Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons,

15   New York. 1999). In this technique, protein or nucleic acid complexes are separated
based on size or charge, for example. In order to maintain the binding interaction during
the electrophoretic process, nondenaturing gels in the absence of reducing agent are
typically preferred, but conditions appropriate to the particular interactants will be well
known to one skilled in the art. Immunoprecipitation is another common technique

20   utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel *et
al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York.
1999). In this technique, all proteins binding to an antibody specific to one of the
binding molecules are precipitated from solution by conjugating the antibody to a
polymer bead that may be readily collected by centrifugation. The bound assay

25   components are released from the beads (through a specific proteolysis event or other
technique well known in the art which will not disturb the protein-protein interaction in
the complex), and a second immunoprecipitation step is performed, this time utilizing
antibodies specific for the correspondingly different interacting assay component. In this
manner, only formed complexes should remain attached to the beads. Variations in

30   complex formation in both the presence and the absence of a test compound can be
compared, thus offering information about the ability of the compound to modulate
interactions between the marker and its binding partner.

- 70 -

Also within the scope of the present invention are methods for direct detection of interactions between the marker and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer may be utilized (see, *e.g.,*

5   Lakowicz *et al,* U.S. Patent No. 5,631,169; Stavrianopoulos *et al,* U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.,* marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.,* marker or test compound), which in turn is able to fluoresce due to the absorbed energy.

10   Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be

15   assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.,* using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in the preformed complex will

20   result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of

25   mRNA or protein, corresponding to a marker in the cell, is determined. The level of expression of mRNA or protein in the presence of the candidate compound is compared to the level of expression of mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA

30   or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA

or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA

5 or protein.

In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo, e.g.,* in a whole animal model for

10 cellular transformation and/or tumorigenesis.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.,* an marker modulating agent, an antisense

15 marker nucleic acid molecule, an marker-specific antibody, or an marker-binding partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the

20 above-described screening assays for treatments as described herein.

It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or

25 sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram,

30 about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of

- 72 -

subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the

5   agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently

10   increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree

15   of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions

20   used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic

25   acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous

30   solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic

water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as

5 bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants.

10 Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about

15 by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required,

20 followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium, and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a

25 powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and

30 used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

- 74 -

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically

- 75 -

acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form
5   as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound
10   and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and
·15 fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (e.g., into the cervical epithelium). A method for lipidation of antibodies is described by Cruikshank et al. (1997) J. Acquired Immune
20   Deficiency Syndromes and Human Retrovirology 14:193.

The nucleic acid molecules corresponding to a marker of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, e.g., Chen et al., 1994, Proc. Natl.
25   Acad. Sci. USA 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can include one or more cells
30   which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

- 76 -

V. Computer Readable Means and Arrays

Computer readable media comprising a marker(s) of the present invention is also provided. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to:

5   magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. The skilled artisan will readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium

10   having recorded thereon a marker of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the markers of the present invention.

15   A variety of data processor programs and formats can be used to store the marker information of the present invention on computer readable medium. For example, the nucleic acid sequence corresponding to the markers can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database

20   application, such as DB2, Sybase, Oracle, or the like. Any number of dataprocessor structuring formats (e.g., text file or database) may be adapted in order to obtain computer readable medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in computer readable form, one can

25   routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the invention in computer readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which

30   match a particular target sequence or target motif.

- 77 -

The invention also includes an array comprising a marker(s) of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development and differentiation, tumor progression, progression of other diseases, *in vitro* processes, such a cellular transformation and senescence, autonomic neural and neurological processes, such as, for example, pain and appetite, and cognitive functions, such as learning or memory.

The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

- 78 -

The array is also useful for ascertaining differential expression patterns of one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

5   VI. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic

10   assays for determining the level of expression of polypeptides or nucleic acids corresponding to one or more markers of the invention, in order to determine whether an individual is at risk of developing cervical cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

15   Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs or other compounds administered either to inhibit cervical cancer or to treat or prevent any other disorder {i.e. in order to understand any cervical carcinogenic effects that such treatment may have}) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the

20   following sections.

A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample involves

25   obtaining a biological sample (e.g. a cervical smear) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (e.g., mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample in vitro as well as in vivo. For example, in vitro

30   techniques for detection of mRNA include Northern hybridizations and in situ hybridizations. In vitro techniques for detection of a polypeptide corresponding to a marker of the invention include enzyme linked immunosorbent assays (ELISAs),

Western blots, immunoprecipitations, immunohistochemistry and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a polypeptide corresponding to a marker of the invention include introducing into a subject a labeled antibody directed against the

5   polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind,

10   thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction.

15   In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

20   There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and

25   immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs.

30   Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain

5   immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known

10   to one skilled in the art.

It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A

15   fluorophore label on the first, 'donor' molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen

20   that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay

25   should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA)

30   (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345 and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real

time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions

5   between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential

10 centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7).

15 Standard chromatographic techniques may also be utilized to separate complexed. molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the

20 relatively different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-

25 6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or

30 charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the

- 82 -

absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of mRNA corresponding to the marker can be determined both by *in situ* and by *in vitro* formats in a biological sample using

5   methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA. For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from cervical

10   cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

15   The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe

20   can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe

25   indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the

30   probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA corresponding to a marker of the present invention in a sample involves the process of nucleic acid amplification, e.g., by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the cervical cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a gene that is not a marker, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, e.g., a patient sample, to another sample, e.g., a non-cervical cancer sample, or between samples from different sources.

- 84 -

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the

5   sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

10   Preferably, the samples used in the baseline determination will be from cervical cancer or from non-cervical cancer cells of cervical tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker assayed is cervical specific (versus normal cells). In addition, as more data is accumulated, the

15   mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cervical cells provides a means for grading the severity of the cervical cancer state.

In another embodiment of the present invention, a polypeptide corresponding to a marker is detected. A preferred agent for detecting a polypeptide of the invention is an

20   antibody capable of binding to a polypeptide corresponding to a marker of the invention, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')$_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking)

25   a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

30   Proteins from cervical cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A*

- 85 -

Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis, immunohistochemistry (IHC) and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can readily adapt known protein/antibody detection methods for use in determining whether cervical cells express a marker of the present invention.

In one format, antibodies, or antibody fragments, can be used in methods such as Western blots, IHC or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody, proteins or cell containing proteins on a solid support. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from cervical cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample (*e.g.* a cervical smear). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing cervical cancer. For example, the kit can comprise a labeled compound or agent capable of detecting a polypeptide or an mRNA encoding a polypeptide corresponding to a marker of the invention in a biological sample and means for determining the amount of the polypeptide or mRNA in the sample (*e.g.*, an antibody which binds the polypeptide or an oligonucleotide probe which binds to DNA or mRNA encoding the polypeptide). Kits can also include instructions for interpreting the results obtained using the kit.

- 86 -

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide corresponding to a marker of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

B. Pharmacogenomics

Agents or modulators which have a stimulatory or inhibitory effect on expression of a marker of the invention can be administered to individuals to treat (prophylactically or therapeutically) cervical cancer in the patient. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens.

Accordingly, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

- 87 -

Pharmacogenomics deals with clinically significant variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, *e.g.*, Linder (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the

- 88 -

identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

5   This invention also provides a process for preparing a database comprising at least one of the markers set forth in Tables 1-4. For example, the polynucleotide sequences are stored in a digital storage medium such that a data processing system for standardized representation of the genes that identify a cervical cancer cell is compiled. The data processing system is useful to analyze gene expression between two cells by

10   first selecting a cell suspected of being of a neoplastic phenotype or genotype and then isolating polynucleotides from the cell. The isolated polynucleotides are sequenced. The sequences from the sample are compared with the sequence(s) present in the database using homology search techniques. Greater than 90%, more preferably greater than 95% and more preferably, greater than or equal to 97% sequence identity between

15   the test sequence and the polynucleotides of the present invention is a positive indication that the polynucleotide has been isolated from a cervical cancer cell as defined above.

          In an alternative embodiment, the polynucleotides of this invention are sequenced and the information regarding sequence and in some embodiments, relative expression, is stored in any functionally relevant program, e.g., in Compare Report using

20   the SAGE software (available though Dr. Ken Kinzler at John Hopkins University). The Compare Report provides a tabulation of the polynucleotide sequences and their abundance for the samples normalized to a defined number of polynucleotides per library (say 25,000). This is then imported into MS-ACCESS either directly or via copying the data into an Excel spreadsheet first and then from there into MS-ACCESS

25   for additional manipulations. Other programs such as SYBASE or Oracle that permit the comparison of polynucleotide numbers could be used as alternatives to MS-ACCESS. Enhancements to the software can be designed to incorporate these additional functions. These functions consist in standard Boolean, algebraic, and text search operations, applied in various combinations to reduce a large input set of

30   polynucleotides to a manageable subset of a polynucleotide of specifically defined interest.

- 89 -

One skilled in the art may create groups containing one or more project(s) by combining the counts of specific polynucleotides within a group (*e.g.*, GroupNormal = Normal1 + Normal2, GroupTumor1 + TumorCellLine). Additional characteristic values are also calculated for each tag in the group (*e.g.*, average count, minimum count,

5   maximum count). One skilled in the art may calculate individual tag count ratios between groups, for example the ratio of the average GroupNormal count to the average GroupTumor count for each polynucleotide. A statistical measure of the significance of observed differences in tag counts between groups may be calculated.

10   C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for cervical

15   cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one

20   or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi)

25   altering the administration of the agent to the subject accordingly. For example, increased administration of the agent can be desirable to increase expression of the marker(s) to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent can be desirable to decrease expression of the marker(s) to lower levels than detected, *i.e.*, to decrease the

30   effectiveness of the agent.

D. Surrogate Markers

The markers of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states, and in particular, cervical cancer. As used herein, a "surrogate marker" is an objective

5 biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (e.g., with the presence or absence of a tumor). The presence or quantity of such markers is independent of the disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of

10 particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (e.g., early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is reached (e.g., an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV

15 RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate markers in the art include: Koomen et al. (2000) J. Mass. Spectrom. 35: 258-264; and James (1994) AIDS Treatment News Archive 209.

The markers of the invention are also useful as pharmacodynamic markers. As

20 used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a

25 pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to

30 the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug in vivo. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection

of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected

5 due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct

10 observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda et al. US 6,033,862; Hattis et al. (1991) Env. Health Perspect. 90: 229-238; Schentag (1999) Am. J. Health-Syst. Pharm. 56 Suppl. 3: S21-S24; and Nicolau (1999) Am, J. Health-Syst. Pharm. 56 Suppl. 3: S16-S20.

The markers of the invention are also useful as pharmacogenomic markers. As

15 used herein, a "pharmacogenomic marker" is an objective biochemical marker which correlates with a specific clinical drug response or susceptibility in a subject (see, e.g., McLeod et al. (1999) Eur. J. Cancer 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker is related to the predicted response of the subject to a specific drug or class of drugs prior to administration of the drug. By assessing the

20 presence or quantity of one or more pharmacogenomic markers in a subject, a drug therapy which is most appropriate for the subject, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein for specific tumor markers in a subject, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be

25 present in the subject. Similarly, the presence or absence of a specific sequence mutation in marker DNA may correlate with drug response. The use of pharmacogenomic markers therefore permits the application of the most appropriate treatment for each subject without having to administer the therapy.

VII. Experimental Protocol

A. Subtracted Libraries

Subtracted libraries are generated using a PCR based method that allows the

5   isolation of clones expressed at higher levels in one population of mRNA (tester) compared to another population (driver). Both tester and driver mRNA populations are converted into cDNA by reverse transcription, and then PCR amplified using the SMART PCR kit from Clontech. Tester and driver cDNAs are then hybridized using the PCR-Select cDNA subtraction kit from Clontech. This technique results in both

10   subtraction and normalization, which is an equalization of copy number of low-abundance and high-abundance sequences. After generation of the subtractive libraries, a group of 96 or more clones from each library is tested to confirm differential expression by reverse Southern hybridization.

      SEQ ID NOS: 1-705 were identified through the above-described subtractive

15   library hybridization technique, wherein the "tester" source for the subtracted libraries was comprised of cDNA generated from four independent stage IB cervical tumors. The "driver" source for the subtracted libraries was comprised of cDNA generated from at least three independent samples of normal ectocervix that were manually dissected to isolate the epithelial component of the tissue. In some cases, the driver also included

20   cDNA generated from B-lymphocytes, T-lymphocytes, and other white blood cells, in activated and resting states.

      SEQ ID NOS: 706-1428 were also identified through the above-described subtractive library hybridization technique, wherein the "tester" source for the subtracted libraries was comprised of cDNA generated from four independent CINIII

25   cervical samples. The "driver" source for the subtracted library was comprised of cDNA generated from six independent normal ectocervix samples that were manually dissected to isolate the epithelial components. The "driver" source also includes cDNA generated from B-lymphocytes, T-lymphocytes, and other white blood cells, in activated and resting states.

30

B. Proteomics

Proteins that are secreted by normal and transformed cells in culture are analyzed to identify those proteins that are likely to be secreted by cancerous cells into body fluids. Supernatants are isolated and MWT-CO filters are used to simplify the mixture

5 of proteins. The proteins are then digested with trypsin. The tryptic peptides are loaded onto a microcapillary HPLC column where they are separated, and eluted directly into an ion trap mass spectrometer, through a custom-made electrospray ionization source. Throughout the gradient, sequence data is acquired through fragmentation of the four most intense ions (peptides) that elute off the column, while dynamically excluding

10 those that have already been fragmented. In this way, approximately 2000 scans worth of sequence data are obtained, corresponding to approximately 50 to 200 different proteins in the sample. These data are searched against databases using correlation analysis tools, such as MS-Tag, to identify the proteins in the supernatants.

15 ### VIII . Summary Of The Data Provided In The Tables

Table 1 shows 1428 novel nucleotide sequences identified through subtracted library experiments. These 1428 novel sequences were determined to be novel through various BLAST searches of available databases. The sequences of Table 1 were reinterpreted and those sequences are set forth in Tables 2 and 3. Table 4 sets forth

20 additional sequence (*e.g.,* full-length sequences) for the sequences of Tables 1-3.

The contents of all references, patents, published patent applications, and databases cited throughout this application are hereby incorporated by reference.

Other Embodiments

25 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

30 What is claimed is:

- 94 -

Claims

1.   An isolated nucleic acid molecule selected from the group consisting of:

        a)   a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleotide sequence of Tables 1-4, or a complement thereof;

        b)   a nucleic acid molecule comprising a fragment of a nucleic acid comprising the nucleotide sequence of Tables 1-4, or a complement thereof; and

        c)   a nucleic acid molecule comprising the nucleotide sequence of Tables 1-4, or a complement thereof.

2.   A vector which contains the nucleic acid molecule of claim 1.

3.   A host cell which contains the nucleic acid molecule of claim 1.

4.   An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleic acid comprising a nucleotide sequence of Tables 1-4.

5.   An antibody which selectively binds to a polypeptide of claim 4.

6.   A method for producing a polypeptide comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

7.   A method for detecting the presence of a polypeptide of claim 4 in a sample comprising:

        a)   contacting the sample with a compound which selectively binds to the polypeptide; and

        b)   determining whether the compound binds to the polypeptide in the sample to thereby detect the presence of a polypeptide of claim 4 in the sample.

- 95 -

8.   A kit comprising a compound which selectively binds to the polypeptide of claim 4.

9.   A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample comprising:

a)   contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and

b)   determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample to thereby detect the presence of a nucleic acid molecule of claim 1 in the sample.

10.   The method of claim 9, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

11.   The method of claim 9, wherein the sample is isolated from cervical tissue.

12.   The method of claim 9, wherein the sample is a tumor sample.

13.   A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1.

14.   A method of assessing whether a patient is afflicted with cervical cancer or has a pre-malignant condition, the method comprising comparing:

a) the level of expression of a marker in a patient sample, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4, and

b) the normal level of expression of the marker in a control non-cervical cancer sample,

wherein a significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer or has a pre-malignant condition.

15.   The method of claim 14, wherein the patient has CIN.

16.   The method of claim 14, wherein the patient has SIL.

5   17.   The method of claim 14, wherein the marker corresponds to a secreted
protein.

18.   The method of claim 14, wherein the marker corresponds to a transcribed
polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

10

19.   The method of claim 14, wherein the sample comprises cells obtained
from the patient.

20.   The method of claim 19, wherein the sample is a cervical smear.

15

21.   The method of claim 19, wherein the cells are in a fluid selected from the
group consisting of a fluid collected by peritoneal rinsing, a fluid collected by uterine
rinsing, a uterine fluid, a uterine exudate, a pleural fluid, a cystic fluid, and an cervical
exudate.

20

22.   The method of claim 14, wherein the level of expression of the marker in
the sample is assessed by detecting the presence in the sample of a protein
corresponding to the marker.

25   23.   The method of claim 17, wherein the presence of the protein is detected
using a reagent which specifically binds with the protein.

24.   The method of claim 23, wherein the reagent is selected from the group
consisting of an antibody, an antibody derivative, and an antibody fragment.

30

25.   The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide or portion thereof, wherein the transcribed polynucleotide comprises the marker.

5

26.   The method of claim 25, wherein the transcribed polynucleotide is an mRNA.

27.   The method of claim 25, wherein the transcribed polynucleotide is a

10   cDNA.

28.   The method of claim 25, wherein the step of detecting further comprises amplifying the transcribed polynucleotide.

15   29.   The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide which anneals with the marker or anneals with a portion of a polynucleotide wherein the polynucleotide comprises the marker, under stringent hybridization conditions.

20

30.   The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with cervical cancer by a factor of at least about 2.

25   31.   The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with cervical cancer by a factor of at least about 5.

- 98 -

32. The method of claim 14, comprising comparing:

a) the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-4, and

b) the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer,

wherein the level of expression of more than one of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with cervical cancer or a premalignant condition.

33. The method of claim 32, wherein the level of expression of each of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with cervical cancer.

34. The method of claim 32, wherein the plurality comprises at least three of the markers.

35. The method of claim 32, wherein the plurality comprises at least five of the markers.

36. A method for monitoring the progression of cervical cancer or a premalignant condition in a patient, the method comprising:

a) detecting in a patient sample at a first point in time, the expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4;

b) repeating step a) at a subsequent point in time; and

c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer or a pre-malignant condition in the patient.

37.   The method of claim 36, wherein the marker corresponds to a secreted protein.

38.   The method of claim 36, wherein marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

39.   The method of claim 36, wherein the sample comprises cells obtained from the patient.

40.   The method of claim 39, wherein the patient sample is a cervical smear.

41.   The method of claim 39, wherein between the first point in time and the subsequent point in time, the patient has undergone surgery to remove a tumor.

42.   A method of assessing the efficacy of a test compound for inhibiting cervical cancer in a patient, the method comprising comparing:

a) expression of a marker in a first sample obtained from the patient and exposed to the test compound, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4, and

b) expression of the marker in a second sample obtained from the patient, wherein the sample is not exposed to the test compound,

wherein a significantly lower level of expression of the marker in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting cervical cancer in the patient.

43.   The method of claim 42, wherein the first and second samples are portions of a single sample obtained from the patient.

44.   The method of claim 42, wherein the first and second samples are portions of pooled samples obtained from the patient.

45.   A method of assessing the efficacy of a therapy for inhibiting cervical cancer in a patient, the method comprising comparing:

        a) expression of a marker in the first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, wherein the marker is
5   selected from the group consisting of the markers listed in Tables 1-4, and

        b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy,

        wherein a significantly lower level of expression of the marker in the second sample, relative to the first sample, is an indication that the therapy is efficacious
10   for inhibiting cervical cancer in the patient.

46.   A method of selecting a composition for inhibiting cervical cancer in a patient, the method comprising:

        a) obtaining a sample comprising cancer cells from the patient;
15   b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;

        c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4; and

        d) selecting one of the test compositions which induces a lower level of
20   expression of the marker in the aliquot containing that test composition, relative to other test compositions.

47.   A method of inhibiting cervical cancer in a patient, the method comprising:

25   a) obtaining a sample comprising cancer cells from the patient;

        b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;

        c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4; and

30   d) administering to the patient at least one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

48.   A kit for assessing whether a patient is afflicted with cervical cancer or a pre-malignant condition, the kit comprising reagents for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-4.

5   49.   A kit for assessing the presence of cervical cancer cells or pre-malignant cervical cells or lesions, the kit comprising a nucleic acid probe wherein the probe specifically binds with a transcribed polynucleotide corresponding to a marker selected from the group consisting of the markers listed in Tables 1-4.

10   50.   A kit for assessing the suitability of each of a plurality of compounds for inhibiting cervical cancer in a patient, the kit comprising:

        a) the plurality of compounds; and

        b) a reagent for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-4.

15

        51.   A method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer or a pre-malignant condition, the method comprising:

        isolating a protein or protein fragment corresponding to a marker selected

20   from the group consisting of the markers listed in Tables 1-4;

        immunizing a mammal using the isolated protein or protein fragment;

        isolating splenocytes from the immunized mammal;

        fusing the isolated splenocytes with an immortalized cell line to form hybridomas; and

25   screening individual hybridomas for production of an antibody which specifically binds with the protein or protein fragment to isolate the hybridoma.

        52.   An antibody produced by a hybridoma made by the method of claim 51.

- 102 -

53.   A kit for assessing the presence of human cervical cancer cells or pre-
malignant cervical cells or lesions, the kit comprising an antibody, wherein the antibody
specifically binds with a protein corresponding to a marker selected from the group
consisting of the markers listed in Tables 1-4.

5

54.   A method of assessing the cervical cell carcinogenic potential of a test
compound, the method comprising:
        a) maintaining separate aliquots of cervical cells in the presence and
absence of the test compound; and

10   b) comparing expression of a marker in each of the aliquots, wherein the
marker is selected from the group consisting of the markers listed in Tables 1-4,
        wherein a significantly enhanced level of expression of the marker in the
aliquot maintained in the presence of the test compound, relative to the aliquot
maintained in the absence of the test compound, is an indication that the test compound

15 possesses human cervical cell carcinogenic potential.

55.   A kit for assessing the cervical cell carcinogenic potential of a test
compound, the kit comprising cervical cells and a reagent for assessing expression of a
marker, wherein the marker is selected from the group consisting of the markers listed in

20 Tables 1-4.

56.   A method of treating a patient afflicted with cervical cancer, the method
comprising providing to the patient an antisense oligonucleotide complementary to a
polynucleotide corresponding to a marker selected from the markers listed in Tables 1-4.

25

57.   A method of inhibiting cervical cancer in a patient at risk for developing
cervical cancer, the method comprising inhibiting expression of a gene corresponding to
a marker selected from the markers listed in Tables 1-4.

Table 1

Sequence 1
GCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGGACATACTGAGAGAATTTGGAATTATAT
GTTATGGTAGAATAAAGATCGAGGTCCATTTTTCTATACATGAAAANTTAAATATTTAG
T
TTGGGATTTGAGACTTCGATCTAGGCCTCTGNATTTCTTTCTAGTTTTTTCCCTACCAT
T
CTTTAATCGGAGTATCCAAGCCCAATCACCCTGTANCCTATGTCCTAAAGCATCTTGAAT
TGNTTGNTTCANGTTTTTNCTTCATGNAGGAGTGTCTTTTGCNCACNCCTCTTAAGCC
TA
TCTGGATCCCCACTTCANNCCTCTGAAGGGTTCTGTTAAAANTTCTAACCCTATCTNT
AT
NGAATTTGTCCCC
Sequence 2
GCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGTC
CGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCCT
TTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATTT
GCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAG
CATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTGG
AATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 3
CGGAGAGGAGTCCTTACTTAGAGTNAAGCTGAAGGAGCATCACAACCCCAAAGACTGTTA
TGTTGTGAAATTTAGGCTGTGTTTTAATAATACTGATGATGATANGATGAAATAGTAAT
T
TATTGATTACTATATCTACTATATGTCCGTAAGATAGCAGGGTCTTTATACTCGGAATC
T
CATTTGATCCTCATAGTTTTTATTGGTGTATTATTATCCTCATTTTACAGATACAGAAAC
TGAGGCTTCAGAGAGGCTGTGTAATCAAGAGTTTGTATGCCTTTCATCTGAGGAGGTTGA
GGACAATCCCAAGTTAGAAAAATAAATGTCTTTAGCATTATTTTTCCTTAATGTTTAGAA
TATTAATAAGTTACTCAGATAATCTATTGGAATTTTCTTCATGGCAGGGGGAAGAGGCTA
GAGTTG
G
Sequence 4
TACTCAGTTTCCTTATCTATAACATGGGGATAATATTANGTATGCTACATCCGTTGTTA
T
GAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTNTACTAAATGGGNAAGG
TCTGGCNGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGGAAGGCTGAGGNGGGG
GCAGTTGGGGAGCGAGGGGTTGTACTACTNCAATGTAACTTGCTTTCTCAGAAATTNAGG
CNAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAACAGTCTCNTGCCTTT
AAGGAGCTTATAGTCTAGTTANGAAACCAGACTTAAACATATGAAAAGTTTAAACATTGG
Sequence 5
CTCTTTCATTGAAAGGAAATTANGGTTGAACCTCCAGGAGCCCGTCAGAGTCTGAGGAGA
GGCTGGCTTNATGTCTAGATACGACGACAGCAAGGCTGCTTAGAGCTAACAGCGCATTGC
CTTTCACTACCGGACTCTCCTTTGCAGCTGCCTTGGTGATCTCATCAGTCAGCATGTC
TC
TAACCCAGAGCCAGGCTGTGCTTTTTTTGTACCT
Sequence 6
CGCGGTGGCGGCCGCCCGGGCAGGTACCTATGACCATCTTACATTATTTTTATGGGTGGG
GGGCATTGGCTGTGGAATGTGGGCAGTAACTTGCACAGTCAGTAACCGTNNGAGTAACTG
GTTGTTGGCATCCCCATTCTGGCACTCCTCCTCTAGGTCTCCACCTCACACGCTGGTTTG
TGGGCGGAGGGGCAGGTTGGTGCCGTGGGGTGTCCGGGCACTGGCTGTGCATGCCTTCTT
CCTCTTCTGTCTCTTGGCCACCTTTTCCAAAAAGTCACCAGTGACCAATTCTCCCAGT

Table 1

GT
TTCTTTGGGACTCAATGCCTTGGGCTTGGCATTGGGTAAAGCCGACTGGCAAGTTTCATT
CTGACCAAGCTCTATAGTAGTCCGGNGTGGACCTCTTGCCCTCCCTGCTCTGCGGAAAGC
TTNCTCAGCCTTTGCTTCTTCACTTATTTACTATTTGCGGGGTCCTGGGGGTACCCTC
GG
NCGCTCTAGAACTAAGTGGGATCCCCCCCGGGCTGCAAGGAATTCGAATATCAAGCCTTA
TCGAATCCGTCNAACCTTCGAAGGGGG

Sequence 7
GGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCTCC
ATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATTGAC
TCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAGTTT
GGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAGGATC
ATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCCGGA
TT
CCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC

Sequence 8
AGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGTCCGCGAAAC
CAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCCTTTTGAGGT
CCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATTTGCAAAACC
ATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAGCATCCAGA
GAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTGGAATCTAAC
TCAGCGGAATTGTATCCGTACCTCGGCCGTTCTANACTAGGGGATCCCCCGGCC

Sequence 9
GGTGGCGGCCGAGGTACCACATGCACTGATAGCTCTCTTTGTATGAACAGGAGCTGTGGC
AGGCCCTATGCCAGGGAGAAAGTAAGATTGGAAAAGAGCTTACCAAGGAGGTGGCATTTG
CACTGTGCTTAAGGGGCAAGAAAAACGTCTTCCAATCAGGAGCCACAAATGCTTGGCTGA
AGTGCTACTGCTCTTTCATCCTGGAGCTGGAACAGACGTCACCAGTCAATCATGATGGCT
GCTGGGTGCACTGGCTAACATCTATAATCCCAGCACTTTGTGAGGCTGAGGGTGGGAAGA
TTGCTTGGGGCCAGGAGTTTGAGACCAGTTTTGGGCAAATTGCAAGACCCTGTCTCTGCA
AAAAAATATAAATGTAGCTGAGTGTGGTGGCACCTGTAGACCCAGCCCCAGCTACTCGA
GAGGCTGAGATGGGAGGATCGCTTGGGCCTAGGAGTTCGAGGCTGCAGTGAGCTATGATT
GCACCACTGCACTCCAGCCTNGGTGACAGAACANGACCTGTCTNTAAAAANCATTAAATT
AAATCAAAAAAAAAAAAAAAAAAAAAG

Sequence 10
GGTGGCGGCCGAACATCCTGTTTTAACTAGCACAGACAAAACCTATGTGTTACTATCAAA
ATAAAATTTAGAAAAACAATTTTCTTATAAAATTTTCTGTTTGTATTTGGACTACATAAA
CTGGCTTTAAAATTGAGAAATATGCCCTAAAACCATAAGGAAAAAGCCAACAGAAAGAAC
AAAAAGATCACAGCAATTAGGCCCGTTCTATTCAATTTTGCCATGAGCTAAAAATCACAT
TCTTCACAAAGTAAATTACCGCCCTGTTTTTTATTCTTAAGCACTAGGGTTAGGATTGT
G
ATCTGAGCTTTACTAAATCGGAAAAGAAAATCTCAATTATAGAACATTTAGTTTATTTAT
ACCTTAATGCCCGGAGAGGTAATATTTTACTTTAAAATGCATAACCCATGTGGACATGCT
AGGTCTTCCAAAA

Sequence 11
GGTGGGGCCGGGCCCGGACCCGGNCCAAGACCTACCCGCCGGNGNANTTGGCCTNGGGCC
CTGGGGTTTCCTCCCNAGGGGAAGCCTTGTAGAATCCACCTNGGAAANCCTTGTNGGGTN
CCGCTTGCCCCGTNGNATGGNTGGNTAGGGGAAGGGCAAAGTACGCCTTCAAGAATAGG
NAAAAAAGGGANGGGGGGGGGGNACCACTCAAGGCCTGGCAAAGGCCAAGTGGGACCAAG
TGGCCCAAGGGGGCTTCTTGGAATGGTGGNTCTCTCACAAGCTTTGTAANAAAGGTGGTG
GAAGAACCAAGCCTTGNCCCTTTTTGTGGGTCGNGNGACCTTGGAATAAAGGGCCAAAAGG

Table 1

AAGTTTTGGTTTCCCTTGGCCCCCNTTTTTCCCTTNTTTGNTTGGAACCTTTTGGGAAA
A
GAAAACCCCCCTTGGGACCTTTTTTTGGTTTTTTTCCTTTGGCNAAAAAAGGGGGCCACCCC
TTGGCCAAATTGGATGGTTCCTTGNATTGGTTTTTCCGGTCGCTTTANGGGGCCAATT
NA
NAANTTGGTTTGTAAAGGGGAAAG
Sequence 12
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTGTTTTGTATTTTTAGTAG
AGATGGGGTTTCACCGTGTTGGCCGGGCTGGTCTTGAACTCTTGATTTCAAGTGATCCGT
CCACCTCAGCCTCCCAATGTGCTGGGATTACAGGTGTGAGCCACCATGCCTGGCCTTTTT
CTTTTTTTTTTTTTAAACGAAAAAATGTTTTTAATTGACAAATAAAAATGATGTATATTTA
TGGTGTTTTTTCTCTTTTGCATCATCAGTCTCTTTCTCATCACTGAAACCTACAAATATT
TTAAAATCTTTCCATTAAAAAAATTTTGCTGATCATTCAACCTCTTCAAATTATTAAGAG
ATACTTACTTTGTATGAAAAATTTTGTCGAGATGTATAATCCATTTTTTTTCTGGGAAG
Sequence 13
TTACTTAGGGCGAATTGCGNCCGAGGTACCAGGTGTCATTCCTGCAGCAGGATTTAACAC
GATGCAGATCTGGCCCCAGTGTGAGCATCTGTGTTAATGGTATCAGACTTAAAGAAGGAA
AGACCTGATTTGACTGCTGTTGGTTTGGTAGTGTTCCCTGATCCGGAGCCAGTTTTGTGG
GAGGGAGTCCCAAAGCAGGTTTGAGCTGTGGTAATGACCGAGTTGATCCTAGAAGACAAA
ACAGTAGAATCGTACCTGCCCG
Sequence 14
TGGCGGCCGAGGTACGGTATTCTCTTCAAACAAGAGCAAGCCCATGATGATGCCATTTGG
TCAGTTGCTTGGGGGACAAACAAGAAGGAAAACTCTGAGACAGTGGTCACAGGCTCCCTA
GATGACCTGGTGAAGGTCTGGAAATGGCGTGATGAGAGGCTGGACCTGCAGTGGAGTCTG
GAGGGACATCAGCTGGGAGTGGTGTCTGTGGGACATCAGCCACACCCTGCCCATTGCTGC
ATCCAGCTCTNTTGATGCTCATATTCGTCTTTGGGACTTGGAAAATGGCAAACAGATAAA
GTCCATAGATGCAGGACCTGTGGATGCCTGGACTTTGGCCTTTTCTCCTGATTCCCAGTN
TCTGGCCACAGGAACTCATGTCGGGAANGTGAACATTTTTTGGTGTGGAAAGNGGGAAAAA
GGAA
Sequence 15
GCCCCTGCCCGGCTGGTTATGTAACAAACAAAGTCTGTGTCTGTGTGGAGTGTTGCAGGA
CGAGTGGAAATGACTGTTTCCAAGTTCATGGCAATTCAGAAGGCCCTTCAGCCAGACTGG
TTCCAGTGCCTCTCCGATGGAGAAGTATCTTGTAAGGAAGCAACTTCCATAAAAAGGGTC
AGAAAGTCTGTTGACCGATCACTTCTTTTCTTGGATAACTGTCTGCGGCTGCAGGAAGAG
TCAGAGGTTCTTCAGAAGAGTGTGATCATTGGAGTGATTGAAGGTGGAGATGTGATGGAA
GAGAGGCTGAGGTCAGCACGAGAGACAGCCAAGCGGCCTGTGGGTGGCTTCTTCTGGATG
GTTTTTCAAGGAAATCCAACA
Sequence 16
CGGTGGCGGCCGCCCGGGCAGGACGCGGGAAGAGGTAATTTTAATGCCATTTTCATGGGA
CACTTGGGAGCTAGATTAGAAGAAGCCAAGACTAGAATCGGGGAGATGAGTTGCAGAGGG
NNGTGGTGAAGGTCTGAAGGAAGGTAGGAAAAGGTCGGACACATTCCAGACATATTTAGG
GGTGGAGGTGGTTGGATATGGGGAGTT
Sequence 17
TTCGCGGTGGCCCGGCCGCCCGGGCAGGTGACTTTAGTCCTCACTCTGTGGGCAGGGGCA
TTACAGCATAGGGGTCCCTTTTTGTCAGGGATTTATGATGGCATCACACGCAGGATTCAGA
GAGCATNAATTGAAAAATACATATGATTGGCTGGGCGTGGAGGCTTATGCCTGTAATCCC
AGCACTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGTCTG
ACCAACATGGAGAAACCCTTTCTCTACTAAAAATACAAAATTAGCCGGGCGTGGTGGCAC
ATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATTGCTTGAACC

Table 1

Sequence 18
TNCCGCGGTGGCGGCCGAGGTACGATTCTACTGTTTTGTCTTCTAGGATCAACTCGGTCA
TTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACTGGCTCCGGATCAGGGA
ACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATT
A
ACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACA
CCTGGTACCTGCCCG

Sequence 19
CCGCGGTGGCGGCCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTT
T
TTTTTTTTTTTTTTNCCCCCGGGAGAGGAATTGGGAAGAGCAAATTGCTGCTGAAAATT
TC
TACATTGATCCAGACAAACAAGTTAGAGCAGGCTGAAAAAGAACCCTTGGTGTTTTTCTG
TGTTCAACCAGATCAACTGGAAAAGTATAGATACCTTAATTAGCACTGTGCTCTGNGGGA
TTCTGGTCAGCCTGGCCCAGTGGTTTTTTTTCCCCTGAACACNCCTGAAAGGGGAGCTCAT
AATGACTGCTGTGCAGGTGGGCGGGGAGGGGGCTTCCTATTTGATTTAGNGGCTGATCAA
TGCCAGTTACCAATTNTNGGTNGCCCCATTTATACATGGNGGAAAAAAAGTACCT

Sequence 20
GAGGTACCCAATTTTTTTTAAGTTCTAAGGTAGCTTTCTCAAAGAAAACCATTTCAGGGT
G
TCCATTAAAAGAGCATCTGCGAATTGTTTTTGCAGGGACTCCTAATCAGTCAGGAGAAGT
AGAATGTAAGCAAAGTCACAAACCTCCCGTAAGAATTTGGTTCACCAGGACACAGCTCCT
CTCTTATGAAGGGATGAGAAGCAGACCCCAAACCCAGTGCCACAGTCTCCCTGGAAACAG
CAGCAGGCTTGGGGAATGCTTCCAAAAGGCTATGCCATTCAAGGTCTCAGGTTTTTTGGT
TAAAAATACAACTTAGGCCAACTGCAAGTGGCTCATGCCTGTAATTAATTCCAAC

Sequence 21
GTGGCGGCCGAGGTACGATTCTACTGTTTTGTCTTCTAGGATCAACTCGGTCATTACCAC
AGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACTGGCTCCGGATCAGGGAACACTAC
CAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACACAGA
TGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACGCCTGGTA
CCTGCCCG

Sequence 22
CGCGGTGGCGGCCGAGGTACAGAGTAGAGAGAGTTCTGCAGGGATGAAGTGGGAGACGTT
GATAGGACCAGACCAGACCAGGCCTTGTAGGCCATGGAAGGACTTTGGATTTTACACCAA
GTGCAACAGGTAACTGCTGGAGGGAATTCAGCAAGAGAGTGACAGGAGCTGATTGACAAT
TTGAACGCCCACTCTGGCTGCCATGTGGCAAATAGATTGTAGGAAGAAAAGAAGAAAAGG
AAGAGAGCAGTTTGGAAGCTACTACTGTTGTCCCAGAAATATGTAATGGTGGCTTGG
C

Sequence 23
CGCGGTGGCGGCCGAGGTACANAGTAGAGAGAGTTCTGCAGGGATGAACGTGGGAGACGT
TGATATGGACCAGACCAGACCAGGCCTTGTAGGCCATGGAAGGACTTTGGATTTTACACC
AAGTGCAACAGGTAACTGCTGGAGGGAATTCAGCAAGAGAGTGACAGGAGCTGATTGACA
ATTTGAACGCCCACTCTGGCTGCCATGTGGCAAATAGATTGTAGGAAGAAAAGAAGAAAA
GGAAGAGAGCAGTTTGGAAGCTACTACTGTTGTCCCAGAAATATGTAATGGTGGCTTGGC
CCAGGTTGGGGT

Sequence 24
CCGCGGTGGCGGCCGAGGTACAAAAAAAGCACANGCCTGGCTCTGGGTTAGAGACATGCT
GACTGATGAGATCACCAAGGCAGCTGCAAAGGAGAGTCCGGTAGTGAAAGGCAATGCGCT
GTTAGCTCTAAGCAGCCTTGCTGTCGTCGTATCTAGACATGAAGCCAGCCTCTCCTCAGA
CTCTGACGGGCTCCTGGAGGTTCAACCTAATTTCCTTTCAATGAAAGAGTGGGTTTCCAT

Table 1

GGTACCTGCCCG
Sequence 25
CCGCGGNGGCGGCCGCCCGGGCAGGTACGCGGGAGGCACATTCTTTTCTACGTGAAGAGT
TTTGTAAACTGAACTTTGTTTTCAGTTCCGGCTCCAGCCATCCTGGGGTNGCTTGCCA
AT
AGATGAATCCCACTCGTTTGACCCATGACGCTCCTTCTTTTCATTTCTCCCTCTTTCCC
C
ACAGCAGTGCATGTCCACCATACCACCTGAGAGTCTGTGGAATCTAATTTTCTGTTATAC
TTCTTTCCTTACAC
Sequence 26
GCGGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCT
CCATCACACGCCCCAGAAAGGACAAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATT
GACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAG
TTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAGG
ATCATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCC
GG
ATTCCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 27
ACGCGGCGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCT
CTCCATCACACGCCCCANAAAGGACAGTAGCCAGCTTNTCTGGATGCTTTGCCAAGCAAT
TGACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCA
GTTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAG
GATCATAGTTTCTTGGAACTCTCTGTAAGNCNCAACTTGGTTATCGCCGGACATAATTGG
ACCCGGTATTTCCGGCTCAGNCATCTTCACCTTTCATCTAAGGNTTGCATNTTCCGGGCC
CGNTCTAAGAACTAGTGGGATCCCCCCGGGGCCTGCAGGGAATTCCGATAATCAAAGGCT
TAATCTGAATACCCGGTCGGACCCTTCGGAGGNGGGGGGGGCCCCGGNTACCCCAAGCTTT
TTTGGTTTCCCTT
Sequence 28
CGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTAGCTACATCGT
TGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTACTAAATTT
TAAGGNCTGGCAGGCGCGGTGGCTCACACCTGGNATCCCAGCACTGTGGAAGGCTGAGGT
GGGGGCAGTGGGGAGCGAGGGGNTGTTACTACTCCAATGTAACTGCTTTCTCAGAAATTA
AGGCAAAAAGTCTTACTGACCATGTNAAGGAAATCCAACAATTATAAACAGTCTCTGCCT
TTAAGGAGCTTATAGTCTAGTTAAGAAACCAGACTTAAACATATGAAAAGTTAAACATTG
GCCAGGCACAGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGGCCAAGGCAGGAGGAT
CACCTGAGGTCANGAGTTCGAGACCAGCCTGACCAGCNTGGAGAAACCCCATCTN
Sequence 29
GCGGTGGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTAGCT
ACATCGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTA
C
TAAATTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGGAAG
GCTGAGGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTTCTC
AGAAATTAAGGCAAAAAGTCTTACTGACCATGTAAAGGGAAATNCAACAATTATAAACAG
TCTCT
Sequence 30
GGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTACGTAGCTACAT
CGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTACTAA
A
TTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTATCCCAGCACTGTGGAAGGCTGA
GGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTTCTCAGAAA

Table 1

TTAAGGCAAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAACAGTCTCTG
CCTTTAAGGAGCTTATAGTCTAGTTAAGAAACCAGACTTAAACATATGAAAAGTTAAACA
TTGGCCAGGCACAGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGGCCAAGGCAGGAG
GATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGACCAGCATGGAGAAACCCCATCTTTA
CTAAAAATACAAAACTAGTTGGGCATGGTGGCGCATGCCTGTGATCCCAGCTACTTGAGA
GGCTGAGGCGGGAGAATCACTTGAACCCGGGAGGTCGAGCGGCCGCCCGG
Sequence 31
CCCGCGGTGGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTA
GCTACATCGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTT
C
TACTAAATTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGG
AAGGCTGAGGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTT
CTCAGAAATTAAGGCAAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAAC
AGTCTCTGCCTTTAAGGAGCTTTATAGTCTAGTTAAGAAA
Sequence 32
GCGGCCGAGGTACGTATGCACTTGCTTGCCATCTAAGCAGGGACAATGGCAGTTCATATC
ATGATGTTACTTTGATTCTCTGACCAAACTGGCCTGTGAGCACCCTGGGCCTTTCTTC
CT
CTGTCAAAGGCCTTAAGACAGGTTTACCCTGTAGCCAGGTCTGGAAGACAGAGCTGGGTT
AAAGCTGGGTGGGAGAAGTGAAAAAGGTCAGGTTTACATTCCTACGCGGAAAAGGATGTA
ACACGGGGCCACATCCTATGCCCAATCCCAAGGCAGGGAGGCAGGGAAGTGGCTGCCAAA
CCTGTTGTAGGAGAGTAATAAATGACTTGAGAGTAAGCCTAAGCAAACTCAAGTGGGAAG
GGGAGTGGGCTGTAAAATAGTTTAAGAGACTCTCTCAGGAAGTCAGCGTAATTGATGTGT
AGAAAGGTAACAGTCAACAGTTCTCCTAACAAGACAGCTTCAAAGCAGCAGCTATAGTGG
AGCATTCCTGAGGCCTGCTGCAGATCAAAGCATGAATGTGCAGACTGGTCCTCTTGCCCA
GCGTTTCTTTC
Sequence 33
CCGCGGTGGCGGCCGAGGTACGTATGCACTTGCTTGCCATCTAAGCAGGGACAATGGCAG
TTCATATCATGATGTTACTTTGATTCTCTGACCAAACTGGCCTGTGAGCACCCTGGGC
CT
TTCTTCCTCTGTCAAAGGCCTTAAGACAGGTTTACCCTGTAGCCAGGCTCTGGAAGACAG
AGCTGGGTTAAAGCTGGGTGGGAGAAGTGAAAAAGGTCAGGTTTACATTCCTACGCGGAA
AAGGATGTAACACGGGGCCACATCCTATGCCCAATCCCAAGGCAGGGAGGCAGGGAAGTG
GCTGCCAAACCTGTTGTAGGAGAGTAATAAATGACTTGAGAGTAAGCCTAAGCAAACTCA
AGTGGGAAGGGGGAGTGGGCTT
Sequence 34
GCGGCCGAGGTACCAGTTAAAGTCTTCTAGCCTGTATCCCCACTCCTTTTTGCCACTTGC
AAATTCGGTAGCCCAGTTACCCAGAGGGAGGCATAGGAGGGAAAACGAAGACTGAAAAGG
GCTAATATGAGTTTTGTCTCTTACAATTTATCTGCATCTTATCCTTCCCCCCACCCCCCA
T
CATTAAATCATTAAACATTCTATCCAAATAGGATGCCCTTCTGTGGAACTGCATATTTG
G
AAACCATACTGCCTGTTTAACTTATGCACTCCACTGGGAACTTACAGTATCTGTTTCCC
A
CAATACTTGCAGTCATATCAGTTACAACCGCTGGGTGTGTATTGGTTCAAAAGGACCTAC
CTACAAGGTTATATCAATCCATTGTCCAATTTGAGAGATTTTTTCTGAATCCAGTTAAA
A
TAATTTTTGGCTACACCTGGGGACACTTCCCAGGACAACAATGACTTGTAGTCTAGTGCC
CAAGAAAGCCAAAAAGGCCCGGCAAC
Sequence 35
GGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCTCC

Table 1

ATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATTGAC
TCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAGTTT
GGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAGGATC
ATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCCGGA
TT
CCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 36
CATNTGTGTTTTATTGTGAAGGGTCCTCAACTGTGTGGCTGATTCAGGCTGTCCCCACTG
CAATGTAGGGAGAGGAGAGAAAGGGATGAAAGTGAAGGCAGGGGGGGGGGATGTTTGTTNC
ACCGGGGTGAACTTCTGCCTGAGCAAGNTGATGTTGGCTTCCGANNGTATTTGGGACACT
TTCTTTCAATACATNTNTTATTTAAGCACTTTATTCTGTGNCTGCTGCCCTG
G
Sequence 37
CCGCGGTGGCGGCCGCCCGGGCAGGⁿACGCGGGGGCAACATGGCGGCCTTAGCAAGCTAT
AGCTGCGAGATTTGAATTACTCCACTCGTAGCTATTGCATTCCTGACGATGGCCTCTGTG
GCTTCGTGCGATTCGCGTCCGAGCTCAGACGAGCTCCCTGGAGACCCCTCTTCACAAGAA
GAAGATGAGGACTATGATTTTGAAGATCGGGTCAGCGACTCGGGTTCATATTCCTCAGCG
AGTAGCGATTATGATGATCTTGAGCCTGAATGGCTGGACAGTGTGCAGAAAAATGGAGAG
CTGTTTTATTTGGAATTGAGTGAGGATGAAGAAGAAAGCCTCCTTCCTGAGACACCAACT
GTGAACCATGTCAGGTTCAGTGAAAATGAGATTATCATTG
Sequence 38
CCGCCGAGGTACTTAAGTTTTTCTTCAGTTACAGCTACCATGTGAAAATAATTCTCTGC
T
TATCAAGTTTACAACTTTAGAATTTCCTGTTTTAAAGTTTTCTCATTTACTTATCACACA
GTCATCTTCTTTTTGCCAAACGCTATAGTAGCACATTAAAAGGAGACTGATGTGAAATCA
ACTCTGTGCAAAAGTATTGGGTGCTTTGGTAGAAGTCTATACAGAAGACACTGGAGACA
CAAAAATGAATTTTGTCCAGGTGAGTTGATGTCAGAAAAGGCTTAATAATGGAGATGAGG
CCGGGCATGGTGGTTCACACCTGTAATCCCACCTGTTTGGGAGGCTGAGGCAGGTAGATC
ACTTGAGACCAGGAGTTTGAGACCAGCCCAGCCAACATGGAGAATCCTGTCTCCACTTTT
.NAAAANTNAAAAANATNNGGTTCCTGCCCGGGCGGGCGCTTAGAACTAGTGGGATCCCCC
GGGCTGCANGAATTTCGATATCA
Sequence 39
TCCCCGCGGTGGCGGCCGCCCGGGCTGGTACGCGGGAAAGCAAAACGACAAGCACGCCCT
GAGCAGAGCCCCGGGAATTCAACCTTTAAGTGGATAACTTGGCTTCTGGTTTGCCAAGGA
ACCAGGGCATCAAACAGATGAAACAGCCTATTGTCCATTTCAACAGGATTTTTCAGGAGT
GGGGATGATCTTTCAAATTATCCACAACTTAATTATTTAATATTTTGATAGTCAATTACC
TAAGACACGGCATCGTCACTGACCAATCAGAAGAGATGCCAGTAGTTGGGCGCAGTGGCA
GCACTTTGGGAGGCTGAGTGGACAGATCACCTGGGGTCAGGAGTTCGAGACCAGCCTGGC
CTACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATGAGCCAGGCATGGTGGGCAC
CTGTAATCCCAGCTACTTGACAGAGTGAGCCTCTGTCTCAAAAAAAAAAAAAAAAAAA
Sequence 40
GCCTCCCCGCGGTGGCGGCCGAGGTACAGTTTAGAAAACTGTGGGGCTGAGTCCTCGGGG
CCGTGGGGCGCAGCGTGGCTGATCACCATCATAACGGGCCTATGGGGATACATTCTCTTA
GACATTTTGAAGTAATTAATGCTCTCGTTAGTGATTAAGTCTGTGAAGTAGTCCTTTGC
A
TAATCAAATCCATGCTTTTCTTTGATGCCATTGCGACAAACAGTGTAATTATAGAAGCG
A
GAATTCTTGATTAATCCAAGCCATTCTCGCCACCCAGGGGGGGATGTAGCTGCCATTATAT
TCATTGAGGTATTTTCCAAAAAAGGCTGTTCTGTAGCCAGTGTTGTTAAGATATACAGCA
AAAGTCCGAGGCTCATGCATGGCCTGCCACGAGGGGGAAGAGCAGTTCTCGTTGTTGGTG

Table 1

TAGACATTGTGATTGTGCACATACTTNCCGGTGAGCATGGAGGACCGTGACGGGCAGCAC
ATGGGGTGTAGTCACAAAGGCATTGATGAAGGTGGCCCCCCATGTT
Sequence 41
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGTGCACATTGTGCAGGTTAGTTACATAT
GTATACATGAGCCATGCTGGTGCGCTGCACCATGGCACATGCATATCTATGTAACAAACT
TGCATGTTCTGCACATGTATCACAGAACTTAAAGTGTAATAAAAAAAGAAAGAAAAACAG
CATGCAATTCAGCCCACACAAAAAAAAGAAGTCAAAGACAGCGAGAATTCTTAAAACAGC
AATAAAAAGTATAAAGTCACTCTAAAGGAATCCCCGTTAGATTAACAACACATTTCTTAA
GAGAAATCTAACAGGCCAGGAGAGAATGGGATGACATATTCAAAGTGTTAAAGGGGGGGA
AAAAACTCCACTCAAGACTACACCCAGAAAAGCTATCTTTCAGAAATGGAGATAAAAACA
TCTTTCCCAGACAAAGAAAAACTAAGAGAATTTACTACCACTCACCAGCCTTACCAAAAA
A
Sequence 42
NTTGGAGCTCCCCGCGGTGGCGGCCGGAGAGCAACCGAGATGAAGGTGAAGATGCTGAGC
CGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAAC
TATGATCCTGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGC
T
ACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGAT
GGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGT
GATGGAGAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 43
ATTGGAGCTCCCCGCGGTGGCGGCCGGAGAGCAACCGAGATGAAGGTGAAGATGCTGAGC
CGGAATCCGGACAATTATGT.CCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAAC
TATGATCCTGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGC
T
ACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGAT
GGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGT
GATGGAGAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 44
GGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTCTACTCTGGAAG
C
TGAGGNGGAAGGATTGCTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGCTATGATCACAAC
ACTGCACTCAAGCCTGGGCAACAGAGCAAGACCCTGACTGTAAAAAAAATTTTTTTACATT
AATTTTTAAAAGTGAGGTTTTTACCTGATGATTGNGTAGGTTTCTCCTAGCTCCAAAGT
A
TCCGGCTCCTACGACTCTAAATATAACCTTCAAGGAAAGNGGAGCTGGTTTACTCTTTTC
TGATAATATCAAGCCATTCCTGGCTGGGCGTGGNGGCTCATGCCTATAATCCCAGCACTT
TGGGAGGCCCCGCGTACCT
Sequence 45
GGGNGGCTCCCACCGCGGTAGGCNGGCCGCCCGGGCCAGGTACGCGGGNAATTCAAGGAT
GGGATTAAAGGATTTAAACCGTTTAGGACCCTAAAAGCATAAAAACCCCTTAGAAAGGAA
AATCTTAGGGCAATACCCATTGGAGGGACCTTAGGGCCTTGGGACCAAAGGACTTTCATG
GACTTAAAAACCACCCCAAAAGGCAATTGGGCAANCCAAAANGCCCCAAAATTAGGNCCA
AATNGGGGATTCTTAACCTTAAAACTTTAAAGGAGGCTTTNTTGGCCCCAGGCCAAAANG
GAAAACTTTCCCCTTCNAGANGGNGGGACCCNGGGCCANCCCTTTCCNGGGAATNGGGGG
GGGAAAAATTT
Sequence 46
GGAGCTCCCCGCGGTGGCGGCCGAGGTACTCGGGAGATCGTGCCACTGCCCTCCAGCCTG
AGAGAAAGAAACTCTGTCTCTAAAAAAAAAAAAGAAAGAAAGATGTCAGTGCTATTTATAG
TAATACAAAAATTTAATGTAATTTTTTGTCAAAATCTCAATGGTATATTTTTGCAGATTTT

Table 1

TCAAATTATATATATATGATTTATAAATTATTGTTATAGATTCCTGGAAAGTTAATCCAT
CTCACCATTACATAATACCAATCTCTCTCGGCCGGGCGCAGTGGCTCACGCCTGTAGTCT
CAGCACTTTGGGAGTCCGAGGCGGGTGAATCATGAGGTCCAGAGATCGAGACCATCCTGG
CCAACAAGGTGAAACCCCATCTCTACTAAAAAT
Sequence 47
CTAACCTCACATTTAATTGCGTTTGCGCTCACTGCCCCGCTTTTCCAGTCGGGGAAACCT
TGTTCGTGCCAGCNTGCAATTTAATNGAATCGGGCCCAACNGCCGCCGGGGGGGAGGAGGG
CCGGGTTTTTGGCGGTATTGGGGGCGCCTTCTTTCCCGCTTTCCTTTCGCCTCACTT
GAA
CTTCGCCTNCCGCCTTCGGGGTCC
Sequence 48
CGCGGTGGCGGCCGCCCGGCCNAGGTACAAGNGACAATGCTGGATGCCAAGCAGNTCCCC
CCTACCGTCTCACTGCCCCTCAAGACTTCAAGGCCACTCTCCCCATAAACATCATGACTA
CAGATTTAGGTGGAAGAGCAGCCATGTTTGAAGGGCACATGTGATGAGTGGGGGGCAGCA
AGATGCCATTTCTGCATCTCCCAGAAGGGATGAGTCTTTGTCCCGATGCAAGCCCCCTCT
TCGTTGGGCTCCCAGCAGTGCTTNCCTNCTCCACCCTGCACTTCATTTNGTTCTTTCC
CC
CCCNAACTTTT
Sequence 49
GCGGCCGAGGTACAACTAATGGAGCTCAGAAGCTGTCAAGGATATAAGCAGTGCAACCCA
AGACCTAAGAATCTTGATGTTGGAAATAAAGATGGAGGAAGCTATGACCTACACAGAGGA
CAGTTATGGGATGGATGGGAAGGTTAATCAGCCCCGTCTCACTGCAGACATCAACTGGCA
AGGCCTAGAGGAGCTACACAGTGTGAATGAAAACATCTATGAGTACCTGCCCGGGCGGCC
GGCTCTAGAACTAGTGGATCCCCGG
Sequence 50
GGCGGCCGGANGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCCGGAATCCGGACAATT
ATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTAC
ATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAG
TATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGG
CAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAA
TTTGGAATCTAACTCAGCGGAATTGTATCCCGTACC
T
Sequence 51
NGGCGGCCGAGGTACCTCAGCATATATTGGAAGTGTTTTAGAGTTGGTGAGTTCCCCGTG
CCTTCCAGAACTGAACGCTAGGAGGAGCAGNCAGNGAGGACAGACGTCTATGCAGAAACA
TGGNGAACCTCTGGAAATGACACACTCTCCGGGGCNCAGGGGGCCATTCGTCCATCTTTGA
GGTGGACTAATCATGGAGATTCTNGCAGGGCCGGCTGCTATCTCAGATTTTCTAATCGGA
GAAGGAGAGAGATCAACTTCCATCGACTCCAGTCTGTCGGGGGCTGATGAGTGAGGTGGC
AGCAGGCATCCGCGTGGTTTTGTTGAAACTGGACTTTTTATTGTGCTGAAAGCTGTTT
GT
TGTGATGATCTCATACTTTGNAGTTGNTCTATCTGCANCACTGACTTTC
Sequence 52
TCGTTNGAAGCCCCCCCGCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTGG
CA
TTCTGAAAATTCATGAGGCTGTGTTTTAGGTGAGGCTATTTCTTCATTCACTGAACNG
GG
CACCCAACAGGCTCTTAATATGAAGACTTGGGCCCTTCCTGAGTTCTAGAAAAGCATTTT
TACTAGTTCTTCAGTAATTTCCCCTCCCCTTCATTCTCTGTTCTCTTTTCCTCGGACTC
C
AATTGGATCTTGGGCCTCTAAGTATAGGCAAGATCATGTTTCTAAAAAGGTTCTTAGAGG
GAGGGAGTTCCTGGGAGTGTTATGTGGGGTGGTGCANAAGGTGCTAACAGGTGGNTTTNT

Table 1

CTTTAGGATGAGCAGGTGG

Sequence 53

GTGAAGATGCTGAGCCGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACAG
AGAGTTCCNNGAAACTATGATCCTGCTTTACATCCTTTTTGAGGTCCCACGAGAATATATA
AGAGCTTTAAATGCTACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTG
GATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTC
CTTTCTGGGGCCGTGTGATGGAGAGGTTAGAAATTTGGAATCTAACTCAAGCCGGAAATT
GTAATCACGTACCTCGGCCCGCTCTAAGAACTAGTGGGATCCCCCGGNGCTGCAGGGAAA
TTCCGATATCAAGGCTTTATCGATACCGGTCNACCCTNGAGGGGGGGGGCCCCCGGGTACC
CCAANCTTTTTGG

Sequence 54

CCCCCCGCGGGGCGGCCGAGGTACACTGGGAAAATGAAGAACTTAACTACATAAAAATAG
AGGGACAGTCAAAACTTCACAGGGGGGGAAATCAAGTTAAATTCAGAGCTGGATTTAGATG
ATGCCATTCTAGAGAAGTTTGCTTTCTCCAATGCTCTATGCCTTTCTGTAAAACTGGCA
A
TTTGGGAAGCATCACTGGATAAATTTTATTGAATCTATTCAAGNCAATTCCTGAGGCTT
T
AAAAGCTGGGAAGAAAGTGAAACTATCTCATGAAGAAGTTATGCAGAAAATCGGTGAACT
CTTTGCTCTAAGGCACCGTATAAACTTTGAAGTTCAGGACCTTCCTGATTACTCCTGA
TT
TCTTACTGGGGACAGGAGAAAACCNNGGGAAGGGACTTTACCGATAAAAACCGTGGTCAA
ATTCCTTTAGCCATTTGGCCCCGAAAGANGTTAAGGGTCCAATGAAATTGAAA

Sequence 55

TAGCAGGAGCCCCAGGAGTCTGAGCGGNGGGACCCTCATGTCCATGCCTGTTGTCCCTGG
ACNTGAAGACCTGAACTCCCCCCGCGTACTCTCGGCCCGNTTCTTAGGAACNTAGGTGGG
ATTCCCCCGGGCCTGCTAGGGGAATTTCCGAATATTCAAAGGCTTAATTCGAATACCCCG
GTCCGAACNCTTCGNAGGGGGGGGGGGGGGCCCCCGNNTTACCCCAAGC

Sequence 56

GCGGCCGAAGAGCACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGT
CCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCC
TTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATT
TGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAA
GCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTG
GAATCTAACTCAGCGGAATTGTATCCGTACCT

Sequence 57

CAGGGAATGGGNGGNGGCTNCACCTGGGGANNCCTGAGGCCCGTGTTTGTGGAAGATGTA
GATTCCTTCATGAAACAGNCTGGNAATGACGACTGCNGATACAGTATTAAAGAAGACTGG
ATGAACAGTACCT

Sequence 58

CGGCCGCCGGGCAGGTACGCGGGCTATTGTGATTCCCAGTGACCCATAGAACAGGATTTC
ACTAGTCCTATGACATGTGACTGGGCTTGGGAAGTTCNCGTGTCAGNTCCAAAAATCCTA
AGGTGGGATCTTCGCTTTGTGAAGCAAATTAATTACACAACCAAATATTGCCACATTCT
T
GAGGTCTATTGACACAATGGGAACTTCAACCCCTACTTAGCTTAGCATTTTTTTTTTTCA
A
GAGTGAAAAGTGGTCCACGTAGAGCACAATATAATTTAAGTAAAGGAAGATTAAAACATA
TTTTTATCCATTTCTTATGGTGGNNNNATTACATGTTTTAGATTTGAGGTCCCCCTCTC
A
GGAAAACCCTTTCAACTTCGTATTATTCACTCCTGAGTAGTATGGGGGTAGAAAAATGAG
TGGGAAATCAGTTTGGTCCACTATTTTCCCGAGTCTTTCTTGCACTTGCAAATACTTTC
A

Table 1

TCAAATATTTTACCAAAAATTCTCANGCNCCTGTTTACCAGGATGGTGGTATCACNATC
A
GGGCTCAAACCAAAGNTTACAGGAAATTCTNTTGGNGGGTTTTTTATCCTGGGACNATTC
TAAATTTTAAAAAAACCTAAAAAAGGTTATTTATTTCTTCNCNAATTTATTCANNTGNTTT
TTTAAA
Sequence 59
CACGCGGGAAAGATCAGTTGNTTTACCTTGGCATTCAAAGACTTTTCTTTGACTCCCATG
GTTCTCAAAGCGTGATCCTGGTCCACCACCATCAGCATGGNNGGNGGGGAACGTGTTAGCA
CTGCAAATTCTCATTCCTCCCTAATTTTCTGAATCANAAATTACGGAGGTGGAGCCCAGC
AATCTGTTTTAACCAAACTTCCACATAATTCTAATTAATTTATGCTTTGGAGAACNCGC
T
GATCTAGTTTGTCCCTCTCATTTTGCAGGCAAAGAATTGAATTCTAGAGAGGTTAATTG
A
CCTTGTCCAGTCATACAGCTAGGGTCTGTTTTCTATTATTTATTTATTTATTTATTTTA
TTTTATTCACTTTACCCCCCAGGTATTCATAGNTTTCTTTCTAAATACTCCATATTTGGA
CTTGACTTTTTACAAGTTTGTAATTACCAAATAAAGTCTAAAGATGGGGAAAGGTTGTGG
GAAAACTTTATAGAGAACATGAGATTTTGACTGAACCAGTNAACATTAAGTAGAGAGNAA
AAAGAAAGGGGTGTTCTAAAGCAGTAGGGACCACAGTGAATAAAGGGAGAAGATAGGGAA
GNTTTAAAAAAAA
Sequence 60
ACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACG
AGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGNGATGGAGTCAATTGCTT
GGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAG
AATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 61
TCCACTCCCGCGGTGGCGGCCGAGGTACACGTTACTGTTCCGTCGTATTTTGTAGTCTCT
GTTCTGCCCTTTGGAACATCTNTTCGGTGTTCCTGTGGGATCTCTCTACTGCATTNTA
CT
TTATGTAATAATCTGTTCAATAAATAATTTTTAAAAGGAGACAACAACGCCGCAGGTGAT
CTGGAGGCTCCTGGAGGACCTCAGCGACTCAGGTCCAGTCCAAGGAGGGCCGCAGATCAG
GCTGAAGGATGGATCCACATGTTTAGAGGAGATCGAGAAATGCAGAAGAGAGATGCAGCA
GAGAAATGCCACAGAAAGGGGAGCTGGAGAGAATCAAAGCATGAGAGGAATTCAACCTGC
TGTCACTGGAAGGGGTCCAGATGGAACGCTTGAGAAGAAACGTGTGTAGCATCTAGGAGT
AAAGACTCGCCCTGGCTGACAGCTAGTAAGGAAATGGGAACCTCANTGCTGCAGCCTCAA
AGAATTGACTTTAA
Sequence 62
TGGCGGCCGCCCGGGCAGGTACAATGATGGCTGTCAACTTCGTTTGTTTAAAAAAAGACA
ATTTGAGCAGGACGACCCTCTCCAATCTGGGTAGCATGGTTAGCCTGTGCAGTAACAACG
TAGGCTCGGAGGATGGGTACCT
Sequence 63
TGAGTGAGCCTAACTCACATTTAATTTGCGTTTGGCGCCTCACTGCCCGCTTTTCCAG
TT
CNGGGGAAACNCTGTTCGTTGCCCAGNCTGCATTTAATGGAAATCCGGCCAACGCCGCCG
GNGGNAGGAGGGCGGGTTTTGCCGTATTTGGGGCGGCTCTTTCCCGCCTTCCTTCGGCCT
TCAACTTGACTTCGGCTTGCNCCTTCGGGGTCNGTTTTCTGGCTTGCCGGGTCGAGNCCG
GGNTATTCAANCCTTCAACTTCNAAAGGGGCCGGGGNAATTACCGGGTTTAATTCCCAAC
CAGGAAATTNAAGGGGGGGGAATAAACCGCCNAGGGAAAAAGGAAAACANTTGTTGGAAGC
CAAAAAA
Sequence 64
GGGCGNTGGGCTGGAGGAGNGGAGCGGCNNCAGNAGGGGGGCGCCGGCCNCCCCAGCAGA

Table 1

NGNCTCCAGCAGCAGNNGNANCTCTGAGGCTCCANCNCCCACAGCACCGAACAGNGGGNN
CCAGCNNCCACCAGGGGACCCNGGANCCCGGGCGACGGCNGANCCAACNCNGAAGGAGNC
NNAAACCTNNNCNNTTGAGCGGNGGGNNCNCNCCCGCGACCCCGAGCAAAAGGAAGCCCAG
CNGGAGGGGCGGNGGANNGACGCCCNCGGGGGGCACAAACAACCNNCNAAAGGAAGAANN
NGCCACCCACCAANCCNNANCAANACAACAAANGAANCAANACAAACANAACCCAAAAAC
GAGNAAAAAAAAAA
Sequence 65
ACCTTTTTTTTTTTTTTTTTTTGGAGGAGATGGACAGTGTCAGTCTCCTGATANGGNGG
T
GATGGGTAGGTAATTTAAAAGCTTCTATTATAAAATCTAGTCTCTCTGACACTGCCCTG
T
CCACTGCAGTCACATCTCCCAATACTGAAGGATCCTGAGAATACCGAGCNGGTCATGACA
CTTACTCACGTCATTCACCANTTTTTTTTGNACCTGCCCG
Sequence 66
GCGGTGGCGGTNTCCCGGGCAGGCCACGCGGAAATCCCCTAACTTCCTTGCTATCTTCCC
ATCCCATATTTAGGTTAGATAGAGAAGTGTGTATGTGTGTGTGTGTGTGTTGCTCGCA
CAGTGATGAACTGTAAACATAAATGAAGATATGGAAAAATACATCAATTAGGACAACATG
ACAATTTCATTAGACTCCTATCAAAGAGTATCAGTTCACAGTTNNTNTAGATACTAGTA
T
AAAATTCAGATCTTGACTGTTTTCTGGGGATAAAGCANGGCTTTACAATTTAGCAGTNTG
NAGCTAGCTTGAAACAGTAAAACAACAACAGCAGAGCCTTAAGTGTATTTTTGTGACCTA
AAACATGAACTCAGGGTTTCCAAATTCCTAACAA
Sequence 67
AGGTACTTGAAGGATAAGAAATTACTGTGTCAAATTACCCACAAGTTAAATGCCCATGTT
CCAGACCTGTGGCTCTTAGTATCAGGCTTGTGATAGAGAAAAGGCTGCTATGAATTCTAC
TCAGTGTGCTTAGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 68
GGATAAGAAATTACTGTGTCAAATTACCCACAAGTTNTTTGCCCATGTTCCAGACCTGTG
GCTCTTAGTATCAGGCTTGNGATAGAGAAAAGGCTGCTATGAATTCTACTCAGTGTGCTT
AGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 69
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCATTTCATCTTGCACCCGCAATAC
CAGGGATTGTTGCGAAGAATCAGTTGTGTTATATTGTCCAAATCATCAAAGATACCCTGA
GGTAAATTACTTAGGTTATTATTGGACATATCCAGTCGATAGAGCTGCCTTAGATAAGAA
AAAGCATTTGGGGGCACCCGATTGATGTGGTTATCTTGAAGATAAAGCTTCCTCAGGTTT
GTGCCTGGAAGGTTTACTGGTGCAGCAGTCAGGGAATTCCGCACCAGGGACAGCTCTGTC
AAATTAACTAGGTTGAAGAAAACTTTGTCACCTAAACCATGATTGTTCAACAGGTTTCCA
TCTAGAACCAGGCGTTTTAGACTAGTGAGACCTTGAAGAGATGGTGATGAAATAGTGGAT
ATGCGATTATCATCCAAGCGTAGTTCTTCTATAGTCCTGGGCAAACCCCAGGGAATTGTG
CTAAGGTGATTACGGGACAGGAAAGCAGTCGGAGATAGTTGCTGTCTCGGAATGCTCCC
TCTTNTATGCTAACTGCAGAGACAGAGTTGNCATCTAAATGTAATTCTTCCAGATAGG
Sequence 70
NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTGAATAAAAGGCTTTGGTTTCTCTG
ATGTCTTCCAATCAATCACACAGAGCTTGCCCTGATACTCAGCCACACAGTCCAGCAGAC
CTATATAGTTTAAGGTTTCATGTTGAACAGCACTTTCAAGAGCTCGCACTCCACTGAC
AT
CTTTCAGAATATGCTGGACACTTTCAATGTAACCAGACTTGAGGAGATTTTCATCTCTC
T
CTTTTAAGGTTTCCTGGGGTGAAAGTATGCTTTCCAAGGCTTCGTGGAACCGTTTCCC
TT

Table 1

GTAAAAAGACGTTTGAAGTGTATTCTTTAAAGCCATCTTCTCCCAGTTCCAGAATCATC
C
CGCTGTTTCCACCTCTCCAACAAAGAAAACCTGTTGTTTTGGTCATGGTCTGCTGAAGGA
CTCGGGTCACACTTGGTATCACATTCCTTTGCAAGGGGATTTTCAAA
Sequence 71
AGGTACTTGAAGGATAAGAAATTACTGTGTCAAATTACCCACAAGTTAAATGCCCATGTT
CCAGACCTGTGGCTCTTAGTATCAGGCTTGTGATAGAGAAAAGGCTGCTATGAATTCTAC
TCAGTGTGCTTAGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 72
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATATATCATTTATTCAAGAGGCAGA
TTTTAAACGTTTTTGTAAAAAGCTAAATAACACCCAGAGTGACTCAAAAAATTTCTCAA
C
TTTGCCCAAGTGAATAGTAAGTCTAGAGTTTTTTGGGTTTTTTTTTTGTGACAGAGTTT
C
TCTCTGCCGCCCAGGCTGGAGTGCAGTGGCGATCTTGGCTCACTGCAACCCCTGCCCG
Sequence 73
GGCGGTTNTGGGGGGCAACACCGANCCGCAGAGNCACACTNGCAACAAAAGGNACTTNTT
TGGGGGGGGGGAAAAACCCCGGCCCCNCCNGNCCAGCNGGACCATCNATTTNNTCCNCCNC
CNCGGAGCNGCNCCCNAAAAAGCNCANAACAGNAGAGANCAGNNGNCNCNGGNNGCAAAN
CNAACANANANNCANGCAANGGAGGNGNANCNCCATGCTTTTTNGNNGGGGGGGGGNNGCG
CNACGCNCCCNNGAAGAAAAAAACGCCNCAGNAACGGGGGGGGGGNAGGACCCAGCCNGG
GCGGNCGCNCNAGAACCAAGNGGAACCCCCCGGGCCNGCAGGAAANCCGAAANCAAGNCN
NANNGAAACCCGNNNAACCNAGANGGGGGGGGGNCC
Sequence 74
CCGCGGTGGCGGCCGCCGGGCAGGTACCTTGTGAGAAGAGGAAGAAGGTGATAAGAACTA
AGATCAGAGCATAGTAGAGAAAGTAGCCCTGTAAACAGAGGAGAAGCAGAAAGAGAGAGG
GGAGGACAGAGCTTTTATTTTGCTCCAGGTTAAAAAGAAAAAAAAAGCACATTCAACTCT
ATGTAGTGTCTGTCCCAGGTCCTAGAACTGGAATAGACCAACCAAGCCCAACCCTTCTTA
AAAGTAAGACTNGGTGCTTCCTGATTATATATTCAACTGCCTGGAAGCATGCAAGTAAAA
TTTCCTTGATGGCATTTCTAAGTTTCAAACATATTCTTNCTAACAAATGCATTTACAAAA
AAATATTAGGGATTGNGGTTTTTTTTGGTTNGGACTTTAAAAAAAAAATTGTTTTNAAANC
C
ATAATTGGGGGCCCTACCCCAAAATGGATTCTTCTCCCCTACAGGTGGAGGGTTTCATTT
TTTC
Sequence 75
GCGGCCGAGGTACGCGGGGAGGCGTTGTGGGAGGAGGTGCGGGGAGAGAGGAAGGGGCCT
GTGCACTGAGCNGGCATCAAACTATTAGTGGATGGCCTTGCGTCTCAATCTGCAGTAAAN
AGGAAACTAATCTGAAAGGGAANGANAGGACTGTGTGNCTTTTTATTTTTTAAAATACGG
AGTGTGCANTTTTACTGAATCTTGAATCATGCCC
Sequence 76
CTTGGCCCTTGGNTCGGGGGGCCNTTTTNCCCCCCCAAGGGATGGGGNCCCNTGGCNTANGT
GTTNGNGGGCCCAAATANGAGCGGANAGGTTAAAANCNAAGTAACNAACGACCGTAATCG
TTGTAGTTCCAAATGGGGAAATTGGGGTNTTTTCGGGNGGAACCTTAAGAAAGNGGCCTT
CCAAAATTGGNGGTTNGGGGGGGAAAGGAAAGGAATTCCCCCCTTGGCCAANAAAAAACNC
CCACNCCAAACCCCCAAGGAAAACCGGTTGGGGNTTTTTTGGGCCCCNTNGGAAAGGGGC
NTNGTTCATACCTTGGGNANGGAAGGNAAAAAATGGAATTTTCTTGGGGGGGGGGCTTTG
GTTCTTTTAATTGNAAAAAAAANATTNAATTAACGGACCCATTTTTNCTTCNAACNAAATT
AAAAGGCCCCCCACGTTNNTTCAATTCCATCCCCCAATTTTTTNTCCCCTNCCCCTTTT
T
TTANCCCCTTTTTTTTTCTAAAGNATTGGGCCAAAGNNTTNTCTTCCNTTTNTTTTNCCA

Table 1

A

CCNATTTTNAANGGGGGCCTTGGGGTTTTNGNGTTNTTCAANAANAACNTTTTTTTTT
GN
GGGGTAAGTCCCNACCCGNGNTANCNTTGGGTNCAAGNTTTCNNTTTCTTTGGGGGGGGA
AAAGGCTTGGNGGTTTCCAANGTCCNTCCAATTNTCCTTGGGCCAAANGGGGGGCCTTTT
NCCTTCCCCTTCCCCTTNCTTTGGTNNCTTTTT
Sequence 77
AAAAAGNGAATTCCANCNTGGGGGGGNCTTGGNGAAAAAGCCTTCTTAAACCANGGGCCAA
TTTGGCNCAGGCCCCTAAAGCCTTACCCTGGCCAAGTTTTTTGAAGAGCCAAAGGGGGGGC
CAAGNGGGTTCAACCTTTTAACCCCCTTGCTTGGTTCTTGGAAATTGGTCNTCCCCTTGG
GGGGAACCAAAACAAGGGNAGGGGGCNTGGCCACCTTCAACTTGGGCCTTGGAGGTTCCA
AGAACCAGGAAAAGGAAGGGGGAATCCATTCCGGGGACCTTGGGAAAAGNCCTCCTTGGG
CCAAGGGGGTAATTGGGGCTTAGGCCCCNTGGGGTTTNACCCCCGGTTAAGTTGGAAGAA
AAATTNGGGAAGNAAGGGGGGCCCCAACCCTTGGCCCCCAAGCCNTTAACCACCAAGGAA
ATGGTTTTTTTCCCCCAAGGGGGAACAAAACCAAAGGGGAAGGGGCTTTGGTTGTTTCCCC
ACCTTTGGNACCAAGGTTTTTCAAGNACCAAGGGAAAAGGTTGGGGGAAAACCCCAACCT
TGGGGGNACCCCCGGGGAAAAGNCCTTCNTTANNCCAAAGGNTGGGTTTTGGCCCCCCAA
CCCCTTGGGGGCCTTAANCTTTANAANTTGGGAAGGCCCCTTTTTGGAAANAACCCCCAG
GCCCGGAAAAAAACCCAAAATTTAAAAATTTCAAAAAAGGGAAAGGCCAAGNTTTTCNTT
GGTNCCCNAANAAGGN

Sequence 78
TCCCTTTAAGTGAGGGGTTAATTGCGCCGCTTGGGCCGTAATCATGGTCATTAGCCTGGN
TTCCTGTGTGGAAATTGTTANTCNCGCCTCACAAATTTNCAACACCAACCATTACGGAAG
GCCCGGGAAAGNCATTAAAAGTTGGTAAAAAGCCCTNGGGGGGGTGCCTAAATGGAAGNTG
GAGCCTAANCTTCAACATTTTAAATTTNGCGGTTTGCCGCCTTCACCTGGNACCCGGCTT
TTTTCCAANTTCCGGGGGGAAAACCCCTTGTTCCGGTNGCCCANCCTTGNCCATTTTAAAT
GGAAAATCGGGCTCCAAACGNCCCCGGGGGNGNAGAAGGGCCNGGTTTTTGGCCGGTTATT
TTGGGGGCCNGCCNTTCTTTTNCCGGCNTT
Sequence 79
GAGGTACTTTGGGCCTCTCTGGGATAGAATGTTATTCACGCAGGCACACCAAACAAGAAG
GGCAAGTTTCCAAGGATTTCAACCTGCTTCAATCAAGAATGGGGCGGGGGGGAAAGAATG
AAAGAACCAGGAATGGGTGGCCAAGGCCCACCAGGTTTCGTTTTTNGANTCCTCCCACCC
TTTGGGGTTCCCCTTCCCGGCCCCGAAAAGGTGGAACCCCGNATGGTCCCCTTTCCCATA
ATTGGTTTTAACAGGGTAAAAATAACAACCTNGCAAGAAAATNCTTTCAAAGGGCCTCCC
AAGNCCCTTGCNTTGGAATTGGGTTGGAAGAAGGTGGAAAAGGTTCTTGGTTCCCCCAAG
NACCCCCACCTTGGCCCAACTTGGAAACCCCTTGGTCCTTGGCCGAATTGNTCCAAGGTN
GGGGCCCCCNTTGGTTTTGGGGAATTGGTAATTCCAAGNAAGGAATTGNAAGNGGGAAGC
CCCTTTGGGGGGGNAANGCCCCTTGGGGCCCCAAGGGGTTTTTTCCTTGGGCNTTGGGGTT
AACCCTTGGCCCCCCGGGGGCCCGGGGGCCCCGGNCTTTCTTAAGAAAACCCTAAGGTNG
GGGGAATTCCCCCCCCGGGGGCCTTTNGCNAGGGGNAANTTTTCNCAATTANTTCCAAA
AGNCCTTTAATTCNGAATTNCCCCCGGTTTNGAACCCCTTTTGNANNGGGGGGGGGGGGGC
CCCCGGGGTTNACCCCCAAAGNCNTTTTTTGGGGNTNCCCCCNTTTAAANTNGGAAGGG
GGGTTTAA
Sequence 80
TGGCGGCGATTACTGTGCGAGAGGTAAAGGATATATGTGGCTACGATTACGGCCTCTCT
Sequence 81
GCGGTGGCGGCCGAGGTACAGCCAACCCCCTAGGTGTGGACCAGCTGAGGCACGGTGGGC
ATGATATGCAGAGGGACTTGGGGCTTTGCCAAAGGGTAAGCACAAAGAAGGAGTCACGGG
TTCTGTTCGAGGCACTGTTGGGATTAGGAGCCGGAGGGGACCTACTTTTGCAGGAACCTA

Table 1

GCATAACTTTGTGTGACGAGACTGCACAAGACAAAGCTCANGCAAGTGGCTCAGTAGTTG
GCCAGCCCAGCAGGGTCCTCTGTATGAGTGTGCACCCAGCTGAAGAGAAGAAATGGAGAG
CAGCAATTGGAGCTTNAGGACCGGCTTGCACTGTGGCTCCAGGTTATACCACCACTGCCC
AAAGCAAAAGCTAGAGAAGCAAGTGGAGAAATGCTGGGAGAAAGCTG
Sequence 82
TGGCGGCCGAGGTACGCGGGGGAGTCAGTCTCAGTCAGGACACAGCATGGG
Sequence 83
CGAGGACCTTGTTGCAGCTCTTTATTTCTTAAGTCCCCTCCCCCGAGGTAACACATTT
CT
GCTTTTTTAGCTGTTTCCTCTAGTGTAGGTTCACCTNGCTAATTTTTGATTCAATCACT
T
AACCACCGTTACATACTACAAAATATCACTATATTATGACCATGATTATATTTTNTTTTC
TTTTTCCCTTCATCAAGGAAGTTCATCAAAGAATTTCATCAAAGTTCAATGATGACCTC
T
TTTTAAAATTTTCTTAGTATTCTATGTAACTATCACCGATCTTTTCCCCACACACTTCAA
GAGGCTTTTTTAAANATAATNTTTTACATAGGCCNTTGAGGCACANGATTAACCAAATCC
CTNTTTT
Sequence 84
GTGGCGGCCGANGNACTNNGGCCTATNTGNGANANAAGGTATTNACCNNGNNCACAACAA
ANGCATNNTCCATATTNNAACNGCTCATCATATGGNGNNAANATNNNGACAGANGGTGCA
ANCACNNTNCACTNGATATACNCCTTGGTNCCTCCGGCCGCTCTAGAANCTNANTGGGAT
CCCCCCCGGGGCCTGCAAGGGAAANTTTTCGAATAATCAAAAGCCTTTATTCGGAATAAC
CCCGNTGCNGACCCCTTNCGAAGTGGGGGGGGGGGCNCCCCGGGTAAACCCCCCCAAGACCT
NTTTATGGTTTTCNCCCTTTTTTTAAAGATTGNAAGNGGGGGTTNTAAAATNTAGGCCNG
CC
CGCCTTTTGGGNCNGNTTAAAATTNCAATNNGNGTTACAATTAAAGNCCTTGGGTTTT
TT
CCCCTTGGTTGGTTAGGAAAAAAAATNTTNGATTTTAATTACCCNGGCCTTTNCNAACNAA
AAATTTTTCTTCCACCAACCCAAAACCAAATNAAACCTNAANTCCCCCGNGGGGGNAAGNC
CNAATTAAAAAAAANGATTTGGTTAAATAAGGCCNCTTGGGGGGGGGGTT
Sequence 85
CCGCGGTGGCGGCCGAGGTACTTATATTACATTATGCTCAAATGCAAACACTTATGCTAA
ATGTTATATTTGGGAACAAATTGTGTAAATATACTGATGACGTCAATGGATCATTACAA
T
TAATGTAGGTGCCGTGGGCAGGAAAGCTAACTTTANCTGAAAGCATCTNNAACGTGCTTA
TTTTTCATGGGCCCTCAAAGGAAAGGGATGAGGCCAGCCATAAGGAANGGCTTGGCCAAA
TATAGTTCTTGTTTGTCAAGAACAACAAATCCCATTTCACAACAGAACTAACGCTGGCAT
GCCATTCTNTCCTNAGGTTCTTGGCGTGCAGTGAGCGAGGCCNGGATGGCAGTCAAGGAT
TCATTCCTTTG
Sequence 86
CCCCGCGGTGGCGGCCGAGGTACATCCCTGTTTATCCCATTCCATCCACCGAGGCCCAAC
AGCATGGATGATCTGTTTGCAGGGAAGCCTCCCTGCTCCCGTGACAGCTATCTCACCAGC
TGACACTTTACCATATCTGGCAACAAACTGTTTGCTCTCTTCTTGGATTTCAAATCCAC
C
AGCTTTTACCAGGGCCAGGGCCAGGCCTCCCCCATGCAGAAGATCTTCATTGGCTGCATT
CACCACAGCATCAACAGCATGTGTGGTGAGGTCATCTTTCCACACTGATAACTCTATCCT
AGGAGTCAGCATTTTTCTGAACACTTGCAGAGATTTGCTGTTGCCTTCCTGAACTGGAGA
GACCAGGGTAGAGATACAGCCAAACTTATTCTGGAGGACTTCACACAGCTGACGCTCATT
ATTTTTTAAAATTTTAGAAGTCATTGGTGGTTAATGG
Sequence 87
CGGTGGCGGCCGAGGTACTCTTCAAAATTGTCAAGGTCATGAAAGACAGCAAAAAGTGAA

Table 1

GAATTCTTACAAACTAGAGGAGACAAAGATTGGAGAAGAAACAATGACTGGCTGGGCACG
GTGGCTCATGCCTGTAATCCACTTTGGGAGCACTTTGGGAAGGCCNGAAGAGGGACAGAT
TCATCTTAGNGTTTGGGAAGTTGNGAGAACGAAGCNNTGACTCAACGTTGGTAGAAAACN
CNNCATCCCNTACCTATAATAAATACCAGGAAATTACGCCTTGGGGTCGTNGGTTGGNTG
ACATTGCCCTTATTAAAATNCCCCAGCCTTACCTTTGTGAAAGGGCNCTTCCGGNCAGGGA
AGAAATTNNACCTTTNTATACNCNCGGGGGAGGGGCATGAAGTGTTTTGTTGNGTTTGAA
GCNCCAAAAAAAATTTGGCCGCCCATTTTGGNCAACNTCCCANGCNCCTNGGGGCCAANC
AAAGAAGCCGAA
Sequence 88
GCCCANAAAACCGTAAAAAAGGCCGCCGTTGCTTGGCGTTTTTTCCATTAGGGCTCCGCC
CCCCTTGACCGAGCCATCACCAAAAAAATTCGACGCTCAAGGTCAAGAAGGGTTGGGCGG
AAAACCCCCGACCAGGGAACNTATTAANAGAATACCCAAGGGCCGTTTTTCCCCCCCTGG
GAAAGGCTTCCCCTCCGTGGCGCCTCTTCCTTGTTTTCCCCGAACCCCNTGGCCGCCTTT
NACCCGGGNATTAACCCTTGTTCCCGCCCCTTTTTTCTTCCCCCNTTNCCGGGGGGA
AA
Sequence 89
CGGGCAGGTACCGCTCAGCCTGCTTGGTTGCATCCTCCGCATGGCGAGTCAGCTCTGAGA
TCTGAAGGTCAGCATGCTTACGCTCGGCCTCACATGTGTCAAAGTGATTCTGGATCTCCT
TAAGTCGATCCAACATCTGCAGNTGCTGGTTTTCCCCATTCTCCAGTTCACGTGTTAA
AT
TCTCTACTTGTGATGCCAAATGTGCTTTCTNCTTGTCTTTTCTTTCCATGCACCGTTTN
A
CTTCCTTTAACT
Sequence 90
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATCACAAAGCAGACAAACAG
GAAAGACTGAACCATCTATTTGAAAAAAGTGACTTCATTCAATTGGTTCAGCCACCCGTA
TCTGTAATCTCTCCATTCTGCCCTCTTGATTTTAATGCAGCTATAAAGGAGAGTATTTT
A
AAAGTGCCTCCCAGTAGGAAGAACAGTCACAAGGCACTGTTATATCAATTCAGTGTGACA
CAAGCCCTGATTATTTAATAGTATAACAGCAGTGAATCAGAGTTCTTTCATCTGACTTT
G
CTGACATTNCCAGCAGCTGNATATTTAATTCACAGTTAGGGGCTGGACAAACTACAGCCN
TTGATCAGAATGGAAGCAGGCATCCTTGAGCTTCTTCTAGGAACAAATACAGATGTGCAC
AAAATTTTCATTTATTCAGT
Sequence 91
GATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATCACAAAGCAGACAAACAGGA
AAGACTGAACCATCTATTTGAAAAAAGTGACTTCATTCAATTGGTTCAGCCACCCGTATC
TGTAATCTCTCCATTCTGCCCTCTTGATTTTAATGCAGCTATAAAGGAGAGTATTTTAA
A
AGTGCCTCCCAGTAGGAAGAACAGTCACAAGGCACTGTTATATCAATTCAGTGTGACACA
AGCCCTGATTATTTAATAGTATAACAGCAGTGAATCAGAGTTCTTTCATCTGACTTTGC
T
GACATTTCCAGCAGCTGTATATTTAATTCACAGTTAGGGGCTGAACAAACTACAGCCATT
GATCAGAATGTAAGCAGGCATCCTTGAGCTTCTTCTAGGAACAAATACAGATGTG
Sequence 92
CCCCANGAGGNCACCAAGCATCCCANCACCCTTNNTCCGGGNGGTGNAAANCCCANGGCC
GCCAGGCAANGGCACANCAAAANCCGGGCTGCGNCNNGAGCACNGGGCANCCCGAGAAAA
CAAGGNCNCAACNACNGACNGGCNAAGAAGGGGCCNGCCCCNGGCCAACNNCACCANACA
GNNNAGAGCAATCTTTTTTTNGGGGGGNGGAGCACCGGGACCACCACCCNGACAACAAAGGA
CCCCGGCCGGGGGN
Sequence 93

Table 1

CCCGCGGNGGCGGANATTGGGGGGNGAAACCTNANANCANGGAANCTTTGCTTTNNGNCCA
GATTANATTGGGGGGGNCTTAAANCCCCAGCGGCNNNNGACAGNTAATACACCTCACGTTT
TTNGNAACTGGGGGGGGGCAGNACCN
Sequence 94
TTTCCCGGGCAGGNACAGCTCCATGAGGTCACCAAGCATCCCATCACCCNTTNCCGGCAG
TTGCATGGCAATGGCTGCCAGGCAATGGCACATCAAAATCCGGGCAGCGTCTTGAGCACT
GTGCAATTGAGTCAACAAGGTCTCAACTACTGACTGGCTAAGATGGGGCCTGCCCTTGGC
CAACTTCACCATACAGTTTAGAGCAATCTTTAAAGTGGNCTGAGCACCTGGACTATCATC
TTGACTACAAAGTACCT
Sequence 95
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTGTATGATAACATTGCAGTCAAACATA
TCTTGTGACAGGACAGTTTTTTTGTGGGGAGGAGAATTAGACCAAGTTCGGAGATATATTT
TAGGAACTAAAAGGAACGTAAGATCTGGGGTAGGGGGATGAGCAGCTCCACACCCTGCTC
CTGTGTGAGCTGTGCGCTCCCGACTGGGAAATGTCTAACTCCATCGAAAACATGAGATGA
GGGGCAGGGAAGGGGCTACTTCCAAGCCTTTCATTATAATACTGTGTGTAACCTTTTGCA
TATTTTCAGAAAAGAAACCAGTAAGGTGGGTTCAGTTGTGGGCTCATCCTGACTTAGAAA
ATTTTAAATAATTTAGCCCATTGAAATGTTGATAATATAAGGCATGCATGAATAATAATT
TTTGCTTCTT
Sequence 96
AGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGCTGCGACAAACACCCCACAAAA
TGGCGGCAGCGCCGTCGCCCTAGAATCCCCCGAGTCGCCTCTCCCCGCGTACCT
Sequence 97
AGCTCCCCGCGGTGGCGGCCGAGGTACCTTCCCCTGAGGAGCCCCCTTCAGAGGGGCGAA
GAGCAGTATCTTCAGAGGCCATCCAAGTTTTAGCATAACAAGGAGGGAAAGAGAATGCAG
AGAAGAGGCTGGTGATAGACAAGTTTCATGTTCACAACTTGAATTGCAGAGGTCAAGAGT
TTAAAGAGTTTGGGATGGAAAGAAATCGAGAATTGGGCT
Sequence 98
GCTCCCCGCGGTGGCGGCCGAGGTACCAGCAGAGATGGCTTCAAGATGATTTAGGACTTG
GGTCAGTAGCACTTACTGATGTAGTGGTTTGATACACACTGATTACCTTCTTCCTTTTT
T
ATTCTCTGGCATTTCTCCTATATAACTAGCCACTTTTAAACAATATTTGTCGGCTCTTTT
CTTCTGCTTGTCTGTAAATATTAGGGTTCCTGAGTCCTTACCTAGATTTTCTTCTCTTC
T
TACTCCTGGCCTTTCCTTGGGAGAGTTCATAATTCACCTACTCCATCTAGATATTTGTG
A
TGTCCAAACACATCTCCACGTTAGGCTTCTATTTGTAGCATCAGACCCACACTTTCAA
CT
GTCCACTAGATAGCCTCACTTGGATGCTCTGCAGGCCTAAATAACCTTTGCGGACAGATT
AACAGGGAAAAAATATTAATAGGAAAAAATATAGATTTTTATCTGATGGTAAT
Sequence 99
TGCGTTGCGCTCACTTGCCCGCTTTCCAGTCGGGGAAACCTNGTCGTGGCCCAGCCTGCA
TTANATTGAAATCGGCCAAACCGCCGCCGGNGGAAGAGGGCCGGTTTTGCGGTAATTGGG
GCGCCTCTTTCCGCTTTCCTTCGCTTCACTGGACTCCGCCTTGCGGCTTCGGGTNCNGTT
TCCGGNCTTGGCCNGGCCGAAGGCCGGGTTANTTCAGGCCTCCACNTCAAAAAGGGCGGG
GTAAATNAACCGGGTTAATCCCACCANGAAATTCAGGGGGGGGAATNAACCGCCAGGGAAA
AANGAACCATTGTTTGAAGCCAAAAAAGNCCCANCCAAAAA
Sequence 100
GAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA
ATATGTTTTAATATGCATATCATCCAGGCAGCATAATGTTATATTTCAAAGACAGATTTA
TCCATTGAATTATTGTTTTTAAAAGTTGGGATTCTCTACATAGAACATATTTTCTGAAAT

Table 1

TTCAAGAATATTTTCAGGTAAATTAAGAATTAATTTCTTCTAAGACTATCCAATGNGTCT
CAATCTATTCCATAATATAATCAATGATAAAGATTCACATGTATCACCAAATTCGAGGC
A
GCTTAGTTGAAAAAATTTGAAACAGCTTACTGAATTCCATTTGCTGATTCTGNGGGGGCT
TCCCCAATGGCATGNGTGCTCCTTTGGATGCCTGCAGGGGTGGTCACTGCAAAGTCGTCA
TNTGTGCCACTGGGAGTTGGGGAGGCGGCCTGCTGGGGTTCCCTGGGT
Sequence 101
GGCCGAGCCCAATTCTTGATTTCTTTCCATCCCAAACTCTTTAAACTCTTGACCTNTGC
A
ATTCANGTTGTGAACATGAAACTTGTCTATCACCAGCCTCTTCTCTGCATTCTCTTTCC
C
TCCTTGNGTACTGCTAAAACTTGNATGGNCTNTGAAGATACTGCTCTTNACNCCTCTGAA
GGGGGCTTCCTNAGGGGAAGGTACCTCGGCNCGCTCTAGAACTAGTGGAATCCCCCGNGC
TGCAGGAAAT
Sequence 102
CGGGTCCATAATAATGCAATTAACAAAATCCAGGATTTAAGGATTTNTATAAGATTAAAA
AAAAAATGAGGTGGTGTCGAGTGGGGAGAGAAAAAAGCAGGAAACAAAACTGGTGAGAGG
AAATGACCCCCTGATGAAAGATCTTAAACACCAGGCTGAAGATTTTAGATTTCTACCTAT
TAGAAATGAATATTCACTGAGGTTTGATGAAGAGTCACTGAAGTGTCACAAAGAAAACAA
GATTTGAGAAAGATTCTTGAGAACTCGTGCATAGGAATGAACTGCAATAAGGGGCAGATTA
GAGAAGAACTAGGCCATGAGGGCCTAGTATCCAGAATGAGGCAGAGGGAGGGACGCTGGA
TGTGAGCAG
Sequence 103
ATTGAGCTCCCCGCGGTGGCGGCCGAGGTACTCCTTTCTTGTTTAAACGCCTCACCACTG
ACCACGGAACGTCTTGATAGAGCCATCTAGTAATTCTTAAGTCCTACCTCATCCAACCTT
GTTTTGACTCCTGCAGTGAGCACAGCTGCCCTCACCCTCCCCTCTCTATGCCCTCACCTT
TGCAGGAGACTCTCAATTTCTCAGTCCACATCAGCTCTNAGACCACCAAANGCAAGGGTT
N
Sequence 104
TGGATTGAGCTCCCCGCGGTGGCGGCCGAGGTACACGTCAACACGGGTGGTTGCATGCAT
TCCTCAAGTCTGTATGACTCTACCAAGATACTGTGAAGTTGTCCTTCTGATTGCACAT
GG
GGAGAAAATGCTGAAACTAGTGGCCACAGATGTCTTTAATTCCAAAAACC
Sequence 105
AGCTNCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTCTAGGTATATCATGTGCCCTAATG
TGCTCCTAATATCATAAATGTTTACTTTCCGAAAAGTATTTCTGAAAGGGAGCATATTT
T
GGAAAGTGCATAGGCTTGTAATCATACTTGTTTTCAAGTTTCAACTTTGCTATTCAACT
A
GAATAATCTTGTGCAAAACCTGAGCTGATTTTCTCATCTATAAAATGGAAACAATACTT
T
CTGTGATAATGGGTGCAAAACACAAGGTATACTGGTTTCTTTGCTCTGGATTCAAGTT
TT
CTTCTTAGTTTCAAAATTTTAAAGGGAAACCAAAAATGTTTCATGGNCCNNNCTNGCNGG
NANGGGANTTTTCCCNCNAAAAAAAAAAANTCAACGGGGGGGGGTTTTTNCCNNTGGGGANN
CCCAAAAAGCCGNNTNTNGGCCANGTTTTTNNGNNNCTTTTTGTNAGGGGNTTTNGGGCC
NCCCTGCTTTACCCCNTTTTTTTANATAACNNCCCCCCCTTTTGGNNTNGGGGNGGGGNNT
TATATATNTTTNTGGGGGGGG
Sequence 106
GTAGTGGGCAGCGATNAGGGCTGGGGCTCTTTCCTGAGTTGTGTCAAGGTGAGAGATTGT
GAAGAACTTGGCTTGCAGGGTTTGGGCATCAGCTGCCCATTGAGGGGCCGTTCATTGTCT

Table 1

CAAAGTGAATGTGGGGTGGTTTGATCTGCATGTGTCATTTGTATCCACACAAGTTAATTA
TTCTGCTTTTGTTGTAGTACCTTGGTTGTGAAGCAGAAGCTACCAGGCGTNTATGTGCAA
GCCATCTTATCGCTCTGCATTAAGTAAGATGAGGATTCACTCTTAATTTATGGGCACAT
T
TTAGTTCCTTCCACACAAATTTAAGGCCTTAACTCTTNATTTTTTCCTACANTGGNGGG
T
TTTGGAAGTAATATTCATACGGGCATGGGACCT
Sequence 107
CAGAGAAAGCTTGCCAACGGTGATAAGTAGGTTTGTCTAGCAGCACTGATGCGTCGTGGA
AGTTGATGGTCATGAACATACAGTGTGATAACCTATCTGCCCTCTTGACCTTTTCTAGT
A
GTGCTATGTCATTTTGGTACTAAGGTAGGTGAATTTTCCAAGTGTTCTTGGAAATAAG
GA
AACATCAAGAATAATGTAAAAGCCTCATATACAATAATGAATAATAAAGAATAATGTGAA
GGCTTCATTCAAGGTTGGGGTTTGCCAGATACATTGCAACAAAATGACAGAGCAGCCAAG
GTATTTAGGGATAGTGGCCAAAGTATTGTAATGATGGCTTATGGGAGTGTCAAGCTGGAT
AAAAGAGTGAAAAATGGAAATAAAAAACTAATGGGATTGGTTCNANTCCGAAATAGGCAG
CNCNGCCCCAATGGCNCCCATNGCCCCGGTTTNAAATTAGGGGG
Sequence 108
NCCGGAATGGAATTCTACATCAAGTGTCTGTGCCTCGCTGCTGAAGGATAACCCAGAGTG
CAAGGTCATCTTTGTTGCTGAACAGGGCTGGACCTGTCGCACTTAAGCACACTTAAAGGA
TTCTATTCTTCATTCAGGTCCCCCAGAGAAATTGGCTCCTTATTTTTCTTTACCTATTC
C
TAGACTTCCTTTTGTCTAGAGCCAGTTTTGCAAAGGGCACTTTTATCCATCTCAGTTAT
T
CCCAGAGGTGACAGAATGAGTAAACCATATGGGGCAAATAGCATATATGAGCTAAACCAG
NTAACTGTTAACCAAGGCACATGGTCAATGCCTTAGTATTTTTTTTTTTTTAATTCTTCC
TAAACGGTTATTTTCTAGCTGTACATTCCCAAAA
Sequence 109
GCGTCCGAGACACTTCTCTGACTAACCATAGACTATGTGGAAAATGGTAGCTGGATTGCC
TTTGGGTGGAGTCCTTGCCCTGTGGCATAGGAAACAAAGGAAAGGAGAGAGATGCCCTTT
GAGATTAATGAAAATGCTCTCAGCCAAATAAAATCTAAAAATAGCCTCCTTGTGATACGA
ACGCGTGGCCCCTAAGGGTCCTAAAGAGAGAGCTAGGGGAGGTTCAGCTGGCCACAGAGA
TGCTAAAGGTCAGGAGCAGACTTTTAGGGTTTGCTGTTTTATAGGTTTAAAGACCAGGTC
TGTGTTTTGATAACTGAACTTGCTAATAGCTGGCCACTTGAGTTGCTTCTTCCAGCTCT
T
TGTTTGTTTTAAATAAAGAGATTCAGCCAGTAATAATGGGAAGAGCTGCAAATGACTTCC
CCAG
Sequence 110
GTGCTGCCTGCACTGTGACTAAGACTTTCTGGACTATCATCATGTTTAGGAGTTGATGAG
ATTATAGTTTCATGTAAGTGTATCATTAGATGACAACTCTACATCTTTAGGCATGGAAA
C
AAAAATTTTTCCTGGAAGAAAAAAAAGTGAACATCCAACCTCCATTTAAACAAATTNGAT
TGTTTCTTTGCTATTAAGAAACTCGGTGCTCTTTCTCCCACTCTATTATATTGTCAAAAT
ACATCTGGAGACACTTTATAAACTTTTTCTCCTTTAAATTACCTGGTTTATATATTATCT
CCTGTAGCCTGCATAAACGATAAAGGGTTAAACATA
Sequence 111
GCNCGCGGGATTGGCCGACGCAGCCATGGTAGGTCCAGATCCCGTAGAAGGGAGCGGGGT
CCCATAGGTTACGGCCGATTCCTGGAGCTTCTGGACTGAGGGCCGCGGTAAGCAGTGGTC
TGGGCTCCCGC
Sequence 112

Table 1

CGTGGCCGAGCGGTTTGCATCGCCGCTCGCGCAAGGCCATGAGGTTGGTCTGGGTGAAGA
ACGCATCGATGGCGGCACGGGCCTGTTCCGGCACGTAGACCTTGCCGTCACGCAGACGCT
CCAGCAATTCGCGCGATGGCAGGTCGATCAGCAGCAGCTCATCGGCTTCCTGCAAGACCC
AGTCAGGCAAGGTCTCGCGCACTTGCACGCCGGTGATGCCGCGCACCTGGTCGTTGAGGC
TTTCCAGATGCTGGACGTTGACTGTGGTGAATACGTTGATGCCGGCAGAGAGCAATTCCT
GAATGTNTTGCCAGCGCTTTTCGTGGCGGATTGCCGGGGGCGTTGCTGTGGGCCAGTTCG
TTCACCAGCACCAGTTTTGGGCTTG
Sequence 113
GCGGCCAGCCAGACTGGACCCCTTAGCCTCGAGGCCTTTGCTGAAGCTCATGTGAGGGGG
CGACTGCCCCTGACATGGTGTTGGATTCCAGCTGCTGTGGCCCTGAAGGTGGGTGGTGGG
AAGAACGGGAGAATGAAGCCAGCCTTGGGAGAGGTAGGACGCCAGCCCGGCCCAGCTGCT
TCCAGCATCTGGATCCAGCCTCACCTGAAGCCAGCCACCTNCTGGACTGCAAAGTCATTT
GTNAACACCGAAACACAGGGTTTCTGACCATTGCAACCCAGGGTCCCGGCGTGTCGTGGC
T

Sequence 114
TTGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGAAGCAACTGTCAGCTAGTGAGATTA
CTGTGTATGGCCAATCCAGATAAATAAGACGATCAAGTCTTTATGAAAAGGAAAGAAAAA
TTTGGAATGCACATCTCTGTCCAGCTCAATTCCTCACTCCTTTTTTTAAGATGGAGAGCT
G
TTAGGTTTGTCTACACAGTAGGAAACACCTGATTAAATAACAGCATGGAGCCAATCTTGA
CAAAGAAATTGGCTGCATCCAATAGAATCCCAGGGCCGGTCGTGGTGGCTCATGCCTGTA
ATCCCAACACTTTG
Sequence 115
GGCCGGAATCGTTGCACCAGACNAGGCCCCCAGGGCCCAGCTACTCGAAGAACAAGCCAA
TGGATTGGAACGTCCTAGGACAGATGCCACGGCTTTGACCCAGGCTGGGGGTGCACGGAT
CTCACTGGGGTTAGTTGGTCGGAGGGGGGAAGCCCCATGGGTCCACCAGGATGAGGTGTTT
AACTCTATCAGGGTACCT
Sequence 116
GGGGCTCGTCGGTGGCGGCCAGCGAATTGGTGACGACGCTGATCTTCACGTTGCGCCCGC
GGATCTCGCGCATCACCTCCAGCCCCGTGGCACCCGGAATCAGGTAGGGCGAGACGATGG
TCACTTCGGAACGCGCGCGGCGCATCTGCTCGACCACGTTGTAGCGCACGCTGTCGACAT
CCAGCAGCGGCACGCCGCCGTACGACGCGGTCTTGCCCGATCACGCGGTCAGGCGAATCG
GCATACGCCTCGGCGGTGGTCCAGATCAGGCCGAGCTTGCCGGCGTTTGAAGGTCTTCGA
CCATCGGGCTGTAGCCGAGCAGGGTTCGTTTGGGGCGCCGGGCTTCGGCGGGGGCCGGGC
GTTTGGTGTCGGGGGNCCCGGTGGGCCGGCGT
Sequence 117
GATGATGAGCTCCCCGCGGTGGCGGCCGAGGTACTCTAATGGAGCCCTCAGGACTGTCTT
AAAAAGACAAAAATACCTCCTACAGTTGTTATCATCAACGTCAGTTGCTGGCTTTTCCT
A
AATTTGTCTTCTACCTCAGATCTAAACCATTTGATAACATTAGGGCAATATCATGGCAA
T
CGTGGCCCAGTAAAACCATAGCAAATGTTTTCTCCCTAGGACACTATCTGTTTTCACAGG
AAAATTTTTCTCATAGAAAAACTGTAGGAAAAGCCATGGGATGAGCTGAGAAGACCAAAC
CTATCTCTTGGAAAACAACAGTAGGGAGCGTNGGATTAGGAATGTCCTTGGTGCGTGAAA
CAGGCAGACCAATCCTGAAACATCTTTCTCTGGGGACCGTAAGGCATGGAAAAATTTTCT
ATTACACTTANGGAGGGCTTCTAGGGAAACAGGAAACCGACCAAAAATGGGAATGGGGCC
TTAATTCATTTTTTTT
T
Sequence 118
CTCCCGCGGTGGCGGCCGAGGTACGCGGGGAACCGAGGCAGCAGCGGACGTGAGCGATAA

Table 1

TGGCGGATATGGAGGATCTCTTCGGGAGCGACGCCGACAGCGAAGCTGAGCGTAAAGATT
CTGATTCTGGATCTGACTCAGATTCTGATCAAGAGAATGCTGCCTCTGGCAGTAATGCCT
CTGGAAGTGAAAGTGATCAGGATGAAAGAGGTGATTCAGGACAACCAAGTAATAAGGAAC
TGTTTGGAGATGACAGTGAGGACGAGGGAGCTTCACATCATAGTGGTAGTGATAATCACT
CTGAAAGATCAGACAATAGATCAGAAGCTTTGGAGCGTTCTGACCATGAGGGACAATGAC
CCCTCAAGATGTTAGATCAGCACAGGTGGGATCAGAAAGCCCCTAATG

Sequence 119
GGTGGCGGCCGAGGTACCTGAACACCAGGCTCTTTACGGTCCCCTGGCCAGTGAAAGGGT
CTAATATAAAACACACCGAGGCTGAAATAGCCCGCTGCTTGTGAGACCTTCCTCAAGCTC
AATGACTACCTGCAGATAGAAACCATCCAGGCTTTGGAAGAACTTGCTGCAAAGAGAAGG
CTAATGAGNTGCTGTGCCATTGTGTATGTCTGCAGATTTCCCCAGGGTTGGGATGGGTTC
ATCCTACAACGGACAAGATGAAGTGGACATTAAGAGCAGAGCAGCATACAACGTAACTTT
GCTGAATTTCATGGATCCTCAGAAAATGCCATACCTGAAAGAGGAACCTTATTTTGGCAT
GGGGA

Sequence 120
GTGGCGGCCGAGGTACCCGAGCTACCAGGCTGTGGAATGAGACCGTGGAGCTTTTTCGTG
CTAAGATGCCCGTTACGGAAACATCGCTGTCGTTTCAAGAGCTATGGGCATTGTTTCACA

Sequence 121
GCTCCCCGCGGTGGCGGCCGAGGTACAAGTTTATGTTTTCCTTGGTGTAAGGCTTTAACA
GTTCCCACCTTTCAGCTGCCTGGGCATTGATTGCTCACCTACCACTATGACTAGATATGA
TTCCATGTGCTTTTGACTAGATTCTTTGTCTCTTGTGTATGGAAAGTGAGACTTTAAGT
A
ATAGTTACTGCTGAGAGAAATAGAAGACGTGACAACGTTTGCTTTCCCATTCAGTAGTCA
GCGGTTGAATGGAATTATCTTCGTTTTTGGACTGACAGATTTGTTTTACAATTCAGCTA
T
TCCCAAGCCTTACTATTCAAAGCAGAACCCTTCTGTCTTCTTTCTGTAGTTGCTCTCTC
T
CCCTATATTCTGTTGTATTTTTTTTCAAATAACTTATTACTATCTCAAGTAAAATTGTTTT
ATGTTTTGTTTTTATCTACCCTCTTAATCAGGGCAGGGATATGTCTGTTGTATATTTTA
C
TTTTCCCAAATCATAAAGGTTTTGGG

Sequence 122
CCCGCGGTGGCGGCCCGAGGTACACACTGGGATCTCCTTCACTCATTTTTTTAACCCTGAC
TGGGACACCAGAGACATGCTGCATCTTGTATTAGGTGTTTCATCTTGCAGAATGGCTGTG
CTCCTGAAATATTTCCTGTGAAGAAAATTGTTACAATCCCATTACATCACTGGCTTTTA
T
TATTAAATTGGAATGTTGGCTGGAAACAATTTTAACCC

Sequence 123
GCGGTGGCGGCCGCCCGGGCAGGTACGCGGGTGTGCAACTGCAAACCAGTAACCTGCTAT
GGCCAATTGTGAAGAGATGGGAGTCTCCCCGTATTGCCCAGGCCGGTCTCAAACTCCTGG
GCTCAAGCAATCTTCCCGCCCCACTTCCCGAAGCCCTAGGATTACGGGAGTGAGCCACCG
CACCCAGCCAGAAAAACGTTTCAAATATTGGAAAACCTTACTTTTTTCAATGAGCATTT
T
TGCATCAAGGGGTAACAGGGACATTAGGCTTTTTTTTCTCTTAGACTCCAAACAGTAAGGT
CAGAATTTATCAAGACATTACATAGGAGTAAGGGCACAGCCAGGGGGTGGTGGGGGGGAG
GGACATTTTCCAGCA

Sequence 124
GCTCACCGCGGTGGCGGCCCGAGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGC
TGCGACAAACACCCCACAAAATGGCGGCAGCGCCGTCGCCCTAGAATCCCCCGAGTCGCC
TCTCCCCGCGTACCT

Table 1

Sequence 125
ATTCAACAAATATTTATGCATCAGCTACATGCCAGGATCTGTAATAGATTCTGGGTGTGC
AGTAGTGATTACTGCAGAATGCAGACATGGTCCCTGCATTCTTGAGAGGGAGACAGCAAC
CAAATAAACAATTACAAAAAAGTATGTAACTAATTAACAAGTGGGAGAAGGGAGTGGGAT
TACACAGCAGAAGTGGAAGGAAGGGCCCACTTAGAGTGGTCAAAGGCTTCTTGAAGGTAA
CATGTAAGCTGAGACCTGAAGAAGGATGCAAAAGGGCCAGCATGTAAGGAACAGAGAATA
AACATCCCAGAAATAGAAAATAACACACAAAAACCTAAAGTCATTAAAGAACATGATCAT
CTTTCAAGAACTAACCCTTGAGATCAGAGTAGTTTGATTATAGAGGAAAAGGGTGAGTGC
AATGGAAACGTTAAAAATAGCCCAGATCACGTAGAGCTCTTAGCCTTTTGGTAGAAAAA

Sequence 126
GCTCCCCGCGGCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGA
CAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGC
TTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGA
ACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTG
CTTGGCAAAGCATNCAGAGAAGCTGCTACTGTCCTTTCTGGGGCCGTGTGATGGAGANGT
TAAAAATTTGGAATCTAACTCAAGNGGGNAATGNATTCCGNACCCTNCGGNCGNTNTTANA
ACTAGGGGGATCCCCCGGGGCTGNAGGGAATTCGANTAAAGCTTNNTTANTCCCCGCCAC
CNCNNGGGGGGGGGNCCCCCNNCCCATTTTTTTTTTTTNTTTANGGGGGGNTAATNGCCCCC
GGGGGAAAAAANNNNANAAAAATTTTTTTTNTNGNGGAAAAATTTTCCCCCAAAANTNTNCA
NNAAAAAAAAAAGGGG

Sequence 127
GTGAAAAAACAAGAAAGCTGAGAGAAATCAACATGTTCCCAAGTGCTGTATGTGAACAAT
AAATCTGAGACATACCTCTAAGGCTTTTCCAGAGACAAGAAGCTCTCAACCTGTAAAGAA
TTCCTGGGACATGACTGAGAGCAATGAGAACTCCAGTGNCAGAAGGTTAGCAGATATAGT
GTAGAGCATACACAGATATACTATAGTTCATAACACTGGTGGCTTAGCTGTAAATCACAA
AATAGCACTGGAATTATCTAGTGATCATAGCACATAGTCCAAGAAGAAAAAATTTTGATC
TTGTCTTAAACTTTGTGGAGCCAGTGGTGAAATGAGTCACACAAAGATGCAACAATGATT
GAACCCAGNCCTCTTTAGACTAACATATTCTTGGCCATCACCNCCAATATTACAATAAAA
ATCAAGACCCATGAAGGAGCATACCTTTTTCTGNAAGNAAATATTGNTTACCTCAGCTCT
ATTGGTATTTGATGCAAAACACCCACATGCAATTTGGATCAATAAGACATGGGAAGGGGC
CAAAATGNNACTTCATGCTTAAGGAAAAAAAAGGAGNGGGAAGGAGGNCACCAAAGCNGG
TNCNGNAATGGGTNAACTTGGGGCATTATANGGGGGNGCTTTAAAATACCATTTT

Sequence 128
GCGATTGGAGCTCCCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTTGAAACG
ACAGCGATGTTTCCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAG
CCTGGTAGCTCGGTACCT

Sequence 129
CGCGGTGGCGGCCGCCCGGGCAGGTACAGTCAACGGCCGAAAACCACTGAGCTTTTCCCT
CTGCCTGGCACATATCCACTGCCCTGCCTTCCTTCAGCTGATGAACTCTTCATATGCCTC
CTTTTGGGTGTCAGTGGAAATGTCACTTCTTTCTAGAAGCTTCTCTGGCTCTCCCAGC
CT
GGCCCAGGGCTCCAGCTATGAGCTTCCATAACACCCCTAGTTTTCCTCACATTGCCCTCA
TAGTATATGGAATTTGTTCATTCAATTGCCTGGCTTCCAACAGATGCCAGCTCCAAGAAG
GCAGGAGCTGCTTCTGGGTATTGCTTGCCATCAAGGCCCTCACACCCAACCTAATGCCTG
GGCCAGAGGTAGGTGCTTAATAAAAAATTGTTTGAGGCCGGGGCGTGGTGGCTCACGGCT
ATAATCCCAGCACT
T

Sequence 130
GCCCAAGGGGGGGGCCAACCCACATTATTTGNNTGGGGCNNNCTGCCCNTTTTTTNAAAANNA

Table 1

GAAAANCCTTNNCCCCCCTTTTTATNAAATAAACCCCCCCCNNNGGGGNGNGGGGGGGGG
GGGNGTNATANNNGNANNNNGTCTCNTNTTTTNTCCTTTAATTCCNANAAATAAACTT
GA
CNTTCGCTTGNGCTTNGGNNGGTTTCGGGCTGCGGCGAAGCCGGTATTCAANCTCACTCA
AAGGGCGGNTAATACCN

Sequence 131
CCGCGGTGGCGGCCGCCCGGGCAGGTACCTATCTGCAGAACGGTCATTAGCAGTTTTTCC
AAACAAGCGACTTTTAGCAAATTAACCGTTAATTTTAATGAGATTCAAAAGTTAATAGC
C
ATTCTTAACGTTTTATAATTAGAAGCTGTTATATAATTAGAGCTGGACACCCACATGGA
G
AAACTAATTTGACTGTGCTGCATTTGACTTCACTTTGGTAACAGGAAGCACTTTTTAGT
C
TGTAGACCCTTGGGAGTTGTAGGGAGTTAAAGCTGATCATTATATACTATTATATACTT
A
GGGATACAACCCAAGGGCAACCCCTGGCCTTTATGAAAACCTGGAGTGAGTTATTATTTC
CTGGTAATACAATTCTCTGCCAGCCAGTTGCTGCATCAAAACAGTTCTGATACACACACC
TAAAGTCACCACTTCCTCATTCTGGTCCCCAATAACCCTATAAGCCTCTCCCTTGGAGGT
GACCTCTGCCCTGTGAAGGGTTGGGCTC

Sequence 132
CGCGGTGGCGGCCGAACCGTGGTGGCCGTGATCGTGCCGTTGGCGGACGGAACCTTGAAG
ATGTTCTGGGCGGCCAGCACAATCGCCGCCTTGCCGACGATGACATTGTTGGCCTTCAGC
CCGTCAATATCGCCCTTGATGTCGATGTTCTGGCTCTCCTCATCATGGCTCAGCGCAATG
GCGGCGTTCGCCTTGCCGGTCGCCTCCACGAGGAACAGGGCTGCGGCCGTCGACACATCG
CTGGACGCGAGGGTCAGGTTGCCCTGAAGCAGCCCCTTCTTGTCCTGGGTGACATCACCG
CGCAGCCGCGTGCCGCCGGCAATGAACTGGATATTGCTCAGGCGTTTTTCGTCCTTGTGC
AGGGCAAGTTCCGTGGCAAGATCGGCCCGCACGCCGTCGAGGAACGCCAGACCG

Sequence 133
CGGTGGCGGCCGAGGTACGATAATTCATGCCAATTTCTTTGGGAATACTTGTTTCTGATA
TAATAGGTTACAAAGCAAAATTGAGATGATTTTTAAAATGCCATGCAGTTATTTTTTCT
G
AATAACATAAATTTTAAACAGAGACCTGAAAAAAAACCCCAAAAGTATTAACCTTTAAATA
CATAAACTCAATAGAAATAATTTAACTGCCTTCTCTTCACAAGAGGCAATCAGAAGGCAG
GACTATAGTTTTCTGTGTTTCTTTTCCACAGGAGAGATAATTACATTTCTAGAGACCCA
T
AGAAACAATTCCATAGTTTTAATTTC

Sequence 134
TNGACTCCCGCGGTGGCGGCCGCCAAGTGTTGGGATTACAGGCATGAGCCACCACGACCG
GCCCTGGGATTCTATTGGATGCAGCCAATTTCTTTGTCAAGATTGGCTCCATGCTGTT
AT
TTAATCAGGTGTTTCCTACTGTGTAGACAAACCTAACAGCTCTCCATCTTAAAAAAGGAG
TGAGGAATTGAGCTGGACAGAGATGTGCATTCCAAATTTTTCTTTCCCTTTCATAAAGA
C
TTGATCGTCTTATTTATCTGGATTGGCCATACACAGTAATCTCACTAGCTGACAGTTGC
T
TCCCGCGTACCT

Sequence 135
TTGAGCTCCCCGCGGTGGCGGCCGAGGTACCTCTCCTGCAGGGCCCTCCATTCAGGGTCT
TCCTGGAAAACCCCCTGGAGGAAGCGCTCCTGTTGCAGTCGGAGTGAACACCCGTCTTGT
TTAACCACCAGCAGGGGGATTCCTTTCTGGAGAGTCCATGTAGTCATCATCTCTTTGACC
TCTGCATTTTCCCCCAGAAAGGCGAGCATGTTACTTGTCATCTTGGGATCCGAATGACAA

Table 1

ACTCCACCAGATGTAAAATCACTTTCTAAACAACTATTTGACAGACTGCTCCACAAGTCA
TCATTCTTAGCATTTCTATAGCTGAACTTCTTTAAGTACCTGCC
CG
Sequence 136
AGCTNCCGCGGTGGCGGCCGAGGTACTTAAAAGTATATCANGGGCAGTTTCATGCCACGG
GAGCCAGGGAAGGCACCCAAGGAAGTGATGGAAGAGTAGAAGTTCACCAGGTGCAGCTCA
GGAAAGGGCTCAGCAAATTTCTCTGTAACAGGATGCAGACCCCGCGTCCTGCCCG
Sequence 137
GCCGAGGTACTAAATTTAGCAACTTTATTCATGAGGAACACCAGTCCAATGGTGGTGCTC
TTGTCCTTCATGCTTACATGGATGAACTCTCATTTTTGTCTCCAATGGAGATGGAGAG
AT
TTTCTGAGGAGTTTCTTGCTTTGACATTCAGTGAAAATGAGAAAAATGCTGCTTACTAT
G
CTTTAGCAATAGTGCATGGAGCGGCTGCTTATCTCCCAGACTTCTTGGACTACTTTGC
TT
TAATTTCCCCAACACTCCAGTGAAAAATGGGAAATTCTGGGCAAGAAAGATTTTTGAACC
ACCCCCCATTTTTAAATTTTTTTNACCTCAGGGGGAANNAGGGACNATCCTGGNTGGGGGNCC
CNCACCGGNGGGGGGNTCCNTTTTGGGGGGGAAAAAAANATNTTTNTTGTGGNNCNNAANAAA
AAAAAAAAAANNGGGGGGNTTTNTTTTTCCCNNCCCNTTTTTTTTTNTTNTANAAAAAAAA
C
CCNCTTTTTTTNAAAAAAATTTT
Sequence 138
TNCCGCGGTGGCGGCCGAGGTACTCGGGAGGCTGAGACAGGACAATTGCTTGAACCTAGG
AGGTAGAGGTTGCAGTAAGCCAAGATCGTGCTACTACACTCCAGCCTGGGTGACAGAGTA
AGACTCCATCTCAAAAAAAAAAGAAAAAAATTGACTTTGGAACCTCAGATTACATATCAG
TTTGCATACATGCTAAACAGAGAAATGTCCTCAAAATTCAGTTACTAAAAATTACTGAT
A
TCTCCATGATTAGAACCACACTGTGGTTGTGTGTGTAGTCAAAGGAGGAGAATTTTTAAT
GCTATATAAGCATAACTGATAACTGCTATTACAAATAAATATTCCACAAATTTGGAAAG
T
TATTAGAGGAAGAATTTTTTTTTCCTTGTAATTTCCAGGTGTTTATATTAGTTGGGCCAT
A
GTGAAAATTACATGGAGGAAAGAAAATAGGGAAAATAAGTCACAGAAAAAGAAAA
Sequence 139
TTGGAGCTCCCCGCGGTGGCGGCCGAGCCCAATTCTTGATTTCTTTCCATCCCAAACTCT
TTAAACTCTTGACCTCTGCAATTCAAGTTGTGAACATGAAACTTGTCTATCACCAGCCT
C
TTCTCTGCATTCTCTTTCCCTCCTTGTTATGCTAAAACTTGGATGGCCTCTGAAGATAC
T
GCTCTTCACCCCTCTGAAGGGGGCTCCTCANGGGAAGGTACC
T
Sequence 140
TCCCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTTGAAACGACAGCGATGTT
TCCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAGCCTGGTAGCTC
GGTACC
T
Sequence 141
TNCCGCGGTGGCGGCCGAGCCCATTCTTGATTTCTTTCNTCCCAAACTCTTTAAACTC
TT
GACCTCTGCAATTCAAGTTGTGAACATGAAACTTGTCTATCACCAGCCCCTTCTCTGCAT
TCTCTTTCCCCCCCTTGTTATGCTAAAACTTGGATGGCCTCTGAAGATACTGCTCTTCA
CC

Table 1

CCTCTGAAGGGGGCTCCTCAGGGGAAGGTACCT
Sequence 142
NGGTTGCGCTCACTGCCCGNTTTTTCCAAGTCAGGGAAAACCTTNGCNGGCCCNNTTTNG
TTTTAANANAANNTGNGCCNNCCCCNCGGGGGGGGGGGGGGNNGNTTTTGNATNTNTTGGGG
CCNNTTTTTCCCTTTTCCNNNAAAAAAAAAAAAANCNCNNGGCCCCCNGGNNTTTTTGGGG
GGGNGGGGGGGG
Sequence 143
NNGACCTAACCTNACATTTAAATNGCGGTGGCGGCTTAACTGGCCCGCTTTTCCAAGTCC
GGGAAAAACCCTNTTCCNNGCCCAANCTTTGTANTAAANGAAATCCGGCCCAACCNCNCC
GGGGNGAAGGGNGGGTTTTTNGCNATTATTGGGGCNCTTTTTCCCGTTTNTTTGNTTNNN
NNNANACCCCTTNNGCCNCNGGGGGGGATTGGGGGGGGGGGGGGGGG
Sequence 144
GAGCTCCCCGCGGTGGCGGCCGTTGCCCTTACATCTCTCATTTGGAACGTGACACGGTAT
TAAATAACGGCATATGAAAGCTTAAAAGTCATCAAATACAATCACTGGGTACTTTCGATT
ACCCAAACCAGGCACTTTCCTAAACTCCCCACTTCTTTACTTCTGCGGTCTCCTTTCTT
T
TATTCCCCCGCGTACCTGCCC
G
Sequence 145
ACTCCCCGCGGTGGCGGCCGAGGTACCGAGCTCCNGGCTGTGGAATGAGACCGTGGAGCT
TTTTCGTGCTAAGATGCCGTTACGGAAACATCGCTGTCGTTTCAAGAGCTATGAGCATTG
TTTCACA
Sequence 146
CTCCCCGCGGTGGCGGCCGTTATGCTTAGCCNGTTTATTCTTTATTTTTTTTACTGGAG
TC
ATTGCCAGTGATGGAAACGGTGTTTGCTTCTCTTTCAGTCAAGATCTGCACAAAGTATAG
CATTAGGTGGTATTTATTGTTTATATTATGAGTTCTACATTCATCTTTCCAGCACTCTGA
AGTTATCAGCAAGTTCTCAGTCAGTTCAAGGCATTGGATTCTGCTTGATTTCTTTTTAA
T
TCATTGTTTTTGACCCCTTTGAGAGTTTTAATAGAGAGGAGTCTGGAAGGCAGAGATCTC
CACCACCTAACCGTGAGAAATTTGGAACTAAGGACTTGCACTGGTCCCCAAGTTAACAGG
GGATATACTTCCTGCATTTTCTCTGNTCTTTCTTGCC
Sequence 147
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCAAGGTGGGCATTTTTTTAAAAA
ACCCATGGAAATAAATGCTACTTCTTGTTAGTGTTGTTTGAAAATAAACAAAGAAAATGC
AAACAAAACAAAAACCATGGTCCATTCAAGCTCAAGAGTATTTAACCAATGCTCTGTTGC
CTCTTAAAGGATTGGTAGCTATTTCCCCATCTACAAATACATGACAATTAACTAAGCCCA
ATTCTTTAAAACTATCTGGAATTAGGTCAAAATTATCTAATTTTTTTTCTGATTTAATTAT
GGATTACCGTAATCCAATAGTTGGCAACATTATAAAACCCTAACTTTACCTCATTGGTT
T
GGCTATACCAAGGTCTCATGGACTCTTGGACATAACCACCATTCTTTCCTNCCAACACCC
CGGNGTACTTCAGAGTAAAACCCGGGAGCCTTCATGATAACCATGAAGGCCCGGAAGCTT
CTGGCTTCCAAGGCTTTCTNTNGGCCTNACCTTCCGGTGGTTCCTTTTCT
Sequence 148
GGGTGGCGGCCGAGGTACCTNTGTGCGCGGTGGNCGAAAAGCACCTGGGTCGGGTGCAG
ACTGCGGAGCNGGGCCCTACCGTGTGCGCAGAAAGAGGAGGCGCTGGACTTATCCTACCT
TAAGTTGAAGCAGACCAGCAATTGTTGTGACCTACAATCTCCACACCCATCTTTACTCTG
AGCCAAGGAAGTGTCTGTTCTTGTGCTGAGTTTNAGGGGCCTTCAGCTNGNGGGAAATCC
CNAAGA
Sequence 149

Table 1

AGCTCCCCGCGGTGGCGGCCGAGGTACCTTCCCCTGAGGAGCCCCCTTCAGAGGGGTGAA
GAGCAGTATCTTCAGAGGCCATCCAAGTTTTAGCATAACAAGGAGGGAAAGAGAATGCAG
AGAAGAGGCTGGTGATAGACAAGTTTCATGTTCACAACTTGAATTGCAGAGGTCAAGAGT
TTAAAGAGTTTGGGATGGAAAGAAATCAAGAATTGGGCT
Sequence 150
CNCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATTGCTCTTGAAACGACAGCGATGTTT
CCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAGCCTGGTAGCTCG
GTACCTCGGCCGCTCTAGAACTAGT
Sequence 151
CCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTGTTTTTGTTT
T
TTTCTGTCCCCTCTGAGCCATGGAAGATACTGGAGTTAACAAAAATTTTATAAACTAAAG
AAAGCAACTTTATAATCTAAAAGAAAGCAACTTTCCCTCCTGTCTTTTGAATTCTTATTC
CTGAAAGAATGGATAATGAATCAGGAGATGAGCAAAAACGTATCTTTTACAAAGCTCTAG
TCTTCCAAAAGCCTCTAAACTCAAACGAAACCTTTTTAAAGTAGTTTTGTAAAAGCTCA
A
GGTATGCCATTTCCAGAAAGTTGCAGATGAGCACCATTGGGCATTACCCAAATTCTGTCA
CACATTGAGCAATGAAATTCAGGGAATTGGGACAATGACCTCTTGGGCATATGAAAGAAT
TAAAAGAGGGCTAGGGCTTAGGGAGGGGGGATCTAATCGGGAGGGGATGTTCTGTCCCNA
GCCCTTCCTTCCTTTCT
Sequence 152
TNCCGCGGTGGCGGCCGAGGTACNCCTAAAAAAGTACTGCAGCAGAGAAGAAAACATTGG
ACAAAGAAGAAAGGCGACAGAAGGCTAGAGAGAGGCAGCAGAAATTGCTTGCGGAGTTTG
CTTCACGACAGAAAGGCTTTATGGAAACTGCAATGGATGTTGATTCTCCTGAGAATGATA
TTCCTATGGAGATCACCACGGCAGAACCACAGGTTTCCGAGGCAGTATATGACTGTGTTA
TTTGTGGACAGAGTGGCCCCTCCTCTGAAGATCGACCTACTGGATTAGTTGTACCTGCCC
G
Sequence 153
GCGGTGGCGGCCGAGGTACACCTGCAACTGTGCGAATGGTCCTGTTGCCTCCTGCATTTT
GGCCTCTGTTCTATAAAGGAAGAGTAAAGATGGAGCTCCTCCTGCCTCCATCACGAAAGC
ACATATCATCTGTCCCTTTGGATTTTACTTCCAGGACGCGTGTCGTCCCCAGCGTGTG
TT
GCCTTATGGTGCCGGCAGAGCCTCAGCTATCTGCCTGGGAAGTCGGATGTCCTTGGAGAG
AATTTGGAATGCAGATAATTTTTCTTATTTCTTGAGAGCTTACTTTAATCAGCATGACA
C
TACCTAAACACTGAAGATGGCCTTATATTAGTAAGATTTGCACAAAATTAAGTATACCT
A
TGCAAACTATTACTTTGGTTTTTAGGAGTTTGATCAGATGAAGAAGTNATGGTATCACA
T
ATATATGTAAGAAGGCCAACCCATCATTATTTTTTGNAAGTGNTTTTTATTAAAAACC
Sequence 154
CNCCGCGGTGGCGTNCGGCCCCCGCCTTTTCTGCGGCTTTCAGCTGCGCGTTTCAGGTCG
TCAATGAGGTCGTCGGCATCTTCGAGACCGATGGACAGGCGGATCGTGCCCTGGCTGATG
CCTGCGCCCGCCAGCGCTTCGTCGCTCATGCGGAAATGCTGTGGTGCTGGCCGGGTGGAT
CACCAGGCTGCGGCAATCGCCCACGTTGGCCAGGTGGCTGAAGACCTTGAGGGTTTCAAT
GAACTTCTTGCCCTGCTCGCGGTTGCCCTTGAGGTCAAAGCT
Sequence 155
CGCGGTGGCGGCGCCCGGGCNGGTTATAAAAACGAACATGTATAAACGCTTACGCAAACC
CTTTTTAATGTTCTGAAGTCAGTCTTTGTAAGTGAAATCGCTGGAGACTAGAAAGTATG
A
AATGGCAGTCTACCTGGGCAACCTACAAAAAAATTTAGCTTGAAAAGACTTCAGTCTCCGC

Table 1

TCCCCTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAGAACTGGAAAATTATTTA
GGAAAGTTTGTTAACTACTCTTTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAG
AACTGGAAAATTATTTGGGAAAGTTTATTAAC
Sequence 156
CTGGCGGCCGCCCGNNCTGGTNCTTNCATCTNGGCTNCCTATANGCTNTCTTTTTTACAG
ACGGCCATGAAATGCAATCCAGCTGAAGTATTATCATCTTGTAGCATTTCAAAAGGAACC
GTCGAAGTCATCCAAAGGATGGGAACCACAATGTTCTTGTTGTTCCTTGGGTTTCTTA
AT
GATTTCTGAATCATCATTATTAATTATGGAATTCTCTGGTCGAAAAGTCACATTTGGTT
T
TCTCCTCAGTTTCTCACATCTTTTTTTCTTGCAGCTCTTTCTCAGCTCTTCTTCCTTGCCT
TTTTTTACTGGCCTTTCCTTGTCTTACTTCAGGTGGTTCTATTTTGACCTTTAAGAAGG
T
TGAAGGGTGGTNCAAGCATCACCTTGGTTCNAATAAAATTAATGGTGTTAGGTTTCTGGT
GGCCTTNGTTTAAAACGCAAATGGGGGTTTTTNANGGGGGGANAAGGTTGGGGT
Sequence 157
CCGCGGTGGCGGCCGAGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGCTGCGAC
AAACACCCCACAAAATGGCGGCATGCGCCGTCGCCCTAGAATCCCCCGAGTCGCCTCTCC
CCGCGTACCT
Sequence 158
CCCAGGGCCCAGCTACTCGAAGAACAGCCAATGGATTGGAACGTCCTAGGACAGATGCCA
CGGCTTTGACCCAGGCTGGGGGGTGCACAGGATCTCACTGGNGNTAGTTGGTCGGATGGGA
AAGCCCCATGGGTCCACCAGGATGAGGTGTTTAACTNTATCAGGGNACCTTGCCCGCTCT
AGAA
Sequence 159
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACAGGACCAATGCTGCCCATCCCATGGAAT
TTACAAACATTCTACAGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGG
AGAGGCTGTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTACA
CCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCAT
ATGACTTTGATATTCGTGTGCCTTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCA
A
TAGTCCCACAGATCGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTGCTGGGC
TCGACACACCTCCTGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGC
CAGGTAACAGGTTTCGAACAAACAAGAAGGCC
Sequence 160
TGGCGGCCGCCCGGGCAGGTACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAA
CATTCTACAGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCT
GTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTACACCGCCGA
CCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCATATGACTT
TGATATTCGTGTGCCTTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCAATAGTC
CC
ACAGATCGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTGCTGGGCTCGACAC
ACCTCCTGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAA
CAGGTTTCGAACAAACAAGAAGGCCAAAA
Sequence 161
CGAGGTACCATCCTATTAATACTAACTTCTGCTTCTACATACTGTAGACCTTTCTGGAT
G
ATAGAAATCAATGCAGCGGGTGGGACGAGGGCACCATTTATATTGGACTGACTGATATGG
CTTTCTATACCAAAGGTAAATGCTGAATGAGAAAATCCTGACTCTTGCAAGTATCTATA
T
ACCAAGAAGTTGACCTCATCACTGCTTATACTCATCTTTATTCCCACTTAAACCATGAG

Table 1

G
TCCCAACACAGGATATAACCCATTGGGCAGTGCATTGATGTGGGGGATGTGCAACTGANT
ATNCCGGTCACCCGCCAATCACAAGTTTGCTGGTGTTGATGCTGGAAACGGTGGCCTCCA
ACGCCGCTCCCCCCTCCCGGGAA
Sequence 162
GGCGGCCGAGGTACCTGGCCTGCTGGCATAGTTCTTTGACCCGTTCATATTTGGGCAAGT
GATTTGACTGTTGGATATTCTTGCTGGATTCCTCCTTCTTACGTAGAAATTTGCCTCTT
T
CCACTAGGAATGTATCACGCCAAATTTTGGCCTTCTTGTTTGTTCGAAACCTGTTACCT
G
GCTTTTCTGGGTCCAGAAGTTTGAGGACAGACTTGCCGTCCACATCAGGAGGTGTGTCGA
GCCCAGCAATATCCAGGATCGTGGGGGCCAAGTCAATGTTGAGAACGATCTGTGGGACTA
TTGATCCTGGTTCTACACTTGGACCACGAATAAAAAAAGGCACACGAATATCAAAGTCAT
ATGGCATGGATTTCCCCTTGACCAGTCCAAACTGCCCAATATGGTAACCATGGTCGGCGG
TGTA
Sequence 163
GGGGCCNCGCGTCCGGGTGGCTCTATGTAGTTCTAATTTGCATTTCTCTAATGACTAACG
ATGTTAAACATATTTTTATGTACTTGTTTCATGTACTTGTTGATATGTCTATTCAATTCC
TTTCACCATTTTTATGGAGCTGTTTTTTTTATTATTGAGTTGTAGGATTTCTTTATATATG
CTGCATACCAGGCCTTTGTTATATACATGCTTTGCAATGTACATTGTCTTAAAATCTGT
G
GCTTGCCTGTTCAATTCATTAGTGGTGTTTTGTTAAGCAGTTTTTAATTTTGATGAAGT
G
TAACTTATTCATTTTTTATTATGGTTATTGCTTTATGTTTCAGGTCCCAAATTTTGCCTT
CTCACAAATCACAAACATTATCCTATGTTTTCCTTCAAAAATTATATGGTTTTATGTATT
TTCAATCTCAAAATATTCTCTAATTTTTTTGCTGATTTATTTCTAAAGAAATTTGAGGGA
TTTGCTATAATGG
Sequence 164
CCCCGCGGTGGCGGCCGCCCGGGGCAGGTTATTTAATTTCTTAGTGTCTCAATTTCCTCC
TCTATAAAACAGAGATAATAGTATTTAGCCCAGAGGGTTGTGGTGAAGTGTGAATCATTT
CTCCATGTAAAACACATAGGACAGGCTGGGCATGGTGGTGGGCACCTGTAATCCCAGTTA
CTTGAGAGGCTGAGACAGGAGAATCGCTTGAACCCGGGAGACGGAGGTTGCAGTGAGCCG
AGATAGTGCCACTGCACTCCAGCCTGAGTGACAAGAGTGAGAGTCCATCTCAAAAAAAAA
AAAAAAAAAAAAAAGTACCT
Sequence 165
NCCTGGCATCAGCNATTAGNAATCAACCTGTTAATCCAAGGTCTTTAGAAAAACTTGAAA
TTATTCCTGCAAGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAGAAGG
GTGAGGAAAGAAGATGTCTGAATCCAAGAATCCGAAGGGCCGTCAAGAAATTTTACCTGA
AAGGCAGGTTAGGCAAGGGAAAAGGGGTCTAAAAAGATCTCCCTTAAAAACCAGGAGGGG
GGAAGCCAAAAATCCGATGCCAAGTGCTTTCCCAAAGGGGATTGGGGACCACCACCAAGA
GGGCCTGGCCCTTCTTCCCATCACTTTCCCCTTACCATTGGGGAGGTAATTATTGTCAAA
GGCCATTAAATTTGGTTTCTTTAAGTTTTTGGCAGGTTTACCGCCTTAAAAAAGGGTG
GA
CCCAAATGGATTGGGTCCACCCAAAATCNAGGCTTGCTTACTTACTTCCCTGGTAAGGGA
A
Sequence 166
GTGGCGNCCGTNCGGNCAGGTACTTGCTCAGCCTTTCCAGGCCCCTNTGATGAGCTCTCT
AATCAGCAGGACCAAGGTGTGAAGTGGGAATGAACATGGATCCATCCCATTGGATGGAGA
AGAAAGGTGGACAGCCTGTTCGTCTCTCATGTCAGCCTAGGGCTGGGAACAGTTTGTGAG
GACTTATCTGTTGTACCT

Table 1

Sequence 167
GCNGGCCGCCCGGGCAGGTACGCGGGAATGGGCACNNTGNAGCGCAAGTAGGTCTACAAG
ACGCTACTTCCCCTATCATAGAAGAGCTTATCACCTTTCATGATCACGCCCTNGGGNATC
ATTNTCCTTATCTGCTTCCTAGTCCTGGTATGCCCTTTTCCTNAACCACTCACAAACCA
A
AAACTTAACTAAATAACTTAACAATCCTNAGAACGCCTCAAGGNAAANTAAGAAAACCCG
TCNTGAAACTTATTCCTGCCCCGCCCATCATCCCTTAGNTCCCTCAATTCTGGNCCCT
CN
CCAANCCCCTACCGCCAATCCCTTTTTACAATAAAACAGGACCGAAGGGTCCAAACNGAA
TCCCCTCCCCNTTACCCATTCAAAAAATCAAAATTNGGCCCACCCAAATTGGANNACCTT
GAAACCCCTAACCGAAGTTACCCTTCGGGCCCGCTTCTTAAGAAACTAAGGNGGGAATCC
CCCCCNGGGGGCCTGGNAANGGAAATTTCGGATAATCAAAGCCTTAATTCCGAATANCCCG
GTCCGAACCCTTCGGAGGGGGGGGGGGGCCCCCGGGGTACCCCCANGCTTTTTGGGTTTCC
CTTTTTA
A
Sequence 168
ATNTTCAGGAGACGCTCNGTAGCCCTCGCGCTNTATCCTNCGGNACAGTTCTGCGGAAGA
AGTGGCTCACGCCTTCCAGAGCCACATCATCGCGGNCGAAAGNGAAGCCCAGAGAGAGGT
AGGTGTAGGAGGCCTGCAGGTACCTCGGCCGCTCTAAGAACAANGNGGATCCCCCCGGGC
TGCAAGGGAATTCCCTTANCAAAGCANTANTNAAACCCGTCCGNCCNNNCAGGGGGGGGG
CCCCGNTACCCNAANCTTTTGNNNCCCNTNATAGAGAAGGGNGAAAAAATNANGCCCNCC
TNGGGGCAGNAAAAAAATGGGGACAATAAAGCTNTTNNNCNNGGGGGGNTNAAAAANTTGT
TAAATCCCCCNACCANNAATTTTTCNCNAAACAAAAAAATAAAAAANCNCCGNGGANNGAN
AAAAAAAANNGGGNATAAAACACCCCNGGGGGGNGGGTCCCCNCAAAGNGGGGGGGGGACCN
CCNCCCNAACAATTAATGTGGGGNGGGGNGGANANANAATNGCCCTNNTTTTTTNTANNGNG
ANNAAAAAANNCTTGGNGCNGNCCCNNACTTCTANNTAAAAAAAAAANACCCCCCCNCCCCN
CCCGGGGGGNNAGNGNGGGNNNGNTTNACTTTANNNGGGCNANNTTTTTCCNCCTTATNNAA
AAAAAAAAAAATACNNGGCACNNGGGAAATTTNGGGGGGGGGGG
Sequence 169
TTTTGAAGCCCNCTTNCCGCGGNGGCGGCCGCCCGGGCAGGTACTTCCACTATTATTGAA
TGTATTCTGTATTATAATTGTATATTTGATTGCCTATCTCCCCTCAACTGCATTATACAT
TTTCATGGGTGAGCCAATGTCTTTTTCACTCTATTTCAGTGCCCTGCACATTTTCTGGC
A
CATAGTAAGCATCCCATGAGTATCTGATGAATAAATGTATTTCCAAATTCAGGTTCAGT
A
TCCTTAATCTGAAAATACAAAATCCGAAATGCCATAAAATTCAAAGCTTTTTGAGGACTG
ACCTCGTGCTCAAAGGAAATGCTCATTGGAGCATTTTGGACTTCAGATTTTCAGATTAGG
GATATTCAACCCGTAAGAATAGTGCCAATATTCCAAAATTCAAAAAAGTCTGAAATCCAA
AACACTTCTGGTCCCAGGTATTTTGGATAAGGGATACTCAACCTGTACCGTAAAATACAT
GCATACTTTCGATAGCACATGTGAAGGTATCTCTCTAAAATTGACCTCATTGGTTTCGT
T
CTCAAGCAAACTGACCTGGGGCCACTCAACATGGCTTTTATCGNGCCTGATGTTAATGCA
TGTCTCTTTTTACAATA
Sequence 170
AAGTCTACATTTTATGTAGTGGTTAATGTTTGCTGTTCATTAGGATGGTTTCACAGTTA
C
CATACAAATGTAGAAGCAACAGGTCCAAAAAGTAGGGCATGATTTTCTCCATGTAATCCA
GGGAGAAAACAAGCCATGACCATTGTTGGTTGGGAGACTGAAGGTGATTGAAGGTTCACC
ATCATCCTCACCAACTTTTGGGCCATAATTCACCCAACCCTTTGGTGGAGCCTGAAAAAA
ATCTGGGCAGAATGTAGGACTTCTTTATTTTGTTTAAAGGGGTAACACAGAGTGCCCTTA
TGAAGGAGTTGGAGATCCTGCAAGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAA

Table 1

ACAATGAGGAACATTTCATTTGACCCAACATCCTTTAGGAGCATAAATGTTGACACTAAG
TTATCCCTTTTGTGCTAAAATGGACAGTATTGGCAAAATGATCCACAACTTCTTATTCT
C
TGGCTCTATATTGCTTTGGAAACACTT
Sequence 171
GGCGGCCGCCGGAGCGGCGCGGAGCATGATGGAAGTCGTAGTAGGAAATGGCGTCGTGGC
ATTGAGGGGGCATCCCTCCTAGAACCTCCAGGAAAAGCTCGCGGAAGACGAGGTTCTGCG
GAGAGAGAGGCTCCAAGCAGTCTGGGAAGTGTAGTCCAGTTGGCTTAGCAGTAGTTTCGT
TGGGGGGGAGCCCGAGGTTCCGGGAAGGGGCTAGGCCGGCTTGAAAAGAGATTATGACTG
TACCTCGGCCGTCGAGCGGCCGCCCGGGCAGGTACAACTTTTATACAACTCAGGAGATTA
AAAAAAAATCTCCACAAGAAGAAGCAACTCANCAGGCCCTGGCATTAAAACATTTCCCAG
AATAAACAGATATGCATTGCATTAAAGGTAATTTTCAAATATTTAAGTTACACCAAGATT
TCCCTCCAATATGTGCCTTTCTCAAACCAATGCAACTAATTCATTGCTAATACTGGGG
CA
TGAATTTTTTGGCAAATGTTTATGGTTTTACTTTCTTCATTAATCAAAAAANT
Sequence 172
CGGGTACANATTTAAGGTAGATGGACTCAGGGTAAGGATAGCTACAGCTGTGTGGGGCTG
AAGGTCTGTGGCACTGAGCTACTGGGGAAGGAGGGCTCTGTTTTCATNGTGACACACTGA
GTTAATAAAGCACTTACTGAGGGAGCCAGAGCCCAAACTCTAAATGTGCTGTAGAAAAAG
GGCCAAGTCATTGACTGCACCACTCCTTCAGCCAGAGGTAGAAAGGATTTACTCTTCAGC
CATCTGGTAGAGCCCCAAGAACAAGTTACATGTGGACAAAGGGAGGGAGAGGTATCATGG
TGATTAATAAATNCAAACAAAGCTGAATGATAAGNACCCCAGGATGGAATACAGTCTGAG
AAAGGCCTGGGCAAAG
Sequence 173
GGGGCCGGGGCCCCCGTAGGGGGTTACCCNCCGNGGGGTTATTAAGGGGGTTGGNAAAAAAAAA
AAACCACCTGGCNCANTTTCCAACCCAAANGGTNCAAANGGGGAAACCCCCCAANGGGGG
CCCAGGCCTTGGGGAAAAGTTGTTTGGGGNAAGCCCACCAAACCAATTGGNCTTGGTNGG
GGAGGCCAACCCACCAATGGNCCTTGTTGNGTAAGAAATNTGGGCNAGGGNGGGTTGGTTC
CTTGNAAAGGGTATTTGGGTGGTTNCGTTAANTTTGGGGAAAAAGGAAATTTTTTTTAAGG
GTTATTTGTTAAGAAAGCCAAAGGGTTTTGGAAAAAAATGGGGAATTTGGGAAGAACCTG
GCCAATTGGGGTTGGGGCCCATTAAAANAATTGGGGAAGGNAAAAAATTTTGGCCCCCTTG
GGTNAAGNCCANTCCTTAAGGTTCCTTAACCTTTTGGAAAANGGGGAAAAGGTTGGGGGA
AGGNAACCCANTTAAAAGGGGGNANGGGANGGACCCAAAAAAAAAAAACCCAGGGGGGGTNT
TTTGGTTNGGNCCCCCAATTAAAAAAAAAGGGTTAATTTTTTTTTTTTTTTTCCAAAAAAAG
G
GAACCCANCCCCCCAAAAAGGGAAATTGGGTTGGGGGGGTTNAAAAAAAATTGGGGAAAAA
AAAAAATTTTTAANTTTTTAAGGGTTTTTCCAAACCTTTTTTCCCCCCTTGGCCTTGGG
C
CCCAANTTGGGAAAAAAANCCTTTTTTTTGGGCCCCNTTTTTAAAAAGGNAAAAAGGGGGG
TNGGGCCCTTGGGGGNAANTTTTTNCCCCCAAAAAGGGGGGTTTTTTTTGGGTTNAAAAA
AAGGGGGGGNCCAANTTTCNTTTCCGGGGGGTTTAAAAAAAAGGGAACCCTTGGGCTTTTTTT
TT
Sequence 174
GGCGAGCGGCCGCCGGGCAGGTACCCTAGGGTGTTGTTTAAAGGACTTGATAACCAGCTT
GAAGAGGTTCCTACTGACCAGAAATGGAATGAAATTTAAGCATCAATAAGGGTAATAACT
GCAAGAGACTGACATCCACTATGGTTTAAATCCATGAGGTCACAATGATACTTAATTTT
T
CATTATTCTGAAAACCAGTAAATAAAGGCTAAGATTCAACAAGCATTTATCCAGCCTTTC
CTCAATGAAATATATCNTAAGAGAACCGAATAGTTAACATAGAGACATGGCCGGGCAAGG
TGGCTCTCGCCTGTAATCCCAACACTTTGGGAGGCCCGAGGTGGGAAGATTGCTTGAGCC

Table 1

CAAGAGTTCTAGACCAGNCTGGACAACATGGTGAAACCCTGTGCCTACAAAAAAAAAAAA
AACAAAAAAAAAGGTCCCC
Sequence 175
CAGGACCAAAACCTGGGGATTAAGCTAAGAAGTCTGGTGGAGAGACTCTGTGGACGTAAA
GAAGGGAATGAACACAGAGAAACTTTCAGCCAGATTCCTGATNGTCACCTGAACAAGAAA
AGTCAAACTGGAGTGAAACCATGCAAATGCAGCGTGTGTGGGAAAGTCTTCCTCCCGTCA
TTCATTCCTGGACAGGCACATGAGAGCTTCATGCTGGACACAAACCATCTGAGTGTTGGT
GGGGAATGGANAGAGGACNCCCCCCGNAAACAGAAACCAACCATGGGGAAAAGCCTTCAT
TTCCCCCAGTAGTNGGTGCACCGGCTCACCAGTTAACNACCAACTTNGAAAGGAGACCTT
TATGAATTGCAAGGGTGGTGCGGGGAAAGCCCTTTAAATTCTCCCA
Sequence 176
NCNGGNCAGGACGCGGGGGCCGNGAAGAGCTTTGCATTGTGGGAAGTCTTTCCTTTCTCG
TTCCCCGGCCATCTTAGCGGCTGCTGTTGGTTGGGGGCCGTCCCAGCTCCTAAGGCAGGA
AGATGGCGGCCGGANAGAAGACNAAAAAGTCNCTCGGAGTCGATCAACTCTAGGCTCCAA
CTCGNNATGAAAAGTGGGAAGTNCCT
Sequence 177
CCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTATGAATNATTNATTTTCT
T
TNTCAGAAAAGGATGCGCCTCCACTTAGCAAGGCTGGGCAGGATGTGGTCTCTGCATCTC
CCCACAGACAGGGGTGGTTCTAGA
Sequence 178
GGTGGCGGCCGCCCGGGCAGGTACCAAACCATTTTCACTAGTTCAGGATAGGAATATTCA
TCAGATTGTCTCTGTAAAAGTGAATCACAAAAATTCCACCTGTGTAGGTGTGGGACTGGA
CAGCTGAGTGACAGGGCCCTGGGAAGAACAGAAACCACTTTTCCTCTTTCCTCTGAAATA
TCAGAAGTTAAAAATCTACTCTGAGTTATATGTGCATCAATTTTAGACATATTGCTGAT
T
TTATTATGAAAATGAAGTGCTAAAGACAAAGGATATTTCCATTCCTCTGGACAGGCAGCC
ACAGACCAGCACTGCTTGACCCATGTGTATACACATGTGTGCTTTGTACCT
Sequence 179
GGTACTCACAGTCACGCAAATTCACAGTCTGCGTGCACGGCTCTCCATTCTTCTTCTTGG
CTTTACAGGTTCCCAGGTCAAGAGCTTCACCCATAATTAAGACCTTCTGAGGATGATCGA
TAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGGATCC
CTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAGAACA
AGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTC
CACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCACCCAATCT
A
TTTCTTCCAGCTTCTCTCTGGCCATCTTTTCTTGATCTGAGACAGTCTGATCAGTTTTC
G
GCCGCTCTAGAACTAG
Sequence 180
GGCGGCCGAAAACTGATCAGACTGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAGCTG
GAAGAAATACGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTACGCCACAGAGTGT
GAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGACCTGACACAATG
TGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGACGGAGCAGGGGAC
TGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAGGAGGTGTG
TTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGACCTGGGAAC
CTGTAAAGCCAAGAAGAAGAAT
Sequence 181
GTGGCGGCCGAGGTACTACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTG
GCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCT

Table 1

CCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATG
CTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAA
T
GTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTT
Sequence 182
GCGGCCGAGGTACATGGATACGTTCTCTTCTGGGGGCGGTCTCCAGTCCTTTCTCATGAG
GGAGCACACTCCTCTGCCTCATTGCAGTGGCCTCAGGGATATGGAATTAAGATCCACCTG
GTGTGATGAATAAACCCAGACTCTCAGCAACGCAGGAAAAAAAACAAAAACTGGCTGGCG
ATCTGGAGTAAAGGATCCTCACATCCACGTGAACCAGGAAACTCTGTGCCCAAATCGACG
AAAAAAAAAACACTGGGAGAGCCGAACTAAAAGTCTTTTAGCACGGGTACCTGCCCG
Sequence 183
TCCCGCGGTGGCGGCCCGAGGTACGCGGGGGAGCGGAAAGGGAGACTGTGGGGAACTAGGA
GCAACAGCAGGCATGGACCAAAGCAGTGAAGGATGTATGAAAAAGATTAGCAGTGTGAAT
CTTGACAAACTTATAAATGACTTCTCACAGATAGAAAGAAAATGGTAGAAACCAATGGA
AAGAACAATATACTGGATATTCAGTTGGAAAAAAGTAATTGCCTATTAAAAGTAATGCAA
GCAAAGGAGGTCTCCATTAAAGAAGAATGTGCTACTCTTCATAATATAATAAAAGGGCTA
CAACAGACCATTGAATATCAACAGAATTTGAAAGGTGAAAATGAACAACTAAAAATAAGT
GCTGATCTTATAAAAGAGAAGTTAAAGTCTCATGAACAGGAATATAAGAATAATATTGCC
AAACTTGTAAGTGAAATGAAAATCAAAGAGGAGGGATATAAGAAAGAAATAAGCCAACTT
TATCAGGGACATGCAGAGAAAAGTTGAATTAAATGAAGAAAAGCCCAAAGAACTTATANA
GAAAAAGGNGATGGGAANTTCANAGGTTAATGCCAAGCTTAGAAGTCAAAAAAAAAAAAA
AAT
Sequence 184
CCGCGGTGGCGGCCGAGGTACATGGATACGTTCTCTTCTGGGGGCGGTCTCCAGTCCTTT
CTCATGAGGGAGCACACTCCTCTGCCTCATTGCAGTGGCCTCAGGGATATGGAATTAAGA
TCCACCTGGTGTGATGAATAAACCCAGACTCTCAGCAACGCAGGAAAAAAAACAAAAACT
GGCTGGCGATCTGGAGTAAAGGATCCTCACATCCACGTGAACCAGGAAACTCTGTGCCCA
AATCGACGAAAAAAAAAACACTGGGAGAGCCGAACTAAAAGTCTTTTAGCACGGGTACCTG
CCCG
Sequence 185
CCGGNCGCCCGGCAGGTACGCGGGGGGTGTCCGGCGATGGGCACGGGCATTTCTTCGTTTA
TAGCTGTCTGTTTGCATTCTGATTGGGAACACTGGGATCATTTTCATCATGCCGACAGTG
GTGGTAATGGATGTATCCCTTTCCATGACCCGACCTGTGTCTATTGAGGGGTCCGAGGAA
TACCAGCGAAGCACTAAGTAATATGGATGATTATGACAAAACCTGCTTGGAGTCTGCATT
AGTTGGTGTTTGCAATATCGTTCAGCAAGAATGGGGTGGTGCAATTCTTGCCAGGTTGTC
CTGGTGACAGACGGNTGTCTGGCATTGNNAGAGGGCCACTGGGACATTCNNTANCCANTC
AAAATTAACNAAAGTGNGAGCACNNGGTTTCCCTACCTTTTCNTTTCCCATCAANTNT
AT
ATACCANGGNNGGGCGAATTTGGNGGGCCCCNCGCCCCCTNTTCTTTGGGACTTTTAAAA
CNGTTTGTCNTTTCCNCTTTGGGGNGNGGCCATTTTTATNTTGGGGGGNCCCCTTGGGGA
ANAANAAACCCCCCNCCCCTTTANAAAANNGGNCCCCCCCCCGNGNGGGGGGGNAATTAAA
AAAAAATTTTNCCCCCCCCCCCCCCGGG
Sequence 186
TCCCGCGGTGGCGGCCGAGGTACTCACACGTCACCGCAAATTCACAGTCTGCGTGCACGG
CTCTCCATTCTTCTTCTTGGCTTTACAGGTTCCCAGGTCAAGAGCTTCACCCATAATTA
A
GACCTTCTGAGGATGATCGATAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCAT
GGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTG
AACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTT
CCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAA

Table 1

C
CCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCTTGATCTG
A
GACAGTCTGATCAGTTTTCGGCCGCTCTAGAACTAGGTGGATCCCCC
Sequence 187
GGCGGCCGCCCGGGCAGGTACCAGAGATTCCAGAGAGTGGTCTTTGGAATTTCCCAACTC
CTTTGCTTCAGTGCCCTGATCTCTGAACTAACAAACCAGAAAGAAGTGGCAGCATGGACT
TATCATTACAGCACAAAAGCATACTCATGGAATATTTCCCGTAAATCTGCAGAATCGCTA
CACAGACTTAGTGGCCATCCAGAATAAAAATGAAATTGATTACCTCAATAAGGTCCTACC
CTACTACAGCTCCTACTACTGGATTGGGGATCCGAAAGAACAATAAGACATGGACATGGGT
GGGAACCAAAAAGGCTCTCACCAACGAGGCTGAGAACTGGGCTGATAATGAACCTAAC
Sequence 188
TTTGAANCCCACTTNCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTT
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TGTGCCATTCCTTGTCAATTTCATGCTGCCTACAGCAACAGCATAATACTGCAAACAGCC
ATGATGTCACTCGAAGTGCTCTGTGATTGACAGAGAGGGACAGTCGTAGTCAGAGGTGGC
TCCTCAGAGAATTCAGAACTCACTCGCTGTCCTCCAGGGGCTCATCCCTTGATTTGAGGG
AGGGATGAAATATTCTCTGCATGAGAGAGCAGGGATGGGAAGTGATATAGGTATGTAAGG
ATGGTCAAGTTACTCTAAATGTAGTTAGACAGGACAGCCAGAATACCCGAGGTCTTGGTT
AGGTCCTCTGTAACAAGCCGTAGAGGCCCAGAAATGTGGTGACAGCGAGACACATTTCTT
AACTCTTACACTTGTTGAAATGAGTAGAAGGNGACATTTGGTTTGGAAATCCCTCCCC
A
Sequence 189
CCGCGGTGGCGGCCCGCCCGGGCAGGTACGCGGGGAAGGAAAGCAGCTGCAAACTTCCCA
TCTGCAGTGTTTGTTTGTCTCGGCTCCGGCCATCACTGCCACGATTACCCCTGGATGAAT
TCCTCAGTGGAAATATCAACAAGACTCAGCCCACCTGCACCCAGGTGATTAAAAAGCTTT
ATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACATGGACGCGCGCGACATTTGGTGC
CCTGACTTGGATCAGGGGACCTCCCTTGGGAGATCAATCCCCTGTCCTCCTGCTCTTTGC
TCCGTGAGAAAGATCCACCTACGACCTCTGGTCCTCAGACCAACCAGCCCAAGGAACATC
TCACCAATTTTTAATCAGGAATATTCTGTGAAAAAGACTAAGATATCAAGAGAAATTAT
T
AGTGCACATTATTAGAAGAGAGCTTCAGATGAAAATAAAGATCAAGAAAAAGACTCTTGC
TTTGAGAAAGACACAAAGAAATCACATCATTCTTATTGGGATTACTGGGCTAGCCATATG
CCAGAAAAATGAAACTGGTCCCTTCTTACACCATATACCAAAAGCNGCCCANGATGGNTT
ACTTNAATGTNAAAANCCAAAACT
Sequence 190
CGGCCGCCGGGCAGGTACCATCGCCGTCCCATTGCTCACAGGGACTGGGAAGGCGATGCC
TGGCGGGAGCTGCTGGTGGAGAGACTCGGGATGACTCCTGCTCAGATTCAGGCCTTGCTC
AGGAAAGGGGAAAAGTTTGGTCGAGGAGTGATAGCGGGACTCGTTGACATTGGGGAAACT
TTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGTGGAACTAGAAAATCAAGCTGTA
CCCTGATGCTACAGACGAGGACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGC
ATACAAGGCCATCCCCGTTGCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGG
GAAGGACAGTTATGAAACGAGTCAGCTGGATGACCAGAGTGCTGAAACCCACAGCCACAA
GCAGTCCAGATTATATAAGCGGAAAGCCATGATGAGAGCAATGAGCATTCCCCATGTGAT
TGATAGTCAGGAACTTTCC
Sequence 191
CGCCGGGCAGGTACTCCCTGGAAAGTCCAGCTGAGAAAGCGATCCTGCCCTCTGCTCCTC
CCAGGGTTACCCTCCTGTAAGTCTTCTGCTTAGTGTTCAGAATTGGGGGATGCTGGGACT
GGGCAAGGACTTGTAGGCAACACCCCATAGCCTGCTCATGCCTGTTGGGTTGCCTATGGA

Table 1

TCATTCCCTGCTGGGCTCACTCACCGGCTTCGTATAAGGTCCTTTTTGAGGTTTATTA
TT
TCCTTGTCCATATACTTGATGCTCTTCATTGGCTTGTCTGGGACCTGCCTTAGGTTCT
CC
GAGGCATAAAAGGGCCGGACAGCCCCCGAGTTGGGGGAACTCTGAAGCTTCTTGGTGGCT
GGAACCTTGGTCATCTTAAAAATCCTTCAGGTTTTAGCCTGTGCCCCCAAGACAAGGATT
TTTCCAGAATCTTCTACTTCAAGTAGTTACTGGTATGAAGAAGTTTCGGCA
Sequence 192
CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTC
T
GGCTTGAAATACAGCTGAAATAACTGAATTTTCTACTTGAAACGTGTGTGCCTCTCCACT
GNGGGGCCAAGGCCCTGGAAATGTAAAGGGCCAATCTTTGTTACAGAGGGGTTCATTGCA
GTGAAGGGCGGGTTCTGCAAAGACAAACAGGTCTCACAGATAGTTGCCCCCGCGTACCT
Sequence 193
NGGCGGCCGAGGTACGCGGGGGGGCTGNAGTAGGCTTCGTCTTCGGNTTTTCTCTTCCTTC
GCTAACGCCTCCCGGCTCTCGTCAGCCTCCCGCCGGC
Sequence 194
CGGCCGCAGCGGCAGCTACAACAACCGCGTCGCTCTCCGCTCAATTTCCAAGAGCCAGCT
TTGAAGCCAAGTGCCCCCGCGTACCT
Sequence 195
CTTCCCGCGGTGGCGGCCGGTGTGCTGTGCTCAGCTGCCTTCCAAAGGAGGAACAGATCG
GCAAGTGCTCGACGCGTGGCCCGAAAATGCTGCCGAAGAAAGAAATAAAAACCCTGAAAC
ATGACGAGAGTGTTGTAAAGTGTGGAAATGCCTTCTTAAAGTTTATAAAAGTAAAATCAA
ATACATTTTTTTTTCAAAAAAAAAAAAAAAAAAAAAAAAAGTACCT
Sequence 196
CGGTGGCGGCCGAGGTACTTTGAGCTCATAAGCTGGTATAAAATATCAAACATTTTGACT
GTTTAAACAACTCAAGATATGTTTTGCAAAATTACAAAACATTATACAGGTGACTTAATT
AATATCTACTCCAATTATACACAACACATCATGCTGAAGATTTAGATTTATTTGAAAACA
CTTAGTCTAATTTATATTAGTGCAGAAAAATCACATTCAATAAACCACAATTGTAGAAG
A
GACAGATAAGTGTGTTTGTCACATTTTCACACAAATATAATTTGATATTTAATTAAGGG
A
TGATGAATCACAATCACCATGGTCGCCGCCTGAGCGCCAACCCCTACCCCGTCGCCTCAT
CGGATCCCCCCCGCGTACCTCGGCCGCTCTAGAACTAGTG
Sequence 197
NCGAGGTACCTGCCTNACAGNGCAGGGCGGTATGCCGCCAAACGCTTCCGCAAAGCTCAG
TGTCCCATTGTGGAGCGCCTCACTAACTCCATGATGATGCA
Sequence 198
TTGCTCAGCCTTTCCAGGCCCCTCTGATGAGCTCTCTAATCAGCAGGACCAAGGTGTGAA
TGTGGGAATGAACATGGATCCATCCCATTGGATGGAGAAGAAAGGTGGACAGCCTGTTCG
TCTCTCATGTCAGCCTAGGGCTGGGAACAGTTTGTGAGGACTTATCTGTTGTACCT
Sequence 199
GGACTTGCTCAGCCTTTCCAGGCCCCTCTGATGAGCTCTCTAATCAGCAGGACCAAGGTG
TGAAGTGGGAATGAACATGGATCCATCCCATTGGATGGAGAAGAAAGGTGGACAGCCTGT
TCGTCTCTCATGTCAGCCTAGGGCTGGGAACAGTTTGTGAGGACTTATCTGTTGTACC
T
Sequence 200
GANGAGAAAGCTGGAAGAAATAGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTAC
GCCACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGA
CCTGACACAATGTGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGAC

Table 1

GGAGCAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTC
AGAGGAGCGTGACTGTGAGTACCT

Sequence 201

GCCGAGGTACTCGGGCAAAGAGGGTGACANGTTCAAGCTCAACAAGTCAGAACTAAAGGA
GCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCA
NAANCTGATGAGCAACTTGGACAGCAACAGGGACAACGAAGGTGGACTTTCCAAGAAGTA
CCTGCCCGGGCGGCCCGCTCTAGAACTAGT

Sequence 202

TGGGGCACAGAGAGGGTTTCAGAGGATCCTTGNGAAACACTAGTTAAAAGATGACCGAGT
GGGGAGAAGTGCGAGGAAAGAAGGAAATTAGTCTGACTGGCTTTCTGTCCTGCACCATTG
ATTCAATGGAGACTGGGCGGGAGGAAATGGAAGACTAGGGTTGGAGATGGGATGGGTGGG
GCAAGGGATGGAAAGGAAAAGGCAGACAACTAATGCGTTCCATTTATAACAAGTAATATA
TATCAAAGCACTTTAAAGGAGATTANAAGGACCCAATCAGGAATANATTTGGGCCAACCT
TTANATTCTTTAGGGAAGGATTCAAAAGTTCCCTCCAAAACCCTAATTTTTGGATGGTT
T
TATTNACTAAAAAAGCCAAAAGACCAAGTTNTGGGTACCCTGCCCCGGGGCCGGCCCGCC
TCTTAAGAACCTAGGTNGGGATCCCCCCGGGGGCCTGCAAGGGAATTTCCGATATTCAAA
GCCTTTATCGGNTACCCGGTCCGACCCTNCGAGGGGGGGGGGCCCCGGGTACCCC
C

Sequence 203

GCGGCCGCCCGGGCAGGTACGCGGGGAAGTCTNTCCTTTCTCGTTCCCCGGCCATCTTAG
CGGCTGCTGTTGGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAGA
AGACGAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGGA
AGTACC
T

Sequence 204

CTCCCCGCGGTGGCGGCCGAAAACTGATCAGACTGTCTCAGATCAAGGAAAAGATGGCCA
GAGAGAAGCTGGAAGAAATAGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTACGC
CACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGACC
TGACACAATGTGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGACGG
AGCAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAG
AGGAGGTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTG
ACCTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAGCCGTGCACGCAGACTGTGAA

Sequence 205

CNCCGCGGTGGCGGCCGAAAACTGATCAGACTGTCTCAGATCAAGGAAAAGATGGCCAGA
GAGAAGCTGGAAGAAATAGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTACGCCA
CAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGACCTG
ACACAATGTGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGACGGAG
CAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAG
GAGGTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGAC
CTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAGCCGTGCACGCAGACTGTGAATTTG
CGTGACTGTGAGTACCT

Sequence 206

TCNCCGCGGTGGCGGCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTC
ATGGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTG
TGAACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGT
TTCCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATAT
A
ACCCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGAT
C

Table 1

TGAGACAGTCTGATCAGTTTT
Sequence 207
TCCCGCGGTGGCGGCCGCCCGGGCAGGTACATGGTTCTTCCTCAGAAAGTGGTTCTTCCT
TAATGTGTTTCTTTTTACCCCTTTTCTTCTTCTTCTTCACAGATGNGGCTTCNTCTTCTG
CCACTTTTTCTTCTTCCTCTTCTTCAACTGAATAGGGTAAGTGTAAAGGCACAACAAAT
T
AACACTGTATCAGATCTCATTCCTTCCAAAAACGTTTGAGTCCTAGTTTTTTTCTGTCA
T
TCTCATCAACTACCCAATGTTTGTTTTGTTTATTTTATAATTGGGAAGGTTCTCCAAGG
C
CTACCACTAACTTTAACGAATGATATAGATAGAGCTCAGAGCAATCTTCTCACGATCATG
AAGTCATGTATAAAAATCAGGATTAAAACAAAGGTCATCTGATCTCCAATCATTATTGGG
AAGGAAAGTCAATTATATTANGAAATGGTTAAGAGCTTGCACTCTGAAGTCAGACGGCCT
GGGTTTAATCTACCTGCTGCACCCTGAAAAATTGGTATTTACCCTT
Sequence 208
CGCGGTGGCGGCCGCCCGGGCCGGTACATGGTTCTTCCTCAGAAAGTGGTTCTTCCTTAA
TGTGTTTCTTTTTACCCCTTTTCTTCTTCTTCTTCACAGATGTTTCTTCTTCTTCTGCCA
CTTTTTCTTCTTCCTCTTCTTCAACTGAATAGGGTNAGTGTAAAGGCACAACAAATTAA
C
ACTGTATCAGATCTCATTCCTTCCAAAAACGTTTGAGTCCTAGTTTTTTTTCTGTCATTCT
CATCAACTACCCAATGTTTGTTTTGTTTATTTTATAATTGGGAAGGTTCTCCAAGGCCT
A
CCACTAACTTTAACGAATGATATAGATAGAGCTCAGAGCAATCTTCTCACGATCATGAAG
TCATGTATAAAAATCAGGATTAAAACAAAGGTCATCTGATCTCCAATCATTATTGGGAAG
AAAGTCAATTATATTAGAAATGGTTAAGAGCTTGCACTCTGAAGTCAGACGGCCTGGGTT
TAATCTACCTGCTGCAACCCTGAAAAATTGTATTTACCCTTGGTGAAGCTCCTATCTAT
A
AAACTTAAGAATGTCTTATCTTACTGGACTGGTACTGGATTAAAAAGA
Sequence 209
CACCGCGGCGGCGGNCGAGGTACACGACATAGGCACATGTGCAAACACAAAGAAGGTGGG
CATGCTGCTTCTTTCTNTCTGCCCCTAGNCCAGGCTCCTTTGCTTCACGNAAGATNNACA
CTTTCCCATTCCTCTGAAGTTGCTGGAAGGACATTTCCCAGGAAGAAACAATTCCTCACT
GCCTATAAACTGTAGTCCCAATGTNGGGATAGTCAANNGAACATGAGAATCANAACCAAT
CTGGGCAAATGGGGNATGGCAAGTAATGGGNGAACACGCACTAACAGGNACAGTATGCCC
AACCT
Sequence 210
GGTGGCGGCCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGG
TTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCNNTGTGAACT
TCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCAT
ATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCC
A
AATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTNCTTTGATCTGAG
A
CAAGTCTGATCAAGTTTTCGG
C
Sequence 211
GCGGTGGCGGCCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGG
GGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAA
CTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCC
ATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACC
C

Table 1

CAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGA
G
ACAAGTCTGATCAGTTTT
Sequence 212
GGNGGCGGCCGCCCGGGCAGGTACTTTTNAAATTTTTTTTTTTTCTGNAGAGACGAGGTCT
TTCTATGCTGTTCAGGCTGAACTTCATGGGTTTATTGGGGATGGCTAANGGATGACATTG
GCTGGTGGTCCTTGATACCAGATAAGCCCTCAGTGTGAAGCAGCTCTTATTTTTCCTT
GT
CTTGAGATTGCTCTTGGAATGGAAATTAGGCTTTTTTGAAGGTGTCGACCCTTTTTGG
TT
CATTTCTTCAGCAGTTACTTTTTATTTTTTTTTAAAATGTTTTGACACACAAGTCTTNTGG
ATAAATGAATCANTTCACCCAANCACCCCGGATTTACTTCTCCTTTGCTCTGGNTNAA
GT
NGNTGAACACNTGTCCCCTTTTGAAGAAATCTGGGNCGACAGCTTATGTATCCCCATTCA
CCCACAACACCCCCAAAAAAAAAAAAAAAAAATTTATTGTCTTGGGGTTCCCCAGGGGAGNTT
ACCCTTTTTAATGGAAGAAAGGTNCCATTCTTGNGGAAAGAACCCCTNGGGAATGNTTTC
AANAAGGAAACCTTTCCCTGGGGGAAAAACAACTTGNAAAAGGAAAAAATTAAAAGGAAG
GGCCCGGGGCCC
Sequence 213
GCGGNGGCGGCCGTTTGAGAAGCCAGCGCTCACCCACCCGGGGTCTCTGTGCATTGACCT
TTGGGTGCTGACTTGGAGAAAAGCACAAACACGACCAGTCCCCCCGCGTACCTCGGNG
Sequence 214
TCCCCGCGGTGGCGGCCGAGGTACATGCCTACAGATAGTCCCAGCTACTCGGGAGGCTGA
GGCAGGAGAATCGCTTGAACCCAAGAGGCGTAAGTTGCAGTGAGCCGAGATCATGGCACT
GCACTCCAGCCTGGGTGACAGAGAGAGACTCCATAAGAAAAAAAGAAAAAAAAGGGGGGGC
AAAAAGAAACAGATGAAACCAATGTGAATAATTTATTTTAACACAATATACCTAACATAT
TTTTATTTCAATATCTAACCAGTATAAAAATTTACTTGTTTTGCCCTCTAGAGATAGTAA
GCTCCTTAAGTAAACAGAAGTAATACCTGATTAATTAGAATTCCCAACCCTCATCAAGTG
TGTGCTTATATAGAAGAAACCCAGTAAATGTTTGTTGATTGAAAGATATTAATACTCTT
G
CTTGGATGAGAGTGAGGAAAAAGGTATTAAGTATTGGCTTT
Sequence 215
GNGGCGGCCGAGGTACTTTGGAGTCCCCTGGTTTCTCAAGAATTGCCGTTGACTCTTTCT
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TG
GAAGCCGCGAGCGTAGAGGTTCCGCGTGCTCTGCCGGACTTGAGCAGGTCACTGGGTCCT
TTACACTTGTGAATTCGAAGCTTGCCAGATGTATCCTCAATGCATTGCCACTTCTGCC
CC
GGTTGTTCACAGGCTGTCTGGTACGAGATCTCCGACCAGTCTGGGGGCGCTGGCGGCCTG
CGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCTACTCCAAAGAGGATGCA
ACCAAGGGGAAATTTGCCTTTACCACTGAAGATTATGACATGTTTGAAGTGTGTTTTGAG
AGCAAGGGAACAGGGCGGATACCTGACCAACTCGTGATCCTAGACATGAAGCATGGAGTG
GAGGCGAAAAATTACGAAGAGATTGCAAAAGTTGAGAAAGC
Sequence 216
CCGCGGNGGCGGCCGAGGTACTTTGGAGTCCCCTGGTTTCTCAAGAATTGCCGTTGACTC
TTTCTTTGGCTTCTGCTGGCACGGTAACCAGACTCCCTACAACTGCACTCTTTGTCTT
TG
TCATGGAAGCCGCGAGCGTAGAGGTTCCGCGTGCTCTGCCGGACTGTGAGCAGGTCACTG
GGTCCTTTACACTTGTGAATTCGAAGCTTGCCAGATGTATCCTCAATGCATTGCCACT
TC
TGCCCCGGTTGTTCACAGGCTGTCTGGTACCGAGATCTCCGACCAGTCTGGGGGCGCTGG

Table 1

CGGCCTGCGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCTACTCCAAAGA
GGATGCAACCAAGGGGAAATTTGCCTTTACCACTGAAGATTATGACATGTTTGAAGTGTG
TTTTGAGAGCAAGGGAACAGGGCGGATACCTGACCAACTCGTGATCCTAGACATGAAGCA
TGGAGTGGAGGCGAAAAATTACGA

Sequence 217
CCCGCGGTGGCGGCCGAGGTACTATCAAACAACATGATACAATTTAAATGTGTCATAGCA
ACTACTAGTGGTCACCTGAAATCCATTTTCCCCTCCTTCACAGTAAGAGTTTTAGNTG
AA
TGAGTGGCCACTCATAGAGAGATTGCATTTCTGGCTTCCCTTGCAGCCATAGGTAGCCAT
GGGACAAAGTTCTAACCCAGGGGGGGGTCCAATCTTTTGGCTTCCCTGGGACACACTGGAA
GAAGAAGAATTGTCTTGGGCCACACATAAAATACACTGGCATCAAGGATAGCTGATGAGC
AAAAAAAAAAAAAAAAAAAAAAAGTACCTGCC

Sequence 218
CCCGCGGTGGCGGCCGAGGTACCATCCTGTTCNACAGAGCCATTGCCTATTCCTAAATTG
AATCCGACTGGGCGTGCCCCTCCTCGGAACACAACAGTAGACCTTAATAGTGGAAACATC
GATGTGCCTCCCAACATGACAAGCTGGGCCAGCTTTCATAATGGTGTGGCTGCTGGCCTG
AAGATAGCTCCTGCCTCCCAGATCGACTCAGCTTGGATTGTTTACAATAAGCCCAAGCAT
GCTGAGTTGGCCAATGAGTATGCTGGCTTTCTCATGGCTCTGGGTTTGAATGGGCACCTT
ACCAAGCTGGCGACTCTCAATATCCATGACTACTTGACCAAGGGCCATGAAATGACAAGC
ATTGGACTGCTACTTGGTGTTTCTGCTGCAAAACTAGGCACCATGGATATGTCTATTA
CT
CGGCTTCTTAGCATTCACATTCCTGCTCTCTTACCCCCAACGTCCACAGAGCTG

Sequence 219
GTTATTGGTGGTGAAGACCCGNAGCAACAGTGGGCATGTCTTCTCGCGGTCGATCGGNTT
CTCTGGCTCCTTNTTAATTTCCTCCTGGGNAACGCGCGACTCCACCGCCATCTTCCTCCT
ACGGCCTGCGAGACGCTCCCCCGCGTACCTCGGCCGCTCTAGAACTAAGTGGGATCCCCC
GGGCT

Sequence 220
GGCGGCCGAGGTACCATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTG
CTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGG
TAAGGTCAGCAGCACAGTGGCCATGGAAAAAGAAAAACTCTACAGCATATTTCCGAGGAT
CAAGGACAAGTCCAGAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACTTG
TTGATGCAGAATACACCAAAAACCAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGC
CAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAATTTT
C
GAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCTGTGTGGCTCACTTGTTTT
CC
ATGTTGGTGATGAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGTTCACTATA
TCCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGNTACAATTTGTAA

Sequence 221
GCNGGTACAGCAACAAGAATCAGATGCTCTTTAGAGATCCTCCATTTCATTACTCTAACA
TTCTTCAATGTGGTTCCAGCCACGCATAGTCATATAGATACTACATATNCAAAGATAAC
T
TACTGAAGCTTGTTCACAGAACCAAGCTTTCTCCTGGATAAGCTCTTCTNTCCCCTAC
CC
CGCACTTCTTGGGNAAGGTATTACCCCAAAATGCTCTTCAGNGGATTTAAAATAAACAAT
TTTTTAAAAAANANGGACACTTAACACTCACAAAAAAATGGGGGAAATTTTGCTCGGGCCA
TTGGACNGCGGAAACCAAATTACCGGGTTTAACTTCCAAGNATGGCTTGTCATTTCAAAA
ACCTGGTATTGGGGGGTCCCGTTCGGAAAAAAANANATAGGATATTAACCCATNTTTTTCT
CATAAGGACCAAGCTATTCTTACNTTTTTAATCAACCCAAATTTCCTGGGGGGGAAAGGNCC

Table 1

TTTCTTCTTATTTTAGGTCTTCGGGGATAGGTCTTNTANTCCCAATAAATAATTGGGGT
T
AGGTATTCAATCCATAATCCTCCCAGGACCCTGGGTTTTCCCTNGGAAGAAACAAGGGAA
GAGGTCNTTGCCTGGTATCCTCNAAAAGGTTGGAAACCAAGCTTGGCNACTTTATCTTCT
TAAACTTTCTTTTGGGAAGGAACCCCAGGTTTCAAGATATTTTTTTTTTGGGGAA
Sequence 222
ATGGCCGGCCTGCGGAACGAAAGTGAACAGGAGCCGCTCTTAGGCGACACACCTGGAAGC
AGAGAATGGGACATTTTAGAGACTGAAGAGCATTATAAGAGCCGATGGAGATCTATTAGG
ATTTTATATCTTACTATGTTTCTCANCAGATGTAGGGTTTTCTGTAGATGATGATGTCC
A
TATGGCCATATCTCCAAAAGANATGAATCCGACAGCNGATACAAAGTTTTTTGGGCTGGG
TTTATTGCNTCATATAGNNCTTTGGCCCAAATGGNANGCTTCACCCTATATNTTGGGT
TT
ATGGNCTAAATTATTANGACCCANAGGA*.AAGGAGCCTCNTTAATTGGTCTCCCATCTT
GATTTTTCCCGTGGNAAGCACAACCTGCCCTCTATGCATATCTTCCACCATCCCCAAGCT
TTCTCATAAANTAAAAATAACCTACCAATGGCCTGGGTTGCNTCCGTNGGGAATTTGNNT
GGGGAAATTTGGGAAGCCANGTTTTTTTCAAGACCTTNGGNNTTTACAATTCCCTTTGGG
AGAAA
Sequence 223
GGGCGGCCGGAGTGATGCCATCTGCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGG
TCAGCCCATTATCTTTAATCCTGACTTTTTTGTGGAGAAACTCCGACATGAGAAACCT
GA
GATTTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTCATCGATTTACCTGGAACTGA
GTTGGCTCANCTGATGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATC
AGGATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTC
CCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTACACAAAAA
CTTGCGAGTAGAGGGTTTGTTTAGAGTACCT
Sequence 224
CCGCCCGGGCAGGTACTCCCTGATAAAGGGGAATTTCCATGCCGTCTACAGGGATGACCT
GAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAAAGGGTGCAGACGTCTG
GTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCCAGGAGTTCCTCATTCT
GGTGATAAAGATGGGCGTGGCAGCCCACAAAAAAAGCCATGAAGAAAGCCACAAAGAGTA
GCTGAGTTACTGGGCCCAGAGGCTGGGCCCCTGGACATGTACAGACTCTCATTTTATGAT
GTATCCTACTGCATCAGGACATTTGTGTCAATGTCAGGTGACGAGGGGAAATGAAAGTGA
TGAGACGATGAGAGGAGTGAAATACCAAGGACGCCATACTAGGAAACCCAGGTCTATTTG
TTATCAGAGTAAGGATCAAGCCAGATAGCCTGTTATGTAATTTCTCCGATAAAAGATTT
T
GAAAGCAGGTGCTGTGGGCATCTGTATGGGGGAATCGCACTCATAGAATTATTTTCATTT
GTAAATATTTGGTATCAGGCCCAGCAAGGGAAA
Sequence 225
CTCCCCGCGGTGGCGGCCGAGGTACTCACAGTCACGCAAATTCACAGTCTGCGTGCACGG
CTCTCCATTCTTCTTCTTGGCTTTACAGGTTCCCAGGTCAAGAGCTTCACCCATAATTA
A
GACCTTCTGAGGATGATCGATAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCAT
GGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTG
AACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTT
CCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAA
C
CCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCT
G
AGACAGTCTGATCAGTTTT

Table 1

Sequence 226
TTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGATGGATAGCCGCTTGCA
GGAGATCCGGGAGCGGCAGAAGTTACGGCGACAGCTCCTCGCGCAGCAGTTGGGAGCTGA
AAGTGCCGACAGCATTGGTGCCGTGTTAAATAGCAAAGATGAGCAGAGAGAAATTGCTGA
AACAAGAGAAACTTGCAGGGCTTCCTATGATACCTCTGCTCCAAATGCAAAACGTAAGTA
TCTGGATGAAGGAGAGACAGATGAGGACAAAATGGAAGAATATAAGGATGAACTAGAAAT
GCAACAGGATGAAGCTTATCATCAATTCATTGTATAAAAATAAAGAGATTTTCCTGAGAG
AACTGATTTCAAATGCTTCTGATGCTTTAGATAAGATAAGGCTAATATCACTGACTGAT
G
AAAAT
Sequence 227
CNCCGCGGTGGCGGCCGCCCGGGCAGGTACGCAAAGTGATTCAGAGAACGCTGGGGCTCA
CAGGCGCTGTAGCAAACGTGCAACTCTTGAGGAACACTTAAGACGCCACCATTCAGAACA
CAAAAAGCTACAGAAGGTCCAGGCTACTGAAAAGCATCAAGACCAAGCTGTTACTAGCTC
TGCGCATCACAGAGGGGGGGCATGGTGTTCCACATGGGAAATTGTTAAAACAGAAATCAGA
GGAGCCATCGGTGTCAATACCCTTCCTACAAACTGCATTATTAAGAAGTTCAGGGAGTCT
TGGGCACAGACCAAGCCAGGAGATGGATAAAATGTTAAAAAATCAAGCAACTTCTGCTAC
TTCTGAAAAGGATAATGATGATGACCAAAGTGACAAGGGTACCTCGGCCGCTCTAGAACT
AGTG
Sequence 228
GAGCTCCCTCCTACCCCCTAGCTGAGTAGGCCAGGTTTTGGTGCAAAATCTCCCACATTG
GCAAAGTTCCTGCATATGCTGCGCAGTATGNGCCTTGAATAAAAATCCTGAAGATTAGAT
GGTTCAGGCTGCATCATCCCAAAGCAAAGAGCACCTCTTTGAAGCTCACCTGCCCGGGCG
GCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTCAGTANGNAGCTTTAAAACAGTTACATAT

Sequence 229
TGGCGGCCGAGGTACTACAGGATGATGGCTTTCTCTTCCTCTGGGTCACAGGCANGGGCC
ATGGAGTTGGGGAGAGAATGTCTAAACCTCTGGGGGTATGAACGGGTAGATGAAATTATT
TGGGTGAAGACAAATCAACTGCAACGCATCATTCGGACAGGCCGTACCTGCCCGGGCGGT
CGAGCGGCCGCCCGGGCAGGTACTTNNTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTT
TTTTTTTTTTTTTTTTTTTTGGGAACCNGNTACATTGNTCAGTTTTTACTTGNAAAAAGT
NTTATAGAANAGTTTTATTGGAATGTTATTTTATTAAGCCNTTTTCATGGGTTATTTTTT
TTTAAAGTTTAAAAAGTTTTTACAACANGCTGGGNGGGGGGGNTTNCACCTGGCATCCCA
GCACTTTTGGAGGNCCCGGCGGGCANAAACCTGANGGCGGGGAGGTTTAAAAAAANCNACC
CTGNCCANATTGGNAAACCCNTNTTTTTTCTTAAAATTCCCAAATTAAATTC
C
Sequence 230
GGCGGCCGCCGGGCAGGTACGCGGGGGAGTCAGACCCAGTCAGGACACAGCATGG
Sequence 231
CCACCGCGGTGGCGGNCGAGGTACGACGTTTCCATCAGCTTGTCTGTTTCATTCCCTGAT
GTTACGAGCAATATGACCATCTTCTGTATTCTGGAAACTGACAAGACGCGGCTTTTATCT
TCACCTTTCTCTATAGAGCTTGAGGACCCTCAGCCTCCCCCAGACCACATTCCTTGGATT
ACAGCTGTACCTGCCCGGGCGGCCGCTCTAGAACTAGGTGGATCCCCCGGGCTTGCAGGT
AATNTCGGATATCAAGCCTTATNCGATACCCGTCGACCCTTCGGAGGGGGNGGGCCCCCG
GGTACCCCAGCCTTNTTGTTTCCCCTTTTAGGTGGAGGGGGTTTAAATTTGCCGCCGCNT
TGNGCGGTAAATTCAATGGGTTCATTAGGCTTGTCTTCCCCTGTGGTGNAAAATTNGTTA
ATCNCGGCTCACCAANTTTCCCACCACAAACCAATANCGNAGNCCCGGGGGGAGGCCATTA
AAAAGGTNGTAAAAAGCCCTTGGGGGGTTGGCCCTAATGAAGTGGAGCCTAAACTTCACA
ATTAAATTTGCCGTTTGGCGCTTCACTTGCCCCGCTTTTTCCAAGTCCGGGGA

Table 1

Sequence 232
CGGTGGCGGCCGCCCGGGCAGGTACTTTATTTTTTTTTTTTTTTTTTTTTTTTTTNCTTTNA
A
AAAAAAAAAAANGATATTTTAATATATTCAGATCCNCAAATATGAAATAAAACTAAGNNGA
GCTGGTATTCATTTACACATAATTATCTTATACCGTTNGGAATAAGAATTTGGGGCNC
GT
TAGCAAACCAAAAGGCTCAAAAAGACGTCGNGATATTTAGTTCTTGTCTCCCTCTACAAA
NGGGAAGCACTNTTTTATCCGGCATTCCTAGGGGNGTTCCTATTTTCAA
Sequence 233
CGGTGGCGGCCGNCCGGGCAGGACGCGGGGGCCAGTTCTCTTCGGGGACTAACTGCAACG
GAGAGACTCAAGATGATTCCCTTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGT
T
AACCCTATAAACGCCAACAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGT
CGGGGACCAAGGCCCAAATGTCTGTGCCCTTCAACANGATTTTGGGCACCAAAAAGAAAT
ACTTCAGCCACTTGTAAGAAACTGGGTATAAAANAAGTCCATCTGTGGGACAGNAAAAAC
CGACTGTGGNTATTATGGAANTGTTCGCCCTGGGTTATTATGGAGGAATNGGGAAAGGGA
AATGGAAAAGGGCTGCCCAAGNCANTTTTTTAGCCCATTTGACCCANTGGTTTTATTGGG
CACCTTCTGGGGCCATCCGGTNGGGGGGAGGCNCACCCCACCAAACCGGNAAGCCGCCTTA
TTTCCTTGGACCGNCCCTNAAANAAACCTTGAAGGGGGGAAGGGGNGGAATCCGGAGGGGG
AAAAGGGGGGA
Sequence 234
CGCGGAGGCGGCCGCCCGGGCAGGTACAGTATAGGTTGGTTTTGCCTGTTTTGACGCTTT
ATATATACGTAGACACACATACACATGTATATATACACACACACATTTTACATATATATA
TGAAACTGTATAATGTGTTCGCTTCAGTGTCTGGCTGCTTTTACTCAACATTGTGAAAT
T
AATTCCTGTTATCGGNATATGGGTATCNAAATTTGNTTTGCCCTAGTTTTTGCCTTCTC
A
TTGCTTTCTGAATTGGGGGGCAGCTTTGCCCCTCAAGGGGAAATTTAGCAATGTCTGGAGA
CATTTTTTTTTATTTTCATAATTTNGGGAGGGGACATGGGGGGGAGGTTTGGTGGCTACAGG
AACCTTAATTAAGGTTCGAGGGACAGGGGTTAGGTGCTTGAACGGTTNCCACANGTAACA
CTTCGGGCNCGCTTNTAAGAAACCTAGGTGGGATTCCCCCCCNGGGTCTGGCNANGGAAA
ATTCCGANTATTNCNAAGCCTTANTCGANTACCCCGGNCGACCCTTNGANNGGGGGGGGGG

Sequence 235
CGCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAATAATTTTGT
CATTTTTGTAGAGACAAGGTCTCCCATGTTGCCCAGGCTGGTCTCAAACTCCTAGGCTCA
ACTGATCCTCCTACCTCCACCTNTGCCTCCCAATTATCCCCAATTGAGAGATGAAAATTC
TGACAAGCTCTCAAACGTTAACTGACTTGCCCATAAATGACAGTTCCAAAGTTATAAGGG
CCTAGNAACNTTGAATCCAGGTNCTGTTAGNAAATTCTAGGGTTTGAGAAATCCCATATT
TCTNTCCACTTCCCGCGGTACCCTGCCCCCGGGGCCGGGCCGCCTTCTAGGAACNTAGGT
GGGATCCCCCCCGGGGCTTGCAGGGAATTCCGATATTCAAGCCTTATTCGGATAACCCGT
CCGACCCTCGAAGGGGGGGGGGGGCCCCGGGTACCCAAGCTTTTTTGTTCCCTTTTAGTGG
AGGGGGTTTAAATT
Sequence 236
GCGGCCGNCCGGGCAGGNACCTACGCCACAGACAGCCAGAGGGAAAGCGACCCAGACAGC
AGCCCCTCCTCGACAGGCCCACCCTGCAGCTCAGGCACCAAGAAAACAGCCGATACTGGC
AGCCATTGCAGCTCCAAACTGCANNAGGCAAGGCCAATTTTAACTTTTCAATTTACAGTC
GATTTTGAAGAGCTTTCTACATATCCGGTTATGTAAANTTCATATATGTATTTTTTTGGAA
ATCAGTTCTTATANAACCAGCCTCCGATTCAAGTCTTTAGGCTAAAATTTTATAGGTCC
T

Table 1

AAGGGTAGGTATGGTTAACAATTTTGGAACCTTTTTGGTCCTTAAAGAAAAAGGTTGGAC
TTGTTTCAANATANTTTCTNTCTTACCTNGTGAAAAGGAAAATCNTTACTTTTTTCCTAA
TTAAAAAGGAATTCTTGTTACCCTTCGGGCTCCGCTTCTTAGGAAACTTAGGTGGGGATC
NCCCCCCGGGGTCTTGNGAAGGNAAATTTTCGAATATTCCAAAGGCTTTTATTCGAATAC
CCCGGCTCGGAACCTCGGNAGGGGGGGGGGGGCCCCGGGGTACCCCCAAGCTTTTTTNGT

Sequence 237
GCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGGTCAGCCCATTATCTTTAATCCT
G
ACTTTTTTGTGGAGAAACTCCGACATGAGAAACCTGAGATTTTCACTGAGTTGGTGGTCA
GCAATATCACAAGGCTCATCGATTTACCTGGAACTGAGTTGGCTCAGCTGATGGGGGAAG
TGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATCAGGATTCTTCCGGTCTCTCATGT
CTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTCCCCACTGACGGAGGAAGGCATTG
CCCAGATATACCAACTGATTGAGTATCTACACAAAAACTTGCGAGTAGAGGGTTTGTTTA
GAGTACCT
Sequence 238
CCCGCGGTGGCGGCCGAGGTACGCGGGGATTGTGTGCAAAATCAGAGAGGGGTGCAAGGA
TCCTGATTTTTCAGGAGTTCAAGCGACAATGGCAGCCCAATACGGNAGTATGAGCTTCAA
CCCCAGCACACCAGGGGCCAGTTATGGGCCTGGAAGGCAAGAGCCCAGAAATTCCCAATT
GAGAATTGTGTTAGTGGGTAAAACCGGAGCAGGAAAAAGTGCAACAGGAAACAGCATCCT
TGGCCGGAAAGTGTTTCATTCTGGCACTGCAGCAAAATCCATTACCAAGAAGTGTGAGAA
ACGCAGCAGCTCATGGAAGGAAACAGAACTTGTCCGTAGTTGACACACCAGGCATTTTCG
ACACAGAGGTGCCCAATGC
Sequence 239
CCGCGGTGGCGGCCGAGGTACCAGTTAAGTGAACAGCTCGTCTAGGTCTGCTTTTGTAAC
ACCCAAATACAATTAGCACTTCTCTGCTGGTATTCCCTGGGCCGTCTTAATTATCTAG
AG
GCCAGGAGGCAAAGCCTAGCACGTAACAAAGTATGTGCTTTGTAACTGCTGATTAATTCA
GTTTCTTAACTAGGCAGAGCAGGTCATCAGTGTATCTAATTCACACTATTAATACACTG
T
CTTGCTGAAGAGTCTGACCCTGCCCAGGAACCCCCGTTATGGCCTAGCCCCAGNGGGAAG
NCAGTAAAACCTGCCAANAGCCAGGAGAAAAAGGGGGGCCAGTCTTAAGAATGAAGGCC
TAGGTGCTTGGCCTGGAGCTCCCAGTTTTAGGGTCCTGGTTACTGTTTCTGGTTTCCAAC
TTATTAAAATCCAGGGGATGGACCTGGTTACCTCAGATTTCAGGTTGCCTTATGGTAGGA
AAAATAGGAATGCCACAGGCCAAAAAACATTAATTTTGGGGGGGGATGGACTTGGGCAGNC
ACCCTTTTTTTTTTCCCTTTTC
TT
Sequence 240
GNGGNGGGCCGGCCCGAGGTACTTTTTTTTTTTNTTTTTTTGGTATGACTATAGATGGC
TA
GTGNGTCTTTTTATTAGCTATCANCGTTCATTTAACAGACAAAAAATTCAAGTTCAATG
N
NNGGNCATTAAAATACGGAAGAATTAACAATAAGTTCATTAATCAATCTTTCANCTGTT
C
CTATTTTATCACAAATNACTTTTTCCTANAATTGGAANAAGGATNCATGGGAAGGGGACAA
GTCTTGGAAAAACGCAAACCGTAATTGTGTTCTTTCAAATTCCATAAAAGACACTTCAGG
NNCAAAAAAATAAATAAACAAGGNAAGGGCCGCNTCATTACCTNTTAGTTTNGGGGGNGTN
GGAAATTGAATCATGGCCAAGTGCCTAAGNGCNTTTTTGCTGNTNAGTTAACCCNCCGTG
CCCGCGTCNTAGGAAACCTATGNTGNGGATCCCCCCCGGGGCCTTGCCANGNGGAAATTT
CGAATAATCCAAANGCCTTTATCCGGAATACCCCGTCCGGACCCNCCGAAGGGGGGGGGG
GGG

Table 1

Sequence 241
GCGGTGGCGGCCCGGTGTGCTGTGCTCAGCTGCCTTCCAAAGGAGGAACAAGATCGGCAA
GTGCTCGACGCGTGGCCGAAAATGCTGCCGAAGAAAGAAATAAAAACCCTGAAACATGAC
GAGAGTGTTGTAAAGTGTGGAAATGCCTTCTTAAAGTTTATAAAAGTAAAATCAAATTAC
ATTTTTTTTTCCAAAAAAAAAAAAAAAAAAAGTACCT
Sequence 242
TGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAGCTGGAAGAAATAGATTGGGTGACAT
TTGGGGTTATATTGAAGAAGGTTACGCNACAGAGTGTGAATAGTGGAAAAACCTTCAGCA
TATGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTTATTTGGA
G
AAGTTCACAAAGCGCTCTGGAAGACGGAGCAGGGGACTGTCGTAGGGATCCTCAATGCCA
ACCCCATGAAGCCCAAGGATGGTTCAGAGGAGCGTGACTGTGAGTACCT
Sequence 243
GTACGCGGGGTGCTGGGATTACAGGCACGAGCCAGTGCGCCCAGCTGCCTCTGTTTCTTT
TATTAAGCTGTTCTGGACTGTGGGGCTCCTTGGGCAGATGCTGTATTATGGGGATAAGCC
ACACACTTTTTGAACTGGCCCGGTCAGGGGGGACATAACCATTTNCTGTGCCACCCCATC
AATCCCCACCTATTCTGAGTGTAGGCTCCTCCCCTGCTTGAGTAATGGCCACAGATCTTG
GCTCGGCACTCCTAAGCTGCATGTTGAATTCCTGGGACAACAAGACTGGCTTGTGGTTCC
ATTCTCCAGATCCTTGGGTTGGCTTCTGGGTGCACTAGGAGATCTGAAATGCTCTCAGGC
CACCAGGAAAGTACTGGAAGTAAAGTCTGACTCTAAAGAAGATGAAAATCTAGTAATTAA
TGAAGTAATAAATTCTTCCAAAGGGAAAAAACGCAAGGNAGAACATCAAACAGCTTGTGC
TTGTAGTTCTCAATGCACGCAAGGGTCTGAAAAGTGTNCTCAGAAGACTCTNNAAGAGAC
GAAACGAACCCTGTGCCTGTAACTTTTGAGGNGAAAAGAACAAAAATGGCTCTTAGGNGG
TCCCGAAAAAAN
Sequence 244
TCCACCCACCTCGGCCCTCCAGTGTGCTGGGATTACAGGCATGAGCCACGGCACCCGGCC
CTGGTTTGCTTTCTGAACCATGTCAATACAGTACCACCACAGTTGCTATCTCTTGAAC
AT
CTTTCATTAAAACATCACCGTCTAGTTTGAGAATACTTTTAAGCCTGCTGGCCTCCTTT
G
GGGCATTCTTTTTTCTCTTTTCAGCACGCATCTTTCTTTTCCACTTACTCCGTAAGCTT
T
TAGCCATGTTTTACCTTGAGGGCCGAAGTTAACTTCAGCGGGAGTGAACGACAGGGGTGG
GCTCCACTTTATCCAGTGCACTCGGAAGCCGGAGGGCCCCCACCAAAAAGAGCAAGGGGA
ACCCTC
Sequence 245
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACAATTGCTTGAGTGAGTTCATGGTCCGTAGG
AGGATGACCACTAGCCCACCACCTTCCACTGTTTCTACAGTCCTGGNCAGCAAGTTTGGA
GTTAAGGCTTCAAAATCCTGCAGCACACACATGCCGAAGGTATTGCCCAGGATCTTGTGG
GTCTCGTTGTAGTAGCAGTAGCGAATGTTTGTGGCTGCTATGAAGAGTTCAAAGGGGTCG
TCCTGCTTTATGTTCAGTGTTCCATTCTTTATTTTCTTCTGCAGCTGTCGCA
T
Sequence 246
GCGGCCGTGGGGATCAGCGTAGGTGAGCTGNGGCCTTTTGCGAGGTGCTGCAGCCATAGC
TACGTGCGTTCGCTACCGAGGATTGAGCGTCTCCACCCATCTTCTGCGCNGNCACCATCT
ACATAATGAATCCCAGTATGAAGCAGCAACAAGAAGAAATCAAAAGAAGAATATAAAGAA
ATAGTTCTTGTCCCAAAGGAAGGAAACTCTTGAAGGATTGAATTTCAGCCCTTCTTGCAT
CTTGGGATCTCTTGGTTGGGAAACGGAAGGAAANAAATNGGAAGCCTTGTCCCGCAAGNG
CTTTGTCCANANAAAGGGGAAAACCATTCTGGGGAATGGACCCACCTTTAAACCATCTAC
CAAACCTTCCAAGCCCCTTGGGGGGGTNTATTTGGTCCCCAACACAAAAAAATAGAAGTA

Table 1

TAAAGAAATANAGGTTANCCTTCGGGCCCGCTTCTTANGGAACCTAGNNGGGGAATCCCC
CCGGGGCCTTGCCAGGGGAAATTCNGGAATNTTCAAAAGCCTTTATCGGAATACCCCGTC
CGGACCCTTCGGAGGGGGGGGGGGGGCCCCGG
Sequence 247
GGCTTGCTTGACTAGATGAGCTGCTATAGTAGCCAATCCTGTTAGACTTGGACCATTGTT
TGTCTGAAGAANGGGAATCTGTCGCTCGCCCTGAGCACTGTATTTATTCCCCTTACTCAA
GNCCCAAGGGACTTCTCCAAGTAGCCGACAAACTCTGCCGGGCCGCCCGCCATCTTCCGG
GCCCGCTCTAGAAACTAAGTTGGGGATCCCCCCGGGGGCTTGCAAGGGGAAATTTCCGAA
TATCAAAAGCTTATCAGAATAACCCGTCCGAACCTTCGGAAGGGGGGGGGGGGGCNCCGG
GGTACCCCAAGCTTTTTTGTNTCCCCTTTTAAGTGGAAGGGGGTTTAAATTNGCCGCCGC
NTTGGGCGGTAAANTCANTGGGTCATTAGGCTTGTTTTCCCTGGTNGTCGGAAAAATTTG
NNTTATTCCCGCTCACCAAATTCNCACAACAAACAATAACCGAAGCCCGGGGGGGAGGCCA
TTAAAAAGGTTGGTAAAAAGNCNCTTGGGGGGTGGCNCTAAATGGGAAGTNGAGCCTAAA
CTTCACAATTAAATTTGCCGTTTGGCCGCTTCACTGGNCCCGCTTTTTCCAAGT
Sequence 248
CCNCTCCCGCGGTGGCGGCCGAGGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTCTTTTTT
TTTTTTTTTTTTTTTTTTTTNCAGAGACNAGGAATTTAATTAGGGNTGTAACAAATGGTTA
ATTNTAGNAAGAAAAACCAAATTGAATAATTTTCTAACTCACTTGGCAGGGGGGGNCTCG
CANCCNTAATGAACATCACATAATGAAGTTNCTCCTTTCCANATCTATAAACAGGCTCAT
GTAACTAACTGATNCTCAGTAAAANGGNNCATAATCCAAATNTNTNTAACAAANGGGGCT
TGCTATAAAATCTCTTACATTTTAANACTTACTCTTAANAAATCATCTATTCTTCCCTC
Sequence 249
AGACTGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAAGCTGGAAGAAATAAGATTGGG
TGACATTTGGGGTTATATTGAAGAAGGTTACGCCACGGAGTGTGAATAGTGGAAAAACCT
TCAGCATATGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
AT
TTGGAGAAGTTCACAAAGCCGCTCTGGAAGACGGAGCAGGGGACTGTCGTAGGGATCCTC
AATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAGGAGGTGTGTTTATCTATCGATCAT
CCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGACCTGGGAACCTGTAAAGCCAAGAAG
AAGAATGGAGAGCCCGTGCACGCAGACTGTGAATTTGCGTGACTGTGAGTACCT
Sequence 250
CGGCCGGAGTGATGCCATCTGCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGGTCA
GCCCATTATCTTTAATCCGGACTTTTTTGTGGAGAAACTCCGACATGAGAAACCTGAGAT
TTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTCATCGATTTACCTGGAACTGAGTT
GGCTCAGCTGATGGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATCAGG
ATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTCCCC
ACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTACACAAAAACTT
GCGAGTAGAGGGTTTGTTTAGAGTACCT
Sequence 251
TGGCGGCCGAGGTACCAGCACAAACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCG
TCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCAGGG
Sequence 252
AGGTACATTTTACTACGCACCCTTACGCATTCTTTTTCTCACCTCTGTGTGTGTGTGTG
C
GTGCACATGCACACACACAAATGGGTGAAACAATTCTCACCATACCAAGAGCCACCGCGC
CCTGCCGAGAATTTGCATTTCTAACAAGTTCCCAGGTGATGCTGACACTGCTGGCTCATG
GAACCACTGCTGTAGTATTTTCCAAATTATCCTGATTCTAAGAACCACCTATGACCTGT
G
CTGTTTTTTCTGTGGTTACTGGCTCATGTCACATAAATTCTTTTAGGATTCAAACATGT
T

Table 1

TGTGATATTACTCAGTATTTACATCTTGCTTTTACTGCAGCATGATGGAAAAATTAACC
A
CAGGTATATCATAACAAAAAGAACATGAGTTACCATTTTTCACAAAGTTCAGATATATT
T
AAATTAGCCTATTTAATCTTTTTTTTGGGT
T
Sequence 253
GGGNGGCCGGGCCCGCCCGGNCAGGGTACTTTTTTTTTTTTTTTTTTTTTCTACCAGTAG
CC
TATTTCAGATTTATTAAAAAAACACATAGGTAACCGAGTCANAGCTTTGGCTAGGAATGAN
TTGGAAAAGAACTGAAGGCATAATTCCACAGGACATTCACAGTTAGTGTGCTAGAAGACA
NGAGAGGGAAGCAGGGAAAAGTGTTTTTAAGAAAGCATTTGCGGGCCGGGACAAATGGGA
AAGGGCCCGGGCTTTCATCGAAATTCCCTTGTTTTGCCTTGGATCCCACAATCTTGCTTG
GGAAAAGGGTGGGGACAAGAAGGAAGNGCCCAAGGGATGGGGAGCCACCCGATCCCAAGA
CCAAGGAAGTANTTTTGCCGCTCCCGGGANGGGGGGGGCAAATTGGATCCTTTGGAATCCT
TCAATGGGTGGCCTNGGGGGTAGCTTAAGGGGGCCCGGTGGAATCCTCCTTTCTNGCATT
TCCGGGGGCCGGGCNAAATNGCCCAAGGGGGGTACCCTTCGGGCCCGCTTCTAAGAAACC
TAGGGNGGGGGGATTCCCCCCGGGGCTTGCANNGGAAATTTCGGAATATCAAAAGCCTTAA
TCGGATACCCGGCGNACCTTCGAGGGGGGGGGGGGGGGCCCCCGGTACCCAAGCTTTTTGGG
T
Sequence 254
CTCACCGCGGTGGCGGNCGAGGTACTCATGGNTGCTGNAAATCATGGCACGCCCGTTCTG
CAGGGNTNTGCTTAGCCAGGCTCCTNTGAGATCTGGCTATTNTGNCTTGTGGATNNTCAG
TCCCCGNGTACCTGCCCGGG
Sequence 255
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGATTGTGTGCAAAATCAGAGGGGGGGTGCAA
AGATCCTGATTTTTCAGGAGTTCAAGCGACAATGGCAGCCCAATACGGCAGTATGAGCTT
CAACCCCAGCACACCAGGGGCCAGTTATGGGCCTGGAAGGCAAGAGCCCAGAAATTCCCA
ATTGAGAATTGTGTTAGTGGGTAAAACCGGAGCAGGAAAAAGTGCAACAGGAAACAGCAT
CCTTGGCCGGAAAGTGTTTCATTCTGGCACTGCAGCAAAATCCATTACCAAGAAGTGTGA
GAAACGCAGCAGCTCATGGAAGGAAACAGAACTTGTCGTAGTTGACACACCAGGCATTTT

Sequence 256
ANCGCACACCACCACNTCTGATTAATNTTTTGNATTTAAANNTTTAGGTGGGGCTNCACC
ATGTTGCCCAGACTGGTNTTGAACTCCTGAGCTTAAGCAATCCACCTGCCTCGGCCTCCC
AAAGNGTTGGGATCACAGGCGTGAGCCACCGCATCCGGCCTCATGTTCTTTTTCATTAAA
GAGAGAAATCAACTATTCAGGACCGGCCCCCACCTTTCCTCAGGAGTCATTTCTGTTCCG
CACAGGCCTGCTGAACTGGGTGCTTTATATAGGGNANAGGGGGCCTCATTTTTNGTTCCC
CTGNCCCNCAAGCNTTANGGGGCAAAAANAAAACCATCCAANAATTTGGNAAAGGGNNT
TTTTTTTTTTTNAAAATNNGGNNNGGGGGGGGGCCCCCCTCNCTTGNGGTCGGGNGGNTTT
TNCNGGNGNNAAAAAAAAAAAAAAAAAA
Sequence 257
AGCTCCCCGCGGTGGCGGCCGAGGTACTCTGACTTGCAGGGCCCAAGACCGGCCTTGCGA
GCGTCGTTGGCTGATGGGAGTAGAAGCCACAGAGAGTCTTCCTCTTGGAGGTACAGTCAA
TTCTGAGGTTTGGGCGTCATAGACTAAACCCAGAAAACAGAACATTGGGAAGTCTTCGGA
ATATTCTCTATCTTCTTCACCAACGAGTAAGACCGTTTTG
Sequence 258
GGCCACGTGACCGACGCCAACATNGCGGCGCCCAGTGGCGTCCACCTGNTTTTCCGCAGA
GGTTCTCATAGAATTTTCTCTTCACCACTCAATCATATCTACTNACACAAGCAGTCAAG
C

Table 1

AGTCAACAAAGAAGAAATTTCTTTTTTTCGGAGACAAAGAGATATTTCACACAGTATAGTT
TTGCCGGCTGCAGTTTCTTCAGCTCATCCGGTTCCTAAGCACATAAAGAAGCCAGACTAT
GTGACGACAGGCATTGTACCTGCCCGGGCGGCCG
G

Sequence 259
GGTGGCGGCCGGCGGGAGGCTGACGAGAGCCCGGGAGGCGTTAGCGAAGGAAGAGAAAAA
CCGAAGACGAAGCCACTACAGCCCCGCGTACCT

Sequence 260
GGAGCATAAAGNTGTAAAGCCTGGGTGTGCCCTAATGAGGTGAGCCTAACTTCACATTTA
ATTGCGTTGCGCTCACTTGNACCGCTTTCCAGTCGGGGNAAACCCTGTCCGTGCCCAGNC
TGGNATTAAATGGAAATCNGGCTCAAACGNCGCCGGGGAGAGGAGGGCCGGGTTTTGCCG
GTATTGNGGGCGGCTTCTTTCCGCCTTTTCCTTCGGCTTCAACTTGAACTCCGCTTGC
GC
TTCGGGGTNCGGTTTCNGGGCTTGNCGGGGCGNAGGCCGGGTAATNCAGCCTTCAACTTC
AAAAGGGCNGGGGTAAANTAACNGGGTTTATTCCCCACCAGGAAATTCAAGGGGGGAATA
NACCGCCANGGGGAAAANGAAACCATGNTGGAGCCAAAAAAGG

Sequence 261
TGTGTTGAAAAATTGTTATCNNNCTTCACAAATTCCACACAACATACCGANGCCCGGNNA
GTCATAAAGTGTAAAAGCCCTGGGGTGCCTTAATGTAGTGAGCTAACCTCACATTAATTG
CGTTGNGCTCACATGCCCGCTTTTCCAAGTTCCGG

Sequence 262
GGGCGGCCGAGGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGGAAAAG
ATCTGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTG
CTCACGGAGGCACCCCTGAACCCNAAGGCCAACCGGGAGAAAATGACTTCAAATTATTGT
TTGAGACTTTTCAAATGTCCCANGCCCATGTATGTGGCTTATCCAGGCCGGTCGCCTGTC
TTCTCTTATGCCTCTGGNACGCACATCCTGGCATCTGAGCCTGGACTCTTGGAGATNGGG
TGTTCACTCCACAAATTGTTCCCCCATTCTTATNGAGGGGGGGCTATTGCNCTTGGCCCCC
ATGNCCNATCATTGNCNTTCTNGGATTCTGGCCTGGCCCGANGAATCTTCACTTGAACTA
CNCTTCATTGGAAANNATCCCNTGGACCTGGAANGCGTGGGGCCTAATTTCCCTTTCGGT
TTACCTAACCTGGCTTGNAAGCCGNTGGAGGAATTGGTTCNCGGGGGACCAATTCAAAAG
GGAAGAAAANCTGG

Sequence 263
CTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGCAGCCGTTTTT
C
TTACTAGAAGCTAGGCNGAAAGAGTTGTTACTCANATTTCTTGAACTTGAGACGTCAAAG
GTGAGACGCCAGCCAAGGAGAAGGGATGGTCAGGGACCTGCCCG

Sequence 264
CGTGCGGATCTTCTTCTTTTTTGNGGCTTCCTTCANGGGGTCAANAAAACCCTTCTNGGCC
TTTAAAGCCTTCGCTTTGGCTTCAGCTTTAGGAGGGGCAGGAGCTTCCNCCTTCGANNTC
GGCGCCATCTTGNGAAAAGCCCCGCGNACCT

Sequence 265
AGCNNCCCGCGGTGGCGNTNGCCNGGGCANCCCGCGGGGGTGGAAACCTCTTCAGCATTN
GCTTNNNNTCAGGGGGCTAAAAAAACCCANCAACCGGGACCCCAGCTTTTCAGAACTGCAG
GGNAACAGCCATCATGAGNGAGGGCACCAAGAATTCCCTGGAGAAAATCCTTCCACAGCT
GAAATGCCATTTCACCNGGAACTTATTCAAGGAAGACAGNGGCTNNTGGGANCGNGGGG
ATAGAGNGCGCAACCAGGGNGAAANNTTAAACACNGAGNNCAAAGNGGNCGNGGGNCCCN
CGGCCGCTCTAGAACCAGGGGACCCCCGGGCCCGCAGGGAANNCCGANANCAAAGCCNAA
NCGAAACCCGGCNACCNNCGAGGGGGGGGCCCCGGACCCCAGCNNNNNGGNCCCCCNNAA
GGGNGGGGNAAANGNGCCGCCNNGGCGGAAANCAAGGGGCAAAGGCNGGNNCCCNGGGGG
NAAANGGGNANNCCGNNCACAANNNCCNCACAACAACCAAGCCCGGGAGGCANAAAAGGG

Table 1

GAAAAGCCCN
Sequence 266
AGGTACTTTTCTAGGTATTGCTGGGCAAGATCCTTGTTGGAGTCCTCCTCTTTTGCTG
CC
CCACTCAGAGGATAGGCAGAGCAGACTGGCAGACACAACAGCACAAGGAATGCAAGATGC
ATCATTCTCACTGCCCTTACCTTCTTTGTCTACTGGGCTTCTCCCCGCGTACCTGCCC
GG
GCGGNCGNTCGAGCCGCCGGGCAGGTACTACCTGNACCAACTTTTTCATTTGGGCATCAC
AAAGACGAGTCTTCTGATGTTCTATAAGCAATATGNTTATATGAAAGNCAGAAGTTTAGC
GAAAATTCGGCCTAAACAGNAATAAATGAAAATGGANTGGAAATCAAAGNNCTTAAATAG
AACANGAAGGCNGGGCACCGGNGGNTCACGCCTNGNANNCCCAGCACT
T
Sequence 267
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTACCTCATTTCCTACCAATCATT
TTAAGAGAATTTGGTTGTATTTCAAAGAACAAAACAACACAATTTCTGTCCTGCTGTTT
A
TTTTAGCGGTGGTCGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTC
TAACCTCTCCATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCA
AGCAATTGACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTC
GTTCCAGTTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATG
TA
AAGCAGGATCATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAAT
TGTCCGGATTCCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 268
NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTATATGAAAGTCCTCACTTTCAGA
AGCAGAAAAGGAGTAACTAGATGGGCATTTTCTATACCAGCTAAGGCTTTAAACATAACA
ACGTCTACTGAACTATTTTCTACTTACTTTGACTGAATAAGCCAGTGAGATCGTGACTG
C
AAGTGGAAGACCTTCTGGCACTGCGACCACTAAAACTGTAACTCCAATAATGAAGAACTT
CACAAAGTATTGTATATAAATTGGTGTGCACTCAGCAAGCCATGGTCTTTTCTGAACCCA
GAAGGTGTCAATGACAAAATATAATACTAGAATGATAACTGTGATGGCAGGCATCAACAG
ACCTTTCAGAATAGAAATGAAAGAAAAATGTGATTATTAAATTTCCAGACACTAACCCTT
GACAGATATAAATTAAACACTGTAAAGAGTTATAACTTGCTTGATAGTATTGAATTTCT
C
TGAGAAATTACTTCTTTCTTGCACCTTATAACTTGACATTGTCAGATTTAATTTTT
Sequence 269
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATAGTGGAGGCACTGAAAGACCA
GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT
GAACCAACCTCGAGCGGCCGCCCGGGCAGGTACAGATGCACAGGAGGCCATAGGGTTTAG
GCAAAGGGGAGCACAAAAGTTGAAGATGAGGCGCTGCCACCAATGCTGGGACTTCAGGCC
AGGGGCAGGAGCTGAGGAAGCCACAAGGGAGGACATTTTCTGCAGTTGCTGAACCAGTAG
CAACCAGGTCCTGAGAAAGCCCTCTCTTGTGGAAGAATAACAGCCAGGAGGAAAAGCTTT
TCATTCTGCAAAGCTGGGGCAGAAAGTTCTTNTTTGAATCCCGCGTACCTCGGCCCGNTC
TAGAACTANTGGATTCCCCCGGGCTGGAGGAATTC
Sequence 270
GTCTTCGGNTTTTCTCTTCTTTTTTCCAGGGCCTCCAANCCCTCGTCAGCCTCCCGC
Sequence 271
GGGAGGCGNNAGCGAAGGAAGAGANTNTTCGANGACGAAGAAAACCCAGCGCCCCCCACG
NACCT
Sequence 272
TTGGAGCTCCCCGCGGTGGCGGCCGAGTCCCACAGTTAGCTGCAGCAAAACGCAGGCTGC

Table 1

CTCAGGGAAAGGAGCCTGGGTTGATTAACTTGTGTGTCAATGTCCCACCCGTCCCAGGTA
ACATTTTGCCCCCTGAGGTCCGGGGTAATTTAATGGCTGCTGGACAAAACCTCCAAAGTT
CTTGAAAGATCAGAAATGATAGCTACCTGGAGTCCAGCTGTACGGCACTTGGCGTAAAGC
CGCTTCCCTCAAGAGTAACTACAATCTTCCCATGCACAAGATGATTAATACAGATCTTAG
CAGAATCTTGAAAAGCCCAGGAGATCCAAAGAGCCCTTCGAGCACCACGCAAGAAGATCC
ATCGCAGAGTCCTAAAGAAGAACCCACTGAAAAACTTGAGAATCATGTTGAAGCTAAACC
CATATTGCAAAGACCATGCGCCGGAACACCATTCTTCGCCAGGCCAGGAATCACAAGCTC
CGGGTGGATAAGGCAGCTGCTGCANCANCGGCACTACAAGCCCAATCAATGAGAAGGCCG
GCGGTTGCAGGCAAGAAGCCCTGTGGTAGGTAANAAGGG
Sequence 273
TNTTAGGGNCAAACACGGCCCCAGCCCGCGNCCCAGNCNGNGCGAANGATTTTTTCAGGG
NGACAAAAACCCAGGNCACCCACCTGCCCG
Sequence 274
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGCGTCGATGCTATGCGCTCAGTTC
TAGTCAGAATAATCTTGCTCATCCTCCAGCTCCCCCTGTTCCACCAAGGCAGAATTCAAG
CCCTCATCTGCCAAAACTACCACCAAAGACTTACAAACGGGAGCTTTCGCACCCCCCATT
GTACGCGGGGGAGGAGCCTGAGGAAGAGGGCGGCGACGGTGGTGGTGACTGAGCGGAGCC
CGGTGACAGGATGTTGGTGTTGGTATTAGGAGATCTGCACATCCCACACCGGTGCAACAG
TTTGCCAGCTAAATTCAAAAAACTCCTGGTGCCAGGAAAAATTCAGCACATTCTCTGCAC
AGGAAACCTTTGCA
Sequence 275
CAGCGAGCACGCGTNTTCCGCAACCCGAAACCNCCTTACAGGAGGTTTAANACNCANCCC
AACGGGGAGAGNGGGGGAAACATGANGACAGANNNNGGGGGGAANGAAAATGGNACCTCGG
CCGCTCTAGAACTA
Sequence 276
AGGTACGTTCTATTCCTGCTCCTATTAGGTCCTTCTCACCGCACCGGCCCTCGGTCGATT
ACGCCTCTCCAGTTCTGCTGGGGACGTTCTAGCCTCGCCCCANCCGCGTCGATCTTTATG
TTATACCGTCACTCCCAGTGCCCTAATGGAACTATCCCTCCACTACTCCCCCTGGTTCTA
CCCGGCTCCAGAGCCTCTCCCGGCCCACTAATTTATTCCCAAATTCTAGGCCCGGCCCCA
TCAAGCCCTCCCCGCGTACCTGCCCG
Sequence 277
GACTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGAGCGGGCCCTACCGTGTGCGCAGAAA
GTGGAGGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACTCANCT
GTTCGNTGCTTCAGGGCCTGCTGATTTTTGGAAATGTGATTATTGGTTGTTGCGGCAT
TG
CCTGCTGCGGAGTGCATCTTCTTTGTATCTGACCAACACAGCCTCTACCCACTGCTTGAA
GCCACCGACAACGATGACATCTATGGGG
Sequence 278
TTCGCCCGGGCAGGTACTTTCATCCATAAAGGCCTGCAGCTGTTTCACTGATCCTTGCAG
TTCATCCATCACCAACTCCATACAGTCAAAGACTTTGCTCTGGTTCTGTAATATTTTCT
G
GTAGTCAGGTTTTGTATTAAGAACTTCATTCTGAGAAGACCCAAGATATGTCATAGGTTC
CACTTTGACCTCAGTAATTTTGGCCTCAGTTGATCCTCTGGACAATATCTCTTTAGCCT
C
CTGCTGGTAGTGAGGCAAGAGCTGATCCCAAGTCTGACGTTCTAAAGAAAACTTTGTTAT
GTATTCCTTCATCTCAGCCACAGATGCTTCCAAAGAAAAATCTGATGCTTTTCCATTTG
A
ATCTTCAAAACATTTTTGNAGAGTTCCATCAGTTTCCAGGCCGTCTGCAAAATGTTTCA
A
TTCTTCAGAAAGAGAAGATGCTTTGGCTCTAAAACTTTCAAGACTGAAGCCCTTAGTGGC

Table 1

CCTTANGAAAGGGT

Sequence 279
CACTGTTCTTTCTTTCTAATAAAACTTTCTTTTTCGAACCTATACTGTCTTCTGTAAATT
CTTCTTACTACCCTATGACCCGTGAGCCAACCACTTTCCGATGCCAGGGTTCTGACACCT
CACCTGGCATAATATAAAGTGTTTTTTTTTTTTATACCCTTCCACTTGGAAAGACTACAG
A
GGAATCTTGCNCTGCATAGTTCAAACTAAAAAGAGAAGAGTTAATTACCTGAAAAGCAAG
AGAAAACAAGAAGGGGTAAATTTTGAACCAAGGGAAATCATTTAAGAAGTGTCTGGTATT
TTTCAAATTTCTGTCAGTTGTTACATTTGTCATAAGTAAATGTTTAGGAATAAAGGATG
G
AGACATGCTTATTTTATTTAACTCCCCCAAAATTAAAAAANNAAAAAAAANAAAAAAAAAAA
AGTCCCTGCCCGGGCGGCCGCTCGAGATAAC

Sequence 280
CCGCGGTGGCGGCCGGAGTNATGCCATCTGCAGGTTTTGTGATCTGCAATGATTCTTCCC
TTCGAGGTCAGCCCATTATCTTTAATCCTGACTTTTTTGTGGAGAAACTCCGACATGA
GA
AACCTGAGATTTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTCATCGATTTACCTG
GAACTGAGTTGGCTCAGCTGATGGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCTGGCC
CAGCATCAGGATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATAC
TTGGGTCCCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTAC
ACAAAAACTTGCGAGTAGAGGGTTTGTTTAGAGTACCT

Sequence 281
GGGGGGAGACATGTGGAGGTCCCAGCAGAGGCCAACCTGTGTCTCTTCATCTCCCTGGGA
AGGGTGCCCCCGAAGTGAAAGAGATGGCCTGGTGGAAAGCCTGGGAGAATGAATAAACAG
ACTAGGGTGAAATCCATACAATGGGAATGGTAGCAGACAATAAAAAGAAAATGAACTATT
GATGCCCCCTACTGCACAGCAGAAGCTCTGAATCGTGTTCCTGAATGAAAGAAGTCAGAG
ATGAAAAGATGGGCCAGGAGTCCAGTTTCTGGAAGGCCAAGAATCGAAGTAGCAAGCTGC
AAGCCGTTTTCCAGACAAGCNGNGATGTGGGGATGCCACAAGAATTCAGGACTGGAGGGG

Sequence 282
CGCGGTGGCGGCCGAGGTACTTNTNACTGCCAGAGGCTGTGACGNTGTGTATTCNGAGAG
CAGCCTTNCCTGCANTGATNCCATCCCGCAGGAATCNAANTTCTCCCTNGATACNGNGCA
CTCTGCCTGTCTTTCCACNTTTCCCTTTCNCATTTTGCANTACACNGTTCACCACNCT
GC
CCTTAAGGCTTGGAAACTCACNCCACCTTCAAGCNTCCCATGGTTCTCTGCCACTCATGG
GTCNGGGNAACCAGGGTGGACAAGGGGGCCAGAATCAAAGNCGTTCTTTCACCCCCACCC
ATGGGCCAAGGGGGAATGGGGGCCCCAGNNNGGGGTTCCCCAAAGGCANCAAGNAAAANNA
ACTTGGANACTTGGAAGTGGANGGGCCATTGGNAGGCAAGNCCTNGAAAANGCCANAAAA
AGGGGAGGGGNCNGNAACCACCNCAAAAAAAGGTTTGGANGGCCAGNAAAAGGGANANNGG
GCCCCAGGGGAAAAAACCTTTTGGGCCCCATTTTTTTTTCCAATTTTCCAATTGGGCCT
TG
GGCCANTAATTTCAAAGGGGAAGGAATTANCCTTGGGNNAAAGGGGGNTGGGGGGGGG

Sequence 283
TGGCNGCCGAGGTACAGNATTGGAAATGGATCTGTCTTTGGTAAAGATCAGCCTATAATT
CTTGTGCTGTTGGATATCACCCCCATGATGGGTGTCCTGGACGGTGTCCTAATGGAACTG
CAAGACTGTGTCCTTCCCCTCCTGAAAAGATGTCATCGCCNACCAGATATAAGAAAGACG
GTTTGCCCTTTTCAAAAAGACCCTGGGAATGGTGGGCCCATTTCTTTGGTNGGGNCTTCC
CAATGGCNCAAAGNAAAGGGGAAANGGGCNATTGTGAAGAAGGAANANAGTATTTTTACC
TNGAAAAAGGCCATAAATGGTGNANANAAATTCTTTCCANAAATTCCNCAAGNGNGGTGG
CANGCCCCTNTAGTANTAAAAANTANCGNCCCAAAGGAAAGGNTCANGTTTAAAAGGGGTT
TATTTTGTTTGTTNGGGGTAAAATCNCAAGCCCCAAATACCCCAAACTTGNCCCCTGGAA

Table 1

CTTGGCTTTTCNCAAAGGTTCNAGGCTTTCCNATTCTCAATTCCCCCCCAAAAGGGGAGG
AAACCNTTTCC
Sequence 284
GTGGCGGCCGCCCGGGCAGGTACGCGGGGGGCTCTAAGCTGCAGCAAGAGAAACTGTGTGT
GAGGGGAAGAGGCCTGTTTCGCTGTCGGGTCTCTAGTTCTTGCACGCTCTTTAAGAGTCT
GCACTGGAGGAACTCCTGCCATTACCAGCCTNCCCTTTCTTTGCCAGAAAGGGGAGGGGG
GGAAAAACAATNACAATTTTATTTCCATTGGCCCAAGTNCTTGTNTNGCCAATTGNCAAG
TGCTTTTTTTTGGGCCNTTTNTCTTACCCCTTTGCCAAACCAAGAAAACTNAAAATNTTG
N
CNACNCAAANCTTCCCTTTAGTTAGNCGCGGAATNTCNCCGCCCCCACAAGTAAGAAAGT
TCNCNTGGNNAAGNCCCACCAAGANCCTTTTTTTTTTGGCTTTTTTGCCAATTTGGTGA
AG
GGAAG
Sequence 285
TGGCGGCCGAGGTACTAGGTCCCAAATGTTTCAACCGATTTTACCCTATGTTTTCAAGGG
TATTATAGAAGGGGAGAGGTATCCTGTAGTGATGTCCACGTATCTTGGAGTTATGGGTCG
AGTTCTACTACAAAACACTAGTTTTTTTTCTTCACTTACTTAATGAGATGGCCCATAAATT
TAATCAGGAGATGGACCAGCTTTTGGGAAATATGATTGAAATGTGGGTTTGATCGAATGG
ACAACATTACCCAGCCTGAAAGAAGAAAACTTTCAGCTTTGGCTTTGCTCTCTCTTCTGC
CATCTGATAATAGTGTTATCCAAGATAAATTCTGTGGGATTATAAACATTTCAGTAGAA
G
GCCTGCATGATGTCATGACGGGAAGATCCTGAAACAGGAAACTTATAAAGACTGTATGTT
GGATGGTCTCATCTTGAGGGAACCCAAAAGTAACCAGGAAGATGAATGAAACCACCCAC
Sequence 286
GCGGCCGAGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGGAAAAGATC
TGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTGCTC
ACGGAGGCACCCCTGAACCCCAANGGCCCAACCCGGGANGAAAAATGAACTTCAAAATTA
TTGTTTTTGGAGAACTTTTCAAATTGGTCCCCAGGCCCATGGTATTGTGGGCCTTATC
CC
AAGGCCGGGTNGCCTGGTCTTCTCTTATTGCCCTTNCTGGGGACCGCCACAAACNTGGGG
CAATTNGNTGGCCNTGGGAACTTCTTGGGAAAGAATTNGGGTNGGTCCAACCCCCAACAA
AATGGNTCCCCCCCAATTCTTATTGGAAGGGGGGGCCTTAATTGGCCCCTTTTGGCCCCCC
CAAATGGCCCCANTCAATTGGNCCGTTCNTTGGGGAATNCCTTGGGCCTTGGGGCCCGGG
AAGNAATTCTTCAACCTTGGAACTTAACCCCTTCAATGGAAAAGAATTCCCTTGGACCT
TGGAAGGCCGGTGGGGCCTAATTTCCCCTTTTCGGNTTTAACNTAACCTTGGCTTGGNAA
GCCGGTTGGAANGNAAATTTGGTNCCCGGGGGAACCATTTCAAAGGGGGAGGAAAAAANC
TNGGNGGTTTTAATTGTTAAAGCCCTTCTTGGGGNACTTTTTTGAAAAAAA
Sequence 287
CTCCCCGCGGTGGCGGCCGAAAACTGATCAGACTGTCTCAGATCNAGGAAAAGATGGCCA
GAGAGAAGCTGGAAGAAATAGATTGGGTGACATTGGGGTTATATTGAAGAAGGTTACGC
CACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGNGACC
TGACACANTGTGTGTCCTTGNTCTTATTTGGAGAAGTTCACANAGCGCTCTGGAAGACGG
AGCAGGGGACTGTCGTATCGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCA
GAGGAGGTGTGTNTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTT
GACCTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAAGCCGTGCACGCAGACTGTGAA
TTTTGCGTGACTGTTGAGTACCTCCGGCCGCTCTAGAACTANTTGGATCCCCCG
Sequence 288
GCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGTGGAGCGCCTCACTAACTCCATGATG
ATGCA
Sequence 289

Table 1

GGACAGACTGGCTCATNGAAGACATTNACTNTGATGGGACCATTTNAANCNGATAATTTT
TCTCATAACCTGAGAGGAGTNATCCCACGAAGTTTNGAATNTTTGTTTTCCTTAATTGA
T
CGTGAAAAAGAAAAGGCTGGAGCTGGAAAGAGTTTCCTTTGTAAGTGTTCCTTTATTGAA
ATCTATAACGAGCAGATATATGATCTACTGGACTCTGCATCGGCTGGA
Sequence 290
TGGCGGCCGCCCGGGCAGGTACGCGGGGCCCGTAGGAGCCTCTCTCCCTACTGCTGCTAC
ACAAAGACCCTGAGACTGACCTGCAGGAACTNAAACCATGAAGAGCCTGATCCTTCTTGC
CNTCCTGGCCGCCTTANCGGAAGTAACTTTGTGTTATGAAATCACATGAAAAGCCATTGG
GAAATCTTTATGGAAACTTAATTCCNCTTTTNATTTAAANCCAGGGNAAGNNAATATGT
N
AAAAATTCCNCTTTTTTATTANNTCCCCCTCTNCAATCCAAGNANGNATGGGGGAAGCNA
GCNTAAAACCNCTNCNNATNANANAGNTNGGGGTTTCTAAATAAGNAANCCTTTCTTTCTA
AANANGNNCNTNGNGTTCCCACCGATATCTTTTATATATTNNGGGGATTNANCCCCCCNTN
TGNNAGNTTTATNTACTTTNACNNANGCATTTTTTTTTTNNGTGNAAAAAACCCCGCNNT
T
AACCNACCCCAANTNGGGGTTTTTATATTGGGGGGNANTNACCAAAAATGGCCTNGGCCCT
TNTATNANAAATCNGCGCTTTNNCNTTTATAACNAGGGAAAAAAAGCCCCCCCCCANNGG
GGGNNANNCCCNAAATATNTNTAANATNNTTGGNNGGGGGGAAAAAAAAAAAA
Sequence 291
GAGCCCGGGTGGCGGCCGCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTGGGGGAGTTA
AATAAAATAAGCATGTCTCCATCCTTTATTCCTAAACATTTACTTATGACAAATGTANCA
ACTGACAGAAATTTGAAAAATACCAGACACTTCTTAAATGATTTCCCTTGGGTCAAAAT
T
TACCCCTTCTTGTTTTCTCTTGCTTTTCAGGTAATTAACTCTTCTCTTTTTAGTTTGAAC
TATGCAGTGCAAGATTCCTCTGTAGTCTTTCCAAGTGGAAGGGTATAAAAAAAAAACACTT
TATATTATGCCAGGTGAGGTGTCAGAACCCTGGCATCGGAAAGTGGTTGGCTCACGGGTC
ATAGGNGTAGTAAGAAGAATTTACCGAAGACAGTATTNGGTTCCGAAAAAGAAAGTTTTA
T
Sequence 292
CGGTGGCGGCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTTGTTTTTATCTTTT
GGCCTTTTGGTGACTTGGTGCTCCTTGGAGTCACTGGAGTTCTACTTTGAATCCCACT
CT
GACATCAATCGACTGCCTTAATTCCTGGTCCAGCTGCCCGACCCTGACTCTCTNCCGCTC
TTTTCCTCAGGTCGAANGTTTNCTTTAAGATCACGCTGACGTCGGACCCACGGCTGCCGT
ACCTGCCCG
Sequence 293
GTGGCGGCCGCCCGGGCCGGACGCGGGGACATTCGAGTGGGGATTAAGAGAAGGAAGGCT
GCCTTGCTGGAGCTGTGTGGTCTTCTCCAAGTGAGAGTCGCAGGCAATAGAACTACTTTG
CTTTTGGAGGAAAAGGAGGAATTCATTTTNAGCAAGCACACAAAGAAAAGCAGTTTTTTTT
CANGTGCTGACGGCCACCCACCATCATCTAAAGAAGATAAACTTGGCAAATGACATGCAN
GTTCTTCAAGGCANAATAATTGCAGAAAATCTTCAAAGGACCCTATCTGCAGATGTTCTG
AATACCTCTGAGAATAGAGATTGATTATTCNACCAGGATACCTAATTCAAGAACTCCAGA
AATCAGGAGACGGAGACATTTTGGTCANGNTTTGCAACATTGGACCAAATACA
Sequence 294
GCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAGGCACATTCTTTTCTACGTGAAGAGTTN
TGTAAACTGAACTTTGTTTTCAGNNCCGGCTCCAGCCATCCTCGGGTAGCTTGCCAATAG
ATGAATCCCACTCGTTTGACCCATGACGCTCCTTCTTTGCATNNCTCCCTCTTTCCCC
AC
AGCAGNGCATGTCCACCATACCACCTGAGAGTCTGTGGAATCTAATTTTCTGTNATACTT

Table 1

CTTTCCTTACACTCATTTTCCTGTCTTTATTATGATAGTCTAACTTTTTCTCCTCAAAGG
TATAGCTGCCTTGCTTTCATGAAAACACACTTTCCTATTGTGATTTATCAGAGGCCTTT
C
CATATCTCAGCCACTATGCTATGACAGATTTTATAATTAATA
Sequence 295
CNCGCGGTGGCGGCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCCGGAATCC
GGACAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCC
TGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAAGAGCTTTAAATGCTACCAAAC
TGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCA
ATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGTA
GAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGACCCT
Sequence 296
CCGCCGGGCAGGTACGCGGGGGCTCCCTTGTGAGTAGACTATGCAAAGAAAAAGTGGGCCA
CCATATCTGGAAACTACAGTCTATGCTTTGAAGCGCAAAAGGGAATAAACATTTAAAGAC
TCCCCCGGGGACCTGGAGGATGGACTTTTCCATGGTGGGCCGGAGCAGCAGCTTACAATG
AAAAATCAGAGACTGGTGCTCTTGGAGAAAACTATAGTTGGCAAANTCCCATTAACCACA
ATGACTTCAAAATTTTAAAAA
Sequence 297
GCGGCCGCCGGGCAGGTACGCGGGGGGGAGGGCTCCGAAGTCTGGTTTTGGGCGGGAATTG
AAACCGCCGCTGAAGCCAACAAGAATTTGAGAACTGTAAATACCAAGCCTTGAAAGGGAC
CATGGTGCGGCCTGTGAGACATAAGAAAGCCAGTCAAATTCTCACAGTTTGACCACTCTG
ACAGTGATGATGATTTTGTTTCTGCAACTTGTACCTCGGCCGTTCTAGAAACTTANTG
GA
TCCCCCGGGCTNGNAGGGAATTTCCANATTTTNAANCCTTTTTNCGGANCCCCCNCNCCN
CCCCTNAANGGGGGGGGGGGNCNCNNGCCCCNCNNTTTTTNNNTGGCCCCNTTTTTTGNNG
GGGGGGNGAATTTANCNNCCCCNCNGNCGGGGNAAANAAAATAGGGGGGNAAAANTNTTT
TTNTTNNGNGGGGGNAANAAAATTTTTTTTNTCTCCCCCCCAAAAATAAAAAACNCGNCCC
NCTTTCTNTCCCCGNTGGNNGNAAANNANTATNGNGGTCCCCCCNNGNGGGGGGGGGGGAN
ANTTTTTTTTTTTNNNNAATTTTTTTTTT
Sequence 298
GTGGCGGCCGAGGTACTCCCCAGCAAATATTCTTTGTTGGCTTGCTTGACTAGATGAGCT
GCTATAGTAGTCAATCCTGTTAGACTTGGACCATTGTTTGTCTGAAGAACTGGAATCT
GT
CGCTCGCCCTGAGCACTGTATTTATTTCCCCTTACTCANTCCCCAGGGGACTTCTTCCAA
GTAAGCCGACANACTTCTTGCNGGCCCCGCNCGCNCANTCTTTTCCCGGNCCGGCTTCTT
AGTAAACTTAGGTTGGGAATCNCCCCNCGTGGGCCTGGCNAGGGGAAATTTTCGGAATTA
TTCAAAAGGCCTTTATTCNGAATAACCCGGTTCNNACCCCTTTCNCAAGNGGGGGGGGGG
CACCCCGNGTTAACCCCCAAGGACNTNTNTTTGGTGTNCCCCCTTTTTAAGTTGGAAGGG
GGGTTTTAAAAATATTGGCCGACCGNCCTTTTGGGTCCGNTTANAAATTCCAATTGGGGG
GNTCAATTAAGGNCCTTGNTTTATTCCCCTTNGTNGTTGGAAAAAATTTNGTTNTAAAT
T
CNCCGNCNTTTCAACNAAAATTTTTCCCNANNCAACCAAAACCNAATTAACCNGAAGNCC
CCCGNGGGGAAGNCCAATTAATAAAAANNTTGGTTAAAAAANGGCCCCTTGNGGGG
Sequence 299
TGGCGGCCGAGGTACTTCTGTCTTCCAGTTTTCCACTTCAAACTTCTATCTTCTCCAA
AT
TGTTTNATCCTACCACTCCCAATTAATCTTTCCATTTTCGTCTGCGTTTAGTAAATGCG
T
TAACTAGGCTTTAAATGACGCAATTCTCCCTGCGTCATGGGATTTTCAAAGGGTCTTT
TT
AATTCACCCTTCCGGGTTTTAAATCCTCTTTTTTTTAAAAAGAATCCGTCCTTTCAAAAAT

Table 1

TATNTTTAAAATTCACCCTTACCAACCTTTTTAAAAACCTAAAAACCTTTAAAGGCTTGTTT
TAAAGGTCCACCCTTTCATTTTTTTAAATCTAAAAAAGGCCATTTGGCCCCTTTCTAATT
T
GGGNTAATTNAAATTCCGGGGGGCCTCTTGTTAGGTACCCTNTTCTCTTCAAATTTTTAT
C
CTTTTTTTAAAAATTACCATTTTTTTTTTTACCTTCCCATTGAAAGGAAAGGCCTTTNCAT
TCTTTCAAACCCCTTCCCGGTTCAATTGGTTTTTTTAAGGAAAAAAACCCCTTTTTTTNAT
TTCTTTTTTTCCCCTTTTCCCCTTCCAATGGCCCTTAANCTTTCTTTTCCTTNAAAGGGT
GCCTTTCCAATTAATTTTTTTTTCCTTCTTTTAAAAAAAAAATTCCTTTTA
Sequence 300
CGCGGTGGCGGCCGAGGTACTTAAGGTTGACTGGTAATCAGGGTAACTTCTGATACTTAT
CACACAAGATGGTGCCTCAGCATTTAAATAAATGGAGGTAGGGGAGGGCGTGGTGGTAAC
ATACTTTTAAACCAGCGATTGCACAGCAAACCACAATGCAAGGTATTTCTGACTCCCAAG
ATTGCCCGTTTCCTAAAGAGCAATTCTTCTGCAGGCAACAGCAAACCTACCTTTCCTTGC
TAACTGCTTTCAGTAAATTCTTGATGGCCTTCGATTCTGGATTCAGACATCTCTTCTCA
C
CCTTCTTTTTCATTGTAGCAATGATCTCAACACGTG
GA
Sequence 301
TCCCCGCGGTGGCGGCCGGAGTGATGCCTCTGCAGTTTTGTGATCTGCAATGATTCTTCC
CTTCGAGGTCACGCCCATTATCTTTAATCCTGACTTTTTTGTGGAGAAACTCCGACAT
GA
GAAACCTGAGATTTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTTCATCNGATTTA
CCTGGAACTGAGTTGGCTCAGCTGATGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCT
GGCCCAGCATCAGGATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTG
ATATTTGGGTCCCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTAT
CTACACAAAAACTTGCGAGTAGAGGGTTTGTTTAGAGTACCTCGGCCCGCTCTAGAACTA
GGTGGATCCC
Sequence 302
TTGGAGCACCCCGCGGNGGCGTTTTGGGACGCNCGGAACNGCAATGCTTCAGGACCCACA
GGAGCGACTCTTTAAAGGGACCACAAAANCCGCACAGAGCTGCAAACAACTATACATGAT
ATAATATTAGAATGTGTGNACCTGCCCG
Sequence 303
GNGGCGTTTTAGGGCGNAACGGCCCCCCCATCATGGCGGACCCTAGAGAAAGGCTCTTAGG
GGGACCNAAACCCGNNGCCCGAACACAAGGAGANCGACGGCCGCTCTTNAACCAGNGGAG
C
Sequence 304
TCGCCCGAGCTTTCTCTTGTCCATCTTCTCCCGCTGCTGAAATTTCAGTTGCGGGCGCTG
TCACCTCAGGACCCCTCCCCCCGCGTACGCTGGATAGCCTCCAGGCCAGAAAGAGAGAGT
AGCGCGAGCACAGCTAAGGCCACGGAGCGAGACATCTCGGCCCGAATGCTGTCAGCTTCA
GGAATCCCCGCGTACCTGCCCG
Sequence 305
NTTAAGAGCAAAGGCTCATGTTTGCCAAGTCTGTCCTTTTGTAACAAAAAACCCAGCAGC
TTTATCAAGCAGAATTCCACCTGTATTTCTTAACTTGCCAGAGCTGAGTCTCATGGCC
AC
CCTTAGCAGGAGTTGGGGAGGTATTTTTAACAAGGCACATTATCATCTCCCCCACCCAAA
GTGGAGCTATTGCTAATGAAAAAGATACAATGAGATGTTTATGAAATTATCTGTAGCTAT
TAATGTCAGGTTTTTGAAATTTACTGACCTGGAAGAATACTCATAATGCAATGTCAAGT
G
AGAAGCAGGACAAAGAACATTTGCAATACAGTTGTATTTATAAAATTTTGTT
Sequence 306

Table 1

NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGGCAGCGGAAAGCTCAGCCC
ATGTGAGGTGCCTCCTGCCAATCACAGACTACCCTTCCCTGGTCCTGGAGGTTCAAAGAA
TTGCAGGAGGGTAGAAAAGCACCTGGGTCGGGTGCAGACTGCGGAGCGGGCCCTACCGTG
TGCGCAGAAAGAGGAGGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGA
CAACTCAACTGTTCGTTGCTTCCAGGGCCTGCTGATTTTTGGAAATGTGATTATTGGT
TG
TTGCGGCATTGCCCTGACTGCGGAGTGCATCTTCTTTGTATCTGACCAACACAGCCTCTA
CCCACTGGTTGAAGCCACCGACAACGATGACATCTATGGGGCTGCCTGGATCGGCATAT
Sequence 307
CACCGCGGTGGCGGTTTAGCCCGGCGCNAAATCACCATTATTCCCCTTTAGTCACCTCAG
AGGCTTGTTAATGCTTTCTTTGTAATTAGGCTATATCTGGTATCTGTATAATATCTTCA
G
TTCTTCTTTACCAGGGGTCTTACTCTGTTCTGAAACATGGCACCTCAGGCGGCTCCGGCA
GCGCTGGACACAGGAAACTCCTGGGTCCCCGACTCCGGCTCTCCTNGACCCCCTCTTCGG
TTAACTCCGCTTGTTTCTCTACAAAATGGCGCCGGAGGTCCCCCGCGTACCT
Sequence 308
TGGGGNAACCCGCGGNGGCGGTCTTGGGGNCAACACGGAAACCAAACGAACCGCGGCTGC
ACCAGCNGNCTTTTTTNGGGGNGCCAAAAACCCGAGCAGCCGAAANCNGGAACNGCCNCA
GNNGTGTNCCNGCNGAAGAANGNCNANCCCAGAGAGGCCAAAGNACCC
Sequence 309
CCCGCGGGGGCTTTNGGGGGCAANCGAACACCNCTTAAAGGGNNCNCCNTCTAAAAATNT
TTACNGGNAGAANAAAACCCACCAACCGCTTTTTANTATCGAGNGTCAGAAACCNTTCAC
AAGATGGNAAAAAAAAAAAAAAAGAAAAAAGAAAAAAAAAACAAAACCAAAAACAAAAAAACT
TTACAACCACAGCTAAANGCAANNNNNNCCANGGNTCCCAGTCAGCTCCAANNCCAAGGGG
NGCAAAGCCCANNNNNNNCCAAGCATCCAAANGANAGAGACAGGCCAGGAAANNCTNTAT
NCTATGGGGAGCAGCNNANGCAGGGGCAGCCAAACACAAAGCNNCAGGACAAAANGGACC
NGCCCGGG
Sequence 310
CACCGNGGACAAGAGCAGGNGGTNCTTGGGGGGNGNAAAACCCGCNCCGCGANGCAAGAG
GCTCNGCACAACCACTACTNTNCAGAAGAGCCGGGNCCNGNCCCCGGGAAAAAGAGNGCG
A
Sequence 311
CCTGAGGAAAAGCTCGCACCAGGNGGACGCGGATNNGGTANGGGGGGGTAAAANACCCNCC
CCAACAAGCCGCGGGGCAAAANGNCCNCGTACNTCGGCCGCTCGAGAACTAGCGNACCCN
A
Sequence 312
CCCGCGGTGGCGTTTCCNGGCCAGGCACTTGGAGAAAGTATAGCAGCAAACAATGCCTAT
TTTTNACAGGAAACAGAACANATACCCAGAAAAATGCCCTGGCAATCATCAAATCACAGT
TTTCCAACATCAATAAAGTGTTTAACTCCTCATTTGAAAGATGGTGTTCCTGGATTGAA
T
ATTGAAGAATTAATAGAGAAACTTCAGTCTGGAATGGTGGTAANGGATCAGATTTGNGAT
GNGAGAATATCTGACATAATGGATGTATATGAAATGAAACTATCCACATTAGCTTCCAAA
GAAAGCAGGCTACAAGATCTTTTGGAAACAAAAACTCTAGCCCTTGCACAGGCTGATAGA
CTGATTGCTCAGCATCGCTGTCAAAGAACTCAAG
Sequence 313
CCGGGCAGGCCCTTAGCATTAGATTGAGTTATGTTGCTAGGAGATNTTTATTCATCAGCT
GATCATTAAGCATATGGGGCTTACTTGGCCCCCCTATCAATTTGCGTCAAAATAAATTAA
TTGTAGACCTGTCTTGTTTTATGAAAAAGCAATGTGATAGTCTTTAAATTTATCTTTCTA
AACAAGACACAAGTTTACACATTACCCAGCACAGTAACCCCTCTTGGTATTGTTTACCTA
AAAGGAAGAAGTGTAGGAAAAACTGATATAAGTAGAGAGNTTATTTGGG

Table 1

Sequence 314
GNTTGGAGCTCCCCGCGGTGGCGGTCGAGGTACGCGGGGGGTCCTGGAGGTTCAAAGAAT
TGCAGGAGGGTAGNAAAGCACCTGGGTCGGGTGCAGACTGCGGAGCGGGCCCTACCGTGT
GCGCAGAAAGAGGAGGCGCTCAGGAATGCATGAATTGATTAATTAAATGTCGAGAGCTGT
AGATGGCTTTTCTCAAGGTGCTTCAAGTGCAGAAGCCCAAGTGATTGACCCACACACTTA
CCTTTGTGTTCCTTCCAGAAAATCCTCAGGGAGTGCCTTCAGCTTGTGGGAAATCCCGAA
GATGGCCAAAGACAACTCAACTGTTCGTTGCTTCCAGGGCCTGCTGATTTTTGGAAATGT
GATTATTGGTTGTTGCGGCATTGCCCT
Sequence 315
CTAAGCATATGGGGCTTACTTGGCCCCCCCTATCAATTTGCNGTCAAAATAAATTAATT
GT
AGACCTGTCTTGTTTTATGAAAAAGCAATGNGATAGTCTTTAAATTTATCTTTCTAAACA
AGACACAAGTTTACACATTACCCANTTACAGNAACCCCTCTTGGTATTGTTTACCTAAA
A
GGAAGAAGTGTAGGAAAAACNGATATAAGTAGAGAGTTTATTTGGGCCAAGCATGAGGGT
TACAACCCAACTGTATGGAGACAAGTTGGCCTGAACAATACACATTCTTATTAGCAACAG
NTATAAGTAGGNTTTCAAAGAAAAAGAAGAGGCAGNTCCTAA
Sequence 316
TCGNCCGGGCAGGTACAGAGACCTNCTTACTTACCCCCCTTNTCCTTCGGCTGGAGCTCG
GCGAGCGAGAGGCGGCCGCTGGCGTTGGAGAGCGACGGCGGCCCCCGCGTAAGCAGTGGN
AACAACNCAGAGTAACGCGGGAATGAAGAATNTTAGGCGGGTGCACCCAGTTTNCACCAT
GATTAAGGGTNTTTACGGAATAAAGGATGATGTCTTCCTTAGTGTTCCTTGCATTTTG
GG
ACAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAGAGGCCCGTTT
GAAGAAGAGTGCAGATNCACTTTGGGGGATCCAAAAGGA
Sequence 317
TTTCGCCCGGGCAGGTACTTGGAGAAAGTATAGCAGCAAACAATGCCTATAGACAACAGG
AAACAGAACATATACCCAGAAAAATGCCCTGGCAATCATCAAATCACAGTTTTCCAACAT
CAATAAAGTGTTTAACTCCTCATTTGAAAGATGGTGTTCCTGGATTGAATATTGAAGAA
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TAATAGAGAAACTTCAGTCTGGAATGGTGNTNAAGGATCAGATTTGTGATGTGAGAATAT
CTGACATAATGGATGTATATGAAATGAAACTATCCACATTAGCTTCCAAAGAAAGCAGGC
TACAAGATCTTTTGGAAACAAAAACTCTAGCCCTTGCACAGGCTGATAGACTGATTGCTC
AGCATCGCTGTCAAAGAACTCAAGCTGAAACAGA
Sequence 318
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTATTGATGTTGAAGATGAGAAATCT
CCTCAGACTGAAAGTTGCACTGACAGTGGAGCAGAAAATGAAGGTAGTTGTCACAGTGAT
CAGATGAGCAACGATTTCTCCAATGATGATGGTGTTGATGAAGGAATCTGTCTTGAAACC
AATAGTGGAACTGAAAAGATCTCAAAATCTGGACTTGAAAAGAATTCCTTGATCTATGAA
CTTTTCTCTGTTATGGTTCATTCTGGGAGCGCTGCTGGTGGTCATTATTATGCATGTAT
A
AAGTCATTCAGTGATGAGCAGTGGTACGGGTGGGAATAGCACTACACTGTTCATCTAGCC
TTGTAGAATAAGTCCCAGTGAACTGATATTCTGCAGAATCTTCACTGTTAT
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Sequence 319
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTCAAN
G
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GCAAGAGATGTTCACTTGAAGATCTTGCCCTGATTGAAGGCTTTGCCCACATGCTGGAAG
GCCCCCTCCCAGGAAAAGTACCAGACATCAGCTGCCTCTTCTTCATTTTCAGCCAAAGAA
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Table 1

CCCAGATTGTTAAAAAGCTGGCCGTTATAAATGCCCATCTGCAGCAGCCGCCTGTAAAAC
CGGAGAGCTATTTCTGGCTGATCAGAATAGAAGTGGTTG
Sequence 320
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GCTCACGCCTTCCAGAGCCACATCATNTNTGGNCGAAANAGAAGCCCAGACNAGAGGAAG
GNGNAGGAGGCCNGCAGGNACC
Sequence 321
CAAGCGGAGNNAACCGAAGAGGGGNACTTGGGGGGCCAAAAAACCCGGACCCAGGAGNNN
CCNGNGNCCAGCGCNGCCGGTTCCGCCNGAGGGGGGCACNCCCCCGCCAAGGCNGGAGNG
CAGCGGCACAANCCCNGCNCACNGCAGCCNNGANANNCNGGNCNCAGGNGACCAGCACCC
NTGCTNTTTNTACNGGGAAGNNGCNAAGCNACCNGNCAANANAGCANACAAANNGAAACN
GGGGGNGGNGAAGGANCNNAGAAGNNGGANGCCAGGAAANGGGANGAAGACCAAANGGGC
CANGNNNCAGAACAGAGAAGACCCCNGGNAA
Sequence 322
CTCCCGNGACGAAAACACAANNGNTTCTTNCGGGGGACAGAAAACCCAGACCCAGCTNCA
GGGACAGCCTGGACTACTTTNTTTTCACACAAACAAACCTCCCCGCGNANNCTCCTGGGC
CA
Sequence 323
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTTCAATACTTAAAAATAGTCTTCC
ACAAAAATACTTTATTTCTGATCTATACAAATTTTCAGAAGGTTATTTTCTTTATCATTG
CTAAACTGATGACTTACCATGGGATGGGGTCCAGTCCCATGACCTTGGGGTACTTTTTTT
TTTTTTTTTTTTTTTTTTGGAAAGCTCTGCCATAAACTTCTAGCGTGTGCCAATGGTCACC
T
GCCACACTCGCACCAGGTTGTCCGTGTAGCCAGCAAACAGAGTCTGGCCATCAGCAGACC
AGGCCAGGGAGGTGCACTGGGGTGGTTCTGCCTTGCTGCTGGTACCTGCCCG
Sequence 324
GGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTAANGGGGACGT
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AATAAAATAAGCATGTCTCCATCCTTTATTCCTAAACATTTACTTATGACAAATGTAACA
ACTGACAGAAATTTGAAAAATACCAGACACTTCTTAAATGATTTCCCTTGGTTCAAAAT
T
TACCCCTTCTTGTTTTCTCTTGCTTTTCAGGTAATTAACTCTTCTCTTTT
Sequence 325
ATTGAGCTCCCCGCGGTGGCGGCCGAGGTACCATCAAGTTAAAAGCAGAAGATGCTTCTG
GTAGAGAGCATTTAATCACTCTCAAGTTGAAGGCAAAGTATCCTGCAGAATCACCAGATT
ATTTTGTGGATTTTCCTGTTCCATTTTGTGCCTCCTGGACACCTCAGGTAAATTCTCCT
C
AGAGCTCCTTAATAAGCATTTATAGTCAGTTTTTGGCAGCAATAGAATCACTAAAGGCAT
TCTGGGATGTTATGGATGAAATCGATGNGAAGACCTGG
Sequence 326
CCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTAAGGGGA
GT
TAAATAAAATAACGCATGTCTCCATCCTTTATTCCTAAACATTTACTTATGACAAATGTA
ACAACTGACAGAAATTTGAAAAATACCAGACACTTCTTAAATGATTTCCCTTGGTTCAAA
ATTTACCCCTTCTTGTTTTCTCTTGCTTTTCAGGTAATTAACTCTTCTNTTTTTAGTTTG
AACTATGCAGTGCAAGATTCCTNTGTAGTCTTTCCAAGTGGAAGGGTATAAAAAAAAACA
CTTTATATTATGCCAGGTGAGGNGTCAGAACCCTGGCATCGGAAA
Sequence 327
GCTCACCGCGGTGGCGGCCGAGGTACTTAAAACCAAATAAAAAGTGACATTTGAATTTCT
TTTAAAAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACCAGCACA

Table 1

AACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCGTCTACCCGGGAATCCGGGGTCC
CTGACCGA
Sequence 328
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CTCTTTGATTTCCTGGAAGACGACACCATGACAATTTCAAAGAAAATAGAACAAAATGAA
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TCCTGGCCCGGCCTTGGCACATGTTCGTNTTTGTGGTTGTTGCCTGGACAGGCAACTCTG
CAGGGCTGCTTCTCTACGCATCCCTTTGCCTGCCTGCCTGTGCCAGGGGTTGTCAAGGGC
TTTTGGGTCAGAGTGGGCACCCCTTTCTCCAAGGCTCCCTGCAACAGCTGGCCTGTCCCT
GGTGGGGCT
Sequence 329
NAACTTTACAGGATGGCATTTAATACAGATATTTCGTATTTCCCCCACTGCTTTTTATTT
GTACAGCATCATTAAACACTAAGCTCAGTTAAGGAGCCATCANCAACACTGAAGAGATCA
GTAGTAAGAATTCCATTTTCCCTCATCAGTGAAGACACCACAAATTGAAACTCATAACTA
TATTTCTAAGCCTGCATTTTCACTGATGCATAATTTTTCTTATTAAATATTTAAAGAGAC
AGTNTTTTCTATGGGCCATCNTCCAAAAACCTGCTATGNACCATNCAACTTAGGTTCT
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CNTTTCCTGCCTTAAATTTNTAATGGAGNAANGGGTATTTCTTTTCAATTTTTAAAATTT
GCATTTTTTGGGGGAATTATACCTTCCCACCAATCTTTTTGANTNTATTTTTCCTTTGG
A
CCTTAAATCATGAATTTTTTTCAAAATTAANAAGGTTNNAAAGNTTTAAA
Sequence 330
AGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGATNGTTCACTCACTTTCAAAGCCAGCT
GAAGGAAAGAGGAAGTGCTAGAGAGAGCCCCCTTCAGTGTGCTTCTGACTTTTACGGACT
TGGCTTGTTAGAAGGCTGAAAGATCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTT
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CTTCATCCTCAGAATCTGAGAATTCTTCATCACAAGCTATCCGCTTGTCTGATGCTCG
AA
TAGAAATTCTCTTGTCTGGATCTTCTCCATCTTCATCTCCACTGTCTTCATGAACAGCA
T
CTTCTGGAATAGCCTGCATCTGGACACCCAGGTGCATGAGGTAACATGCGCAAATTTTCA
AACAAACCGCTGGTTTATCTTTTC
Sequence 331
CTNCCGCGGTGGCGGCCGAGGTACTAGCAGTTGCCAATGAAGGAGGCTTTGTTCGATTGT
ATAACACACGAATCACAAAGTTTCAGAAAGAAGTGCTTCAAAGAATGGATGGCTCACTGG
AATGCCGTCTTTGACCTGGCCTGGGTTCCTGGTGAACTTAAACTTGTTACAGCAGCAGGT
GATCAAACAGCCAAATTTTGGGACGTAAAAGCTGGTGAGCTGATTGGAACATGCAAAGGT
CATCAATGCAGCCTCAAGTCAGTTGCCTTTTCTAAGTTTGAGAAAGCTGTATTCTGTA
CC
TGCCCG
Sequence 332
CCGCGGTGGCGGCCGCCCGGGCAGGTACCATCTGACTTGGCAATGTAATGACACACACGT
TAGTGTGGGGCACAAACGTGGAATATTAGGAGAGAGCTGGTTCCAGCACCAAATCCAGAG
TCACTCGGGGAAGGAGGTATGGTGGCAACACTTTATGCTTAATATTCAATTCTGCTCCAG
TAGAACATGGTACCT
Sequence 333
CGCGGTGGCGGCCGNTCGGGCAGGTACGCGGGGACTCTGAACGTGCTAAAATGGGAAGGG
AGGCGGTGTTTTGCTGATCTGTTAAATTCTTAGTGAAGTTTCCTTGATTTCCAGTGGCT
G
CTGTTGTTTGAGTTTGGTTTGGAGCAAAACTGAGGTAGTCCTAACATTTCTGGGACTGAA

Table 1

TCCAGGCANGAAAAAAAAAAAAAAAAAAAAAAAAAAAGGTACCT
Sequence 334
CCCCGCGGTGGCGGCCGAGTTTGATTTCTTGCAGTCCTGAGCGATGGAGCCCGGGGGTGC
CTGGTTATTGTCCGCTTTCTCTCTCAGATGCTTGGCTTGTTTTTCAAGAGAACCTTTTT
C
GATATTCATTGCTCCATCGATTGGATCCAGTCCTTGTTCAGAAAATTGTTTCAAGGCA
CT
TAAGGCTGCCTGAAAGCCTTGAATCCTTGCTAAATATTCCAGTTGTTTTGAAGGTTGT
AC
CTCGGCCGCTCTAGAACTAG
Sequence 335
GCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACTTGACTGCTAACAACTTTCAAATTCTT
CTACTTACTCCCTCTTCTTCAGCTTCACATCTGGGAAAACTGATAGGGAAGCCTAGGTAG
GCCTACCTTTGGTGCCAGAGGGAAGCTCAATCCATGCAAGCCCCAGATAATATATGAGAA
CCTCCCCAACCTTACCCTACACCCCTCACCTCCCAATCCAAGCCAGTCTCCTTTCCCTGC
TTTCTCAAACCATGTTTGGACCTGCTTGGAAGCTCCCTCTGCTCTCCCTAGAAAGCTT
CA
TTATGTGAGTGATACATCTTTTCATATCTTCTTGGTGTGTGTGTGTGGTATCATCAGCC
T
CAACATCTGAAGCAAATGTTGGGTGGGGGGGTACCTCGGCCGCTCTAGAACTAGGTGGAT
C
Sequence 336
CTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTCATGAAGGAGATGGCCCCTTTGGGAGC
AACCAGAGAATCACTGAGATCCCAATGGAAACAGGAGGTTCAGCCAGAGGAACCGACTTT
TAAGGGATCACAGAGCTCACACCAAAGACCAGGGGAACAGTCAGAAGCCTGGCTTGCTCC
TCAGGCTCCCAGGAACCTGCCTCAAAACACAGGTCTCCACGACCAGGAGACAGGTGCTGT
GGTCTGGACAGCTGGGCCCCAGGGACCAGCCATGCGTGACAACAGAGCTGTATCCCTCTG
TCAGCAAGAATGGGATGTGCCCAGGCCCTGCACAAAGGGCCCTCTACAGGGGGTGCCACC
CAGAGGAAGGGACAGTCACGTCTCGCTGGCAACAGGGTGTTGCCCTGGGGCTATTGAAGA
GACCAAGACGCTCCTGGCTATTTTTTAAGTAGTTCTCAATTTTTATGGGNAAAACTNCA
A
GACCTTNTTCAGCCAGNAACAGCCCCAGATTCTTACAGGGGCCATTGGGCGGAAGGGACT
CTTGGGAGCCAANGGGTTTTTTT
Sequence 337
CCGCGGTGGCGGCCGAGGTACGCGGGATAATCAAGGTGTACATCCCGGTGGCTGGACATG
CCCTCTTGGGCTTGGCAGATGCCAGTGGATCCATACAACTACTCCGCCTGGTGGAATCTG
AGAAGAGCCACGTGCTGGAGCCATTGTCCAGCCTTGCCCTGGAGGAGCAGTGTCTGGCTT
TGTCCCTAGATTGGTCCACTGGGAAAACTGGAAGGGCCGGGGACCAGCCCTTGAAGATCA
TTAGCAGTGACTCCACAGGGCAGCTCCACCTCCTGATGGTGAATGAGACGAGGCCCAGGC
TGCAGAAAGTGGCCTCATGGCAGGCACATCAATTCGAGGCCTGGATTGCCGCTTTCAATT
ACTGGCATCCAGAAATTGTGTATTCAGGGGGCGACGATGGCCTTTCTGAGGGGCTGGGAC
ACCCAGGGTACCTGCCCCGGGCGGGC
Sequence 338
NAAAACNCCCCCCGGGATAGAAGNNATTTTTTNTCAGGGCACANANTTAGAANCCAGNNG
GNTTNTANACCCAACTGGCAACATCAAGAANGAGCGGGGGGGGGAAAAAANTGACAGGGA
CGGGGAGCGGGCNCACAAGNGGCAGGGAAGGGAGACNCCACCNGNGGGGGGGNCCTGGGGG
CCCNGAAACCGNACAAAGGGGNGGNACACTGGCCGCCGGGNGCCGGGACGGAANNGAAGN
AANNTAAGAAGGGGGANCNCCCCCGGGGGGTGNAAGGGAAAANGGCGAANAANNCAANGC
NCAAAANCNGAAANNCCCGGGNNNAACCCCNCGAAGGGGGNGGGGGGNCCCGGGGGAACC
CCAAGGNGGGGNTGGAATCCCCAAANAAGAGGAGGGGGGCGGAAAATNCCGGCNGCCGCC

Table 1

AAGGGGGNGGNAAAACNAANGGGGGCAAAAAAGGGCCNGGGGNNNNCCCCGGGGGGGGAAAA
AAAAAGGGGGGNAAAANCCCGGCCCAGGAACAAAAAAAAAGGCAAAAAACAAAACCAATNA
ACNGGGANNCCNNGGGGGAGGCCAAAAAAAAAGGGGGGGGGAAAAAAGCCCCGGGGGGGGGG
GGGGCNCNNAAAAAAAGGAAGGGGGGGGGGGGCCGAAAAACNGCCAAAAAAAAATANAANNNNG
GGCGNNTNGGGNNGGCTANCNAAAAANGGGGNACNGGGGGGNNCTTTCCAAANNAAAGGGGG
AAAA
Sequence 339
CGCGGTNGCGGCCNTCNTTTTTGTTTTTTTTTTTTTTTAATAGCTGAAGATTTAGATTTAT
TTGAAAACACTTAGTCTAATTTATATTAGGTGCAGAAAAATCACATTCAATAAACCACA
A
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GCAAGAATCTNTTTTTGNGGTTNCCGGGNCCTCNNGGGGGTTTATTCNNANACNGGGNGCCG
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TGGGCNATTTCCCCCNGNAANAAAAAAAAATTTTTNCCCCGGGGGNATAACCCCCCCCNAG
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NAANAANTTTTTTTTNCNNNGNNAAAAACCCCNCCTTNTAGNGGGGGGGGGGGGGGGGGNGNT
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Sequence 340
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GAAAGAGGAGGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACTC
AACTGTTCGTTGCTTCCAGGGCCTGCTGATTTTTGGAAATGTGATTATT
Sequence 341
GCGGTGGCGGCCGCCCGGGCAGGTACCAAAGAAGATGCAGTTAAAATACTGCCAGTTTTC
CAAGAAATTTTGTAAAGTTGAACATGGCCATCTACTCTTGCCTTAAAACTTTTCTCACC
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CACCCACCTTCCCACATGCATGATATCCAAGGTCGACAGACCTGGATTAGAATCCACTCT
CAAGCTTTATGCAGTGCGTATTGTATTTTCTGCATAAGAAAGGGCTGCCTCTAGAACACA
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ACTTAGTATATTTTTCAAGGAGAGCTAAACCACCTTTTGTAATGTTTGGTTTCTCACTG
N
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Sequence 342
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CATTATAATACTGTTTTAAGAACTTACAGCATCTGCTTTACAAATGGTGTTAGCTACAT
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TCGACACAGCATCTTTAGCCAGTTTTCTTTTGGAAGTTCATCTGATGTCATCTGGAAAC
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GAGTAGCACATTTGCCTGCTCTGTTGGTGGCCTCACAAGCAAGGCAAAGCATTATGGCA
ATCTAGGGTTCCAGAATAACCATAAACATTAAGTGTCACTCCTTGGAAAATGACAGATGT
ATGCAAGTTTAGTTCCCTCAGAGCAATGAAATTCCAATGAAATGAACTATCACTTCTCCA
CTTTCCTTGTCCTATTTTTAATAAGACAAAGAACATCACCATATTAAGTTGAAGTACCT
G
CCCGGGCGGCCGCTCTAGAACTAGGTGGATCCCCCGGG
Sequence 343
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACATCAGAGATGCTCACACCATTCTTTGAGTA
GTTTAAAAACTCATTTTAACCACTTTTTATTCTTTGTATTCAAACCAATCACTGGCAATA

Table 1

GCTCTAAGTAGGTCATCAACTCTCCTCCATGTCTTCTTTCTAATTCTGCCACAGACTCA
C
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GATACTCTTTTCCTCTTAGAGAAACTCTGTGGAAGCTCTGCCTATACTGTGGGAAATAAA
TTCTAGACGCTGGCTTCTTTCTGTAGTAAACATGTGGGCCCTTTAAAATGTTGAACCA
AA
ATGTGCTTCAAATATAGTTTAAGTTATAAAACATTTATGGGGGAGTATGTATGTGCCAA
C
TACAGAGGCTTCAGAGATGAAGAAACAGTTCTTACCCTAGTGTTGCTTAGAATCTAGTAG
TAGTAAGTAATAATTACTAACATATGCATTTACTATATAGGCAATACTAGGGTAAATATT
TTACATAGATTACCTTATTTAGTAGCTCTTAGCTGCTAAAAAAAAAAA
Sequence 344
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTT
GG
GGGAGTTAAATAAAATAAGCATGTCTCCATTCTTTATTCCTAAACATTTACTTATGACA
A
ATGTAACAACTGACAGAAATTTGAAAAATACCAGACACTTCTTAAATGATTTCCCTTGG
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GTTTGAACTATGCAGTGCAAGATTCCTCTGTAGTCTTTCCAAGTGGAAGGGTATAAAAAA
AAAACACTTTATATTATGCCAGGTGAGGTGTCAGAACCCTGGCATCGGAAAGTGGTTGGC
TCACGGGTCATAGGGTAGTAAGAAGAATTTACAGAAGACAGTATAGGTTCGAAAA
Sequence 345
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CTTCTCAAGGATGTCTCAAGGGCTCCGGTGGTGCTCTCCTGCTCTATCCGCTGCTGTGGC
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GAGGCCTTGTAGACTGACCTGTGGCAGAGAGCTCCCTGGGTCCAGCATCTGTTGCCCTCA
CCCTTGACACATGCGGACCCTCCCCAGGC
Sequence 346
GCGATTGGAGCTCCCCGCGGTGGCGGCCGGGGTACAAGAGAAGAAAGACCAGTCCTTGCT
GAAAGACAAGTCTGAATGCTCCACTTTTTCAATTCTCTCTCCATTCTTCAGTAAGTCAA
C
TTCAATGTCGGATGGATGAAACCCAGACACATAGCAATTCAGGAAATTTGACTTTCCATT
CTCTGCTGGATGACGTGAGTAAACCTGAATCTTTGGAGTACCCATTCCCTTGATGTCTAC
AATATCACCTTTCTTATAGATTCGCATATATGTGGCCAAAGGAACAACTCCATGTTTTC
T
AAAAGGCCTAGAGAACATATATCGGGTGCCTCTCCTCTTTCCCTTTGTGTTCGTCATT
TT
GGCGAATTACTGGAAGATG
Sequence 347
AGCTCNCCGCGGTGGCGGCCGCCCGGGCNGGTACCACNGCCCAGCTAATTTTTTTATGTT
TGTAGTAGAGACGAGTTTCACCATGTTGGTCAGGATGGTCTCAAACTCCTGACCTCAGGT
GATCTGCCTGCTTCGGCCTCCCAAAGTGCTGAGATTAGAGGCATGAGCCACCATACCTGG
CTCTTTTGCTTCATCCATCCCTTAATTTCTTTGCTGGAGCATTTTAAAGCAAATATCAG
A
CATACCCTTTCACGCCTCACACTTCAACATGCGGCTTGTTGAAATTCGTGCTCCACTCCA
GCAACTGCTTTCAATCGGAGTTCCATCCTCCGCCGCAGTATGCCCTAACGCAAGCGTTAT
CTTCAGAGCTACCACCAGGNTTCCGAAACTTTTTCGGNGGGAGGCGCTTTNGCCACCACC

Table 1

TNGCCGGGNNAACGGNTNGCGTNAAACCAAACCTTTGAACGGCCAGNCCCCCCGNGGTAC
CTTNGGGCCGGTTTAAAAACTAAGNNGGGGGATNCCCCCCGGGCTGGCAGGGAATTTCGAT
ATTCAAGCTTAATCGATACCCGGCGACCTTCGAGGGG

Sequence 348

ACTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTGACTGCTAACAACTTTCAAATTCTT
CTACTTACTCCCTCTTCTTCAGCTTCACATCTGGGAAAACTGATAGGGAAGCCTAGGTAG
GCCTACCTTTGGTGCCAGAGGGAAGCTCAATCCATGCAAGCCCCAGATAATATATGAGAA
CCTCCCCAACCTTACCCTACACCCCTCACCTCCCAATCCAAGCCAGTCTCCTTTCCCTGC
TTTCTCAAACCATGTTTGGACCTGCTTGGAAGCTCCCTCTGCTCTCCCTAGAAAGCTT
CA
TTATGTGAGTGATACATCTTTTCATATCTTCTTGGTGTGTGTGTGTGGTATCATCAGCC
T
CAACATCTGAAGCAAATGTTGGGTGGGGGGTACCTCGGCCGCTCTAGAACTAG

Sequence 349

CCCGCGGTGGCGGCCGGAAGGAGGACGACGGTGCTGTGCTGTGTATGAAGAGGCAGTGAA
GACTCTGCCAACAGAGGCCATGTGGAAGTGTTACATCACCTTTTGCTTGGAAAGATTTAC
TAAGAAGTCAAATAGTGGGTTCCTTAGAGGGAAGAGGTTGGAAAAAACCATGACTGTATT
CAGGAAGGCACATGAACTGAAGCTTCTGTCAGAATGCCAATACAAGCAGTTGAGTGTTTC
GTTGCTGTGTTATAACTTCCTGAGGGAAGCTCTGGAAGTGGCAGTAGCTGGAACTGAATT
GTTTAGAGACTCTGGGACAATGTGGCAGCTGAAGCTGCAGGTGCTGATCGAGTCAAAGAG
CCCTGACATAGCCATGCTTTTTGAAGAAGCCTTTGTGCACCTGAAACCC

Sequence 350

CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCGTGCTAAAAGACTTTTAGTTCGGCTCT
CCCAGTGTTTTTTTTTTCGTCGATTTGGGCACAGAGTTTCCTGGTTCACGTGGATGTGA
GG
ATCCTTTACTCCAGATCGCCAGCCAGTTTTTGTTTTTTTTTCCTGCGTTGCTGAGAGTCT
G
GGTTTATTCATCACACCAGGTGGATCTTAATTCCATATCCCTGAGGCCACTGCAATGAGG
CAGAGGAGTGTGCTCCCTCATGAGAAAGGACTGGAGACCGCCCCCAGAAGAGAACGTATC
CATGTACCT

Sequence 351

CCCCGCGGTGGCGGCCGCCCGNNCTGGTACTTATAATGCCNNNNNTTNCGGGNTGTGAAT
GGATTACANTGTATCTTTTCAGGGAAACCTATTATTATCAATGTGACTCCACNGGGGGAG
TCCATGGTGATGATGATGAGGAGGAGGATGATGATGATGAGACACCTCTAAACTTGGAAC
AAGTTTAAGACTTTATGAGAGAAGAAAAAAAATCACCAACAAGAATTGTTTGAGGAAAAA
TCATAACTATCCTGTGTTCATTTTTTTTTTTTATAAACAATAAGAAAAAGTTGTTGGATTT
TTTTTTAATGATTTCTTTTTTGGGGGAGGGAATTTTTGTTGCAGTTTTATGGTGGAAAA
T
GCAAAAACCAGAGCCAGGTGCATAATCTTGTAATCTGTGGATATCCCTGGAGCAGGACTG
ANCCT

Sequence 352

NCCGCGGTGGCGGCCGCCCGGGCAGGTTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGT
AACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAA
CAACGCAGAGTCCAGGGAAGCAGTGGTAACAACGCAGAGTACCCGGGGAAAAAAGGCAAA
TAGAATGAGAACCATATTATGTACCT

Sequence 353

CTCCCGCGGTGGCGGCCGAGGTACACCCAGCTTTGTCTCCTGGCCCCAAATCTCCTTTTC
CTTACTTTGGGCATTAACTGCTGTTGAGGTCTCACAGCCTGATGGTCATTATCCCTGA
AT
GGCATAAATCAACAGGCTGTATGAGCATTGTGTGAGATTCTACATGAGGGAGAGCATTTC

Table 1

AAACCCATGACAGATGAGAGAAGTTAGTACACTCTCACTGAACTGGGGATGTTTGACTTA
AAATGATGGACAATAAGATAGTGAGCAGTAAGTGTGCTCTAGGCTAGGCTACGAGAGGCC
ATGAGCTCCTCATCTCTTCTCTGTTCTGAGCTCTCTGATCCACCGCACTTGGGGCAGGGG
GTGCATTCTCTGTGCCTCTCCTGAGTCTACTTTCTGCATCATTGGGTTCTCCCAGCTC
AC
TTCCATAATGTCCTCCTAGGCTGCATTGGAATTTGTGTGTTGTCTAGACCCATGGCCAAN
ACTGTCATTGCCTGTGAGGGAGACCAAGCTTACCCACCCAAGGGCTTTTG
C

Sequence 354
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTT
GC
CTTTAGAAGGTTAAAATGCCAATATAAAGCTAAAACAGTAATCATCAGAGACAGCTCTAA
TAAGGCTTTGCTACTGTTTTTACTATATAAATCTTTACGTGTTAATGGAAAGAAAATTAA
TTCATTCTGTTACTCCATTTTTTTTCTCTCCATATTGTATGCCTGAAGTGAGCTGATGAG
G
GGCAGAAAGATCATACAGTTAGGAATGAAGACATCAGAATGTTCCACTAAACAGATATTT
AACTAGATACTATTATACTACTAAGAATAGCAAGAATGTCTCTCAATTCTGGGAATTTC
T
CCTAGCTCACACAAATGAAACGCACATCTCCATGAATGCTTTCTAATAAATGCTTCCAGG
ATAGTATCATAAACAAAGTCAAAATTAAGAAAAATCAC

Sequence 355
GCTCCCGCGGTGGCGGCCGGAACCGCCATCTTCNAGTAATTCGCCAAAATGACGAACACA
AAGGGAAGGAGGAGAGGCACCCGATATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTT
GGTCCTTTGGCCACATATATGCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGA
ATGGGTACTCCAAAGATTCAGGTTTACTCACGCCATCCAGCAGAGAATGGAAAGTCAAAT
TTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTACTGAA
G
AATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGGACTGGTCT
TTCTATCTCTTGTACCT

Sequence 356
GTTGAGCTCCCGCGGTGGCGGCCGGAGGTACCTGACTGTGGCTCAGATCTGCGTCGCAGCA
GCGAGAGAAGAAATCACTCCATATCCGATGAGAGGAAGGGTGGCACAGAGATGGTGTCTA
CAATTAGAGACATTTCTGACTCCACCTTAGCCTAAGCAAACTTTATGTACTGAGTAACA
T
TTGAAGGTTGTCTTTTAATGGTGGGGGGTGTTTTTTCCTTTTTAAACTACAGTGCTTGC
A
CAAGAGAGGGAGGGACTCAGAAAAGGTTAGGGCAGGTGAGGGAGACAGTAGATGGCCTGG
GATGACTTGAGTCCATCATACTATTGCTTGGCAGGTGTCCTCCCCCATGTTTGATTCA
AA
TTCCATGAGTGACCTACCTTTCCCCAGGAATGGGACTGAGAGGGTAGTCTCCAGCAACTC
AGTCTGCACAGGGCTCCCCGTTCAGGCTGCCTTT

Sequence 357
TCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCATCTGACTTGGCAATGTAACGACACACA
CGTTACGTGTGGGGCACAAACGTGGAATATTAGGAGAGAGCTGGTTCCAGCACCAAATCC
AGAGTCACTCGGGGAAGGAGGTATGGTGGCAACACTTTATGCTTAATATTCAATTCTGCT
CCAGTAGAACATGGTACCACCATTCTTCCAAGTTCAAAAATTATCTTTGATTCATTTTG
T
TCCCCATTCCTCTAATATGTCACCAATTCTGCTGATACATTCTTTGTAATCTCTCCATC
T
ATTTTAATCTGTTATTCACCTGAGCTACACAAACATTCATCTGCACAAGGAGTATTCCA
C
GTGCTGAAAAGACAGAGGATTAAGCCCTCCTTGTGGAGGCATTCACAGTCTGGTTTTAAT

Table 1

ACACAAACCAACAATTATAATACACAGGGATAAAAAAAGTAGAGGCACTTATTGCATACC
TGTACCT
Sequence 358
TTGACTCCCCGCGGTGGCGGCCGAGGTACTTTTCTAGCAGTCTGTGGCCACTCCATACTC
AGCTGAAAACACTGTTTCAGCCCCCTCTCTGGTGACCTCAGCCTTCTCCAGGTGTATCTC
TTGATGATCTTGGAGACCAGCAGCCACAGCTGCTGCTACTCCTGCAGGAGACTGTCAGGC
TGTGGTGGGGGGCAGGGGTGTTGGAGGAGAAGTTGAAAATCCGTGTGTTCTCTGTCCCTC
TGCTCCTCCATCTTAGCTTCTGGAGGAGTTAAGGCACCAAGGGCA
Sequence 359
CGGTGGCGGCCGCCCGGGCAGGTACTGGTGTTGTGATCGGAACGTGTCGATCCCCTCTTC
TCATCACTGCTGCTCCAACTGGATTTATTACTCCGGGAATGGTAGAGAATAAAGATTTGT
AGGAAAGGTGCTGAACTGCCAAGGAAGGCATTTCTTGTGCCGTGTCTGGAACCGTGTATC
CTTACTACATCACTGAACGACACCAAGCACCCCATGCACTTCTGGGTCCAACCTTGGCCC
CTGGAGAAAGACACTGAAATTTGGCCATGCAGGTCTACTTCCCGTAGGGGGGGATTTTTTT
TTANNAANTGTTTNNGCCCCNTTTGAAAAAAGGGNTTTTAAAANCNAAAANAAAANTTT
T
NTTCCCCCCGGGGGGGNNGGNNTTTTTTTTAGGGGGGGAAAANGGNGGTTTTANTCCCCCCN
NNGGNAAAANCCCCCCCNNTTTTTNTTTTTTTGGGGNNGGGGAAAANATTTTTTNGGGGGGTGCN
CNGGNGNNTTTNNNNNANAANNNAAAACCCCCCNTTTTNNTTTTTTTTAANANACCCNCNNN
AANNGGGGGGGTTTTTTTTTTTTTTTAA
Sequence 360
TGGCGGCCGAGGTACCTACTGAAAACTAAACACGCCAGAGGAAATTTGGCCAGTTATCCA
ATTGATGAACTANTAGGATAGAGCCAAACAATCTTTTCAAGAGGGTGTTTGTGAGATATG
GTTGACCAGTGAAGACACGGGGGGCTTATGGCAGAGATATTGGCACCAATCTNCCCACACT
CCTGTGGAAACTGGTTGAAGTGATTCCTGAGGGAGCAATGCTGAGGCTTGGCATGACAAA
TCCGCCCTATATTTTAGAGCATCTGGAGGAAATGGCANAAATCCTTAATCACCCCAGAGT
CTACGCTTTTCTGCACATACCAGTCCAGTCTGCCTCCGACAGCGTACCTGCCC
Sequence 361
GATTGAGCTCCCCGCGGTGGCGGCCGAGGTACTTAAAACCAAATAAAAAGTGACATTTGA
ATTTCTTTTAAAAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACC
AGCACAAACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCCGTCTACCCGGGAATCC
GGGGTCCCTGACCGA
Sequence 362
GAGCTCCCCGCGGTGGCGGCCGAGGTACGTATGCACAGCCTCACACTCTATAAATGTATG
TGTCCTGAATTTCAGAGCTTAATAATGAATTATGGAACTTGATAATGATTGGATCAGGCA
GACAACACCTGATCAGTCCTAATATCAGAAAAGAGACAAGTAGACATTATGTGCTTCCTG
AGGTGAGGCAGTAGTAAGGAAACAACATCACACATGTAGCAGTCTTGGGAAAAAAAATGT
AACCTGTATCTCGTAATGAGGAAACAATCAGTAAAAAAGTCTAGATTGTGGGACATTCCA
CAAACTTGCCTGAACTCTTTAATAATGTCAGTGTCATGAAAGACACACCACACACACACA
CTGCACATCATACACAAACACCACCCCACCACCCACCACTCAGACACACACAAAAGGGCA
ACTCTAATCAATTAAAGGAAACAAAAGAGAATGACAACTACATATAACGTATAATTCTTG
ATTGGATCCTGGATTTAAAAATAAACAGCTATAAAGGATATTTT
Sequence 363
GCTCCCCGCGGTGGCGGCCGAGGTACTTAAAACCAAATAAAAAGTGACATTTGAATTTCT
TTTAAAAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACCAGCACA
AACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCGTCTACCCGGGAATCCGGGGTCC
CTGACCGA
Sequence 364
TNCCGCGGTGGCGGCCGAGGTACAACGCATGAGTCCCGGGAAAGCATGTGGTAACAACGC

Table 1

AGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAG
AGTCCCGGGAAGCAGTGGTAACAACGCAGAGGCTTTCAGCACAGCCCAGGGTGCCCGGGA
CTGAAAACTCCTTCACCAGCCCCCTCCACAGGATATAGAAGACTTAGATCACTACGAGAT
GAAAGCAGAGCCCATTAGTGGGAAAAAGTTGGAGGATGAAGGAATTGAAAAAAAAAAAAA
AAAAAAANGTNCCTGCCCG
Sequence 365
TGACTCCCCGCGGTGGCGGCCGAGGTACCAAGCACTGGGTAAGGCACTTTTGTGGAGCAT
TAGACAGTAACCCTCAAGGAGCTAGAGAACCGGATGGGAGACATGAGCGGTAATTAACTC
ACTTGTTCCCCAGAGTTTCTATTTGTTTTNTTTTCTTTTTCTGTGACTTATTTTCCTATT
TTCTTTCCTCCATGTAATTTTCACTATGGCCCAACTAATATAAACACCTGGAAATTACA
A
GGAAAAAAAATTCTTCCTCTAATAACTTTCCAAATTTGTGGAATATTTATTTGTAATAGC
AGTTATCAAGTTATGCTTATATAAGCATTAAAAATTCTCCTCCTTTGACTACACACACA
A
CCACAGTGTGGTTCTAATCNATGGGAGATATCAAGTAATTTTTTAGTAACCTGAATTTT
G
AGGGACATTTCTCTGTTTAAGCATGTATGCAAACTGATATGTAATCCTGANGGTCCCAAG
TCAATTTTTTTTCTT
Sequence 366
CTCCCCGCGGTGGCGGCCGAGGTACTTTGCATCCTTCAACCCAATCAAGCTGACACTCAG
TATTAACCATCACAAGGCGTGAGGACAGATAGCTGCATCCGCAAAATAGAGAACCAAGAA
ATAGTCCCACACCAAAGTCAGGATCAAATGATTCCTGGACAAGCCACCAAGTCAATTCAA
CTGAGAGAAAGAAGCCTTTGCACCAGTTGGTGCTGGAAGTTCTGGATATGCACCTGGATA
AGTGAACCCCCCTCCGTCACCACACACAAACGTTAATTTGAGATGGATTGCAAACATAAA
AGCTAAAACCATTAACACTTCTTGAAGGTAACATAGAATATTTTGTAATGTTATGATAG
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CAAAAGTCTCTTAGGACACACAAAAAAAATTAACCATAAAAGAAGAAAATGGCTGGGTGCA
GTGGCTCACACCTTTAACACCAGCATGTTGGGAG
Sequence 367
CTCCCCGCGGTGGCGGCCGAGGTACATTGTGATTCAAGAGAAAAGTCACATGCAGGTCTG
AGCTCCTCCAGCAGGCCTTATGTAATGCTAAGATTTTTGGGGAAGATGAAGTTGAACTGA
TGAACTGGCTGAATGAAGTGCATGACAACTGAGCAAGCTCTCAGTCCAGGATTACAGCAC
TGAGGGGCTATGGAAGCAGCAGTCTGAACTTCGGGTTCTGCAAGAGGACATCTTACTCAG
GAAACAAAATGTAGATCAGGCTTTACTAAATGGTTTAGAACTACTTAAACAAACCACAGG
TGATGAAGTTTTAATAATTCAAGATAAATTGGAAGCCATTAAAGCAAGGTACTGCCAGAT
ACCGAATTGAGCATACCACAAAAAAGTTCTCATTTTGTGTCCTCCCATNCCATTCTCCT
C
ACTAACCAAAG
Sequence 368
CTCCCGCGGTGGCGGCCGCCGGGCTGGTACAATGTGCCTGGCACCTTACAAGACACAAAT
ATGCTCTTATAGGCTGGGGAAATAAGAAAATATGAATGAAGCAACCCAGGTCTTGAGCCA
AAGAATTACCTGGGGTCCGTTGAGTTCAAATCTGAAAATTTCTGTCTTTCAAGGTCAGCA
TCGCCCACAAAC
Sequence 369
CTCCCCGCGGTGGCGGCCGCCCGGGCTGGTACGCGGGGGTTTCCGGTTTGGGTGTGGCCG
CATGGCGTGCTGGGGTGCAGGTGGCCGAAGGGGGCGTTACTGTTGCGACTGGCATCCGCA
TCCGGCAGATGTAGATGGAACCAAAGCCAGAAGTTACGCGTCACCCTTGCTCTACAGCCA
AACATGCAGGACTCTAGTAACCCGCGAAATGATGGGATAGCGTTGCAAATCCTTAAAAGA
GTCTTAACGGAGAAGGAAAAATGTTACATTGTCAAAGTCCCAAAGCCTTTCAGCCTGAAG
CCAGGAACAATTGTTCAAAGTTTCTTTGGAACATCAAGGAAGGAAATCCAGATTTTACTT

Table 1

TAAGTGCAATGGGGGAGTCATTAAGGATTTTGTGTAGATACAGCAAAAAGACAACAATCT
TCAAGCCACAATGGCCCTCACCAGAACCCAGC

Sequence 370
CCCGCGGTGGCGGCCGAGGTACTTAAAACCAATAAAAAGTGACATTTGAATTTCTTTTAA
AAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACCAGCAGAAACCA
GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
CGATTCAGTGGCAGCGGGTCTGG

Sequence 371
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACGATTATTTTCAAACAAGCCTACGTCCCTGA
CTAACCGAGTGGAAGGTGTGAGTGGCACTACAAATTCACAAAAGAACTGTAGCCTCAGAT
AATCAAAGGAGAGAAGGTCAGATGCAATCACTGATGCATGCTAGTAATTCTCAAACCTTC
GTTTTCAGAAACGATTGGATTTTCAGATAGATTTGCAGTAAGAGAATAACAAGTCTTTA
T
TTTTTTCATCCCAACTTCTTTCTTGCACATTTTTCTTCTAGCTATATTTAATATCTGTTC
TCCCCACACACTTGCTAATCTACATTTCACAATCTTCTTCACTTTCACTTTGTCTGCAA
A
GGAAATCTACCCTGGGACAGAANAAGCATCTCTTTTTTTTTTCCCCCTGACCCTTGGCA
TT
TTCCTCTCCCTTCAACTT

Sequence 372
GATTGAGCTCCCGNNCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGATGTCTCTTGTC
AGCTGTCTTTCAGAAGACCTGGTGGGGCAAGTCCGTGGGCATCATGTTGACCGAGCTGGA
GAAAGCCTTGAACTCTATCATCGACGTCTACCACAAGTACAAGAGATAGAAAGACCAGTC
CTTGCTGAAAGACAAGTCTGAATGCTCCACTTTTTCAATTCTCTCTCCATTCTTCAGTA
A
GTCAACTTCAATGTCGGATGGATGAAACCCANACACATAGCAATTCAGGAAATTTGACTT
TCCATTC

Sequence 373
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGAAGGAATGGAAACGCCTGGAGAAAGAG
GATGAAATGACGGATGAAGCAGTTGGAGACTCTGCTGAGAAGCCTCCTTCTACTTTTGCC
TCACCTGAGACTGCTCCAGAAGTGGAGACCAGCAGAACTCCACCAGCCTGTGAAACCACG
AACCCTTCAATCAAGAAAAGACCTTTGATCAGGAGAAGACTTCTCGTCTCATTTCTGGGG
ACACATTCAGGATTTCTCCAAAGCAGGTGAAGGTACCTGCCCG

Sequence 374
TCCCGCGGTGGCGGCCGAGGTACGCGCCAGTCACTAGCAGGTCCTTGTGAATCTCCTCAC
GGAGGCACTTGCGAGAGTTAATGGGCAGATGGAAGGAGATGGCAAGGACCAATCTGGGGC
CGAGCAGGAACAAAAGCAGCAACGCTAACGGAAAAGGGCCGCGCCGGGCTGGTGGGCCAG
ACAAACCAGACATGGTGCTCCCCGCGTACTCCTTATACTTATTAAACACAAAATTAATTG
TAAAATAGCCTCAGGCAGGTCCTTCAGGAGGTATCCAGAAGAAGGCATTGTGATCATAGG
AGCTGATGGCTCCGCCTGGGTTACTGCCCCTGTAGACTTCCAGTGGGACAGGATTGGGAG
GTGGGAAGGACAGTGACATGGATGATCCCGGACCCTTTGTAGGTCTAGGCTAACGTGGTG
TGNTTTGNGTCNTTAGCTTTTTAACCAAAAAAAAGTTTAAAAAAAGGTTAAANNANCNT
N
TNNNNNNNNNNNNNTNNAAANNNNGGGGTNCCTTGCCCGGG

Sequence 375
TCCCGCGGTGGCGGCCGAGGTACCTCAGCTGTTGATCTGTGGAGCCTAGGAATCATTTTA
CTGGAAATGTTCTCAGGAATGAAACTGAAACATACAGTCAGATCTCAGGAATGGAAGGCA
AACAGTTCTGCTATTATTGATCACATATTTGCCAGTAAAGCAGTGGTGAATGCCGCAATT
CCAGCCTATCACCTAAGAGACCTTATCAAAAGCATGCTTCATGATGATCCAAGCAGAAGA
ATTCCTGCTGAAATGGCATTGTGCAGCCCATTCTTTAGCATTCCTTTTGCCCCTCATAT

Table 1

T
GAAGATCTGGTCATGCTTCCCACTCCAGTGCTAAGACTGCTGAATGTGCTGGATGATGAT
TATCTTGAGAATGAAGAGGAATATGAAGATTGTTGTTAGAAGATGTAAAAGAGGGAGGTG
TCAAAAATATGGACCAGGTGGTATCTCTACTTTGTTCCAAAG
Sequence 376
GGTCACAGGTCTCGAAAAAGCGGGTGGTGCAATGCTCCATGGGGATGAGGGGAGCACCGC
AGTGGAGCCAGCTCGGTGTGGGAGAGGTACCTCTAAGGTGTTCTTCCTACCTAGCCTAGT
TTTTTTCTACCAACCTAGTTCACCTAGTTTCCTGCCTAACCTCGTTAGATATCACTCTT
C
GCTGCTTCAAGAATACTAAAGCAACACTCCTGATATTAACCTACTACTCAGTTTTTGTG
T
GGCAAAAACAGNAGATCACATCCCATTTGTCTTTTGNGTTCTCTTGGCTGNTTAAGCANC
AANAGTTTAGCACTTTAATTCATTGCTCTACCAAATGGTTTAGTTTGGAAATAGGGGTG
G
ANGTGGACAAGAAGNTTTTGNTTTAATCCCTTCAAAGCCAATTNAACTTGGTTTTTGGT
T
TTAGGTNGAGGAAGGGCCANGNANTNGTTCAAAGGTAGGCCTCAATGNAACCGTTTACCC
CCCN
Sequence 377
GCGGTGGCGGCCGGACGGAGGAGACGGTGCTGTGCTGTGTATGAAGACGGCAGTGAATGA
CTCTGCCAACAGAGGCCATGTGGAAGTGTTACATCACCTTTTGCTTGGAAAGATTTACTA
AGAAGTCAAATAGTGGGTTCCTTAGAGGGAAGAGGTTGGAAAGAACCATGACTGTATTCA
GGAAGGCACATGAACTGAAGCTTCTGTCAGAATGCCAATACAAGCAGTTGAGTGTTTCGT
TGCTGTGTTATAAC
T
Sequence 378
TCCGCCCGGGCAGGTACCAGGTGGTGAAACCAACTGCTGAACGCACAGCCTACCTCCTGT
ATTACCGCCGAGTGGACCTGCTGTAAACCCTGTGTGCCGCTGNTGTGTGCGCCCAGTTGC
CCGCTTNGTAGGACACCACCTCACACTCACTTCCCGNCTCTCTTTAGTTGGCNCTTTAGA
GAGAAACTCTTTCTCCCTTTGCAAAAATGGGCTAGAATGAAAAGGAGTATGCCNTTGGGG
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T
GAAACANGACTTGTTTGCTTGGATTTTAGNAAAATACACAAAAACCCCATAATTNCTGAA
ACAAATTGCTTGANTCCTGGAGATNAAGGAAAGNTGGGATTTNGATTCCCCAAGTCCTCA
TTGCTTAAGTAGGAATAAAATCCTTGCACCCATGCNAACAACCAACTTNGTAAATTTNGG
TGAAAAANTGAAAATTTTAANTCTTNTCCTTTAAAAAAAAAGAAAAA
Sequence 379
GAGGGACTGCTAGCCAGCCAATAAAATATAAACTCCATTTGTCTTAGTTATATAGAACTG
TGTTTCCAGCTTAGAAAAAGTCAAACCAATGACTTNTAGAACAANCTACTCTCATTTTT
T
ATTCAGCCTCTAGAACATGGAAGCTTTAAAAGTGAATTGGCTAAANAGGCAAGACCTTCT
GAAAGTTAACATCTTAATGATTAAAAACAGTAAGTACGCACAACCGAAGCCGTAGAGTCA
CACTTGCAACAAAAGGTTACAANTATTGCTAATGGGGCTCTGTCCGGTNCTGCTTGTCCA
GCTGGACCATCTATTTCATCCCTCCTCCTCTTGAGCTGTCATTTTAATTGC
Sequence 380
NCCGAGGTACGTTAGCTCATTTTCCCTTAAGCGGGTTGTGACGTACGNTGAAATTGCAAA
CGCTCAAACTTCCAACACTTGCGTATACACTTGTAAACCCAGCTTTGNNAAGTGAGACAC
GCATCAAAATCATGATGAACAATTGACCGGCTGCNTNGCAGTCAAGCAGTTGGGTTA
Sequence 381
CCGCGGTGGCGGCCGAGGTACACCATGTGAAGACTGGACTTAAACAGCTACACCACCAGA
AGCCGAGAGAGAGGCTGGAACATAGCCTTCCCTTTGGAGGTAGCCTGGCCCGGNGGGCAC

Table 1

TGTGATCTCAGACTTCCAGCCTTCAGAACTGTGAGACAATATTTTATTGTTTAAGCCAC
T
TATTTTTTGGTACCTGCCCG

Sequence 382
NGGCGGCCGAGGTACTTTTTTTTTTNTNTNTTTTTTTTTTTGAGACGGAGTTTCACTCTTG
T
GGCCCAGGCTGGAGTGCAACGACACGATCTCAGCTCACTGCAGGGCTNTGCCTCCTAGGT
TCAAGCTATTCTCCCTCCTCAGCCTCCCAAGTAGCTGGGATCACAGGCATGCACCACCAC
CNCCCNGGCAAATGTTTTTTTTTGGATGTTTAAGNCNGACGTGGAGTTTCTCCATGTTGGC
CAAGGCTGGTCTCAAACTCCCTGACCTCAAGGGNGATCCACCNTGTCTCAGCCTTCCAAA
GNGCNTGGGGATTTATAGGCNATGGAACCAATNAACGCCCGGGCCGGCAATAAATTTGTT
ATACANNACTACCATGNAGTTAAATCTGCNANTANNATTGGGACCGAATGGTNTAATCCC
TTCNTACTTCTTTAAATTNTTCCCAANNGGACCTTCAATTAATAATAATAAAAATTNGGA
TCCTNTTTTTTTAAAATGA

Sequence 383
CTGCCGAGGTACTCACAGTCACNCAAATTCNGNGGGTGGNTACACGGCTCTCCATTCTTC
TTCTTGGCTTTACAGGTTCCCAGGNCAAGAGCTTTACCCATAATTAAGNGNNTTCTGAGG
ATNATCCGNTACATAAACNACACCTCCTCTNGAACCATCCTTGGGGCCTTCATGGGGGTT
GGGCATTTNAGGNATCCCTTACNAACAAGNCCCCCNTGGTGNCGGNCTTTCCCAGAAGCG
GCCTTTGGTGNAACCTTCNTCCCCAAAATAAANAAACCAAGGGACAACAACATTTGNGGT
CANNNGGTNACCGAAANGAATCAATTTCAATTTTCCAATATGCNTCGAAAGGGGTTTTTC
CCACTTATTNCACACCTTCTTGNGGGCCNNGAACCCTTTCTTTCAAATATTAANCCCC
NC
AAAATTGGTCACCCCAAATCCTAATTTCCTTTCCAAACCTTTCTTCTTCTTGGCCCATT
C
TTTTTCCCTTTTGAANCCTGGAAGAACAAGGTCTTGGAATCCAANTTTTTTCCGGGGN
CN
NCTCCTAAAAAACTAANNNNGGAATNCCCCCCCCGGGCCTGCAAGGGGGAAATTTCCNNTA
NTCAAAAGCTTTAATCTNATTACCCCNTCCAACCCTTCCAAAGG

Sequence 384
AGACTGCAGGAGATGTGGGCCGTGCCAAAGAGATGGATGAGACTGTTGCTGAGTTCATCA
AGAGGACCATCTTGAAAATCCCCATGAATGAACTGACAACAATCCTGAAGGCCTGGGATT
TTTTGTCTGAAAATCAACTGCAGACTGTAAATTTCCGACAGAGAAAGGAATCTGTAGTTC
AGCACTTGATCCATCTGTGTGAGGAAAAGCGTGCAAGTATCAGTGATGCTGCCCTGTTAG
ACATCATTTATATGCAATTTCATCAGCACCAGAAAGTTTGGGATGTTTTTCAGATGAGT
A
AAGGACCAGGTGAAGATGTTTGACCTTTTTTGATATGAAACAATTTAAAA

Sequence 385
GTACTCCGTCTCAGAGGANGGGATGCAAATCTTCGTGAAGACACTCACTGGCAAGACCAT
CACCCTTGAGGTCGAGCCCAGTGACACTATCGAGAACGTCAAAGCAAAGATCCAAGACAA
GGAAGGCATTCCTCCTGACCAGCANGAGNGTTGATCTTTGCCGNGAAAAGCACGCTGNGA
AAGATGGGNGCCGCCACCCTGTGCTTGNACNTANCAACAATCCCATGAAAGGAGGTCTAC
NCCTGGCACCCTTGG

Sequence 386
CTTTTGAAGGCCCCGNTCGCCCGGGCAGGTACTCCCTGATAAAGGGGAATTTCCATGCCG
TCTACAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAA
AGGGTGCAGACGTCTGGTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCA
GGAGTCCTCATTCTGGTGATAAAGATGGGCCGTGGCAGCCCACAAAAAAAGCCATGAAGA
AAGCCACAAAGAGTAGCTGAGTTACTGGGCCCAGAGGCTGGGCCCCTGGACATGTACTCT
CAGAATGTTTGTCATATGCTTCTTGCAATGCATATTTTTTAATCTCAAACGTTTCAATAA

Table 1

AACCATTTTTCAGATATAAAGAGAATTACTTCAAATTNGAGTAATTCAGAAAAAACTCA
A
GAATTTAAGTTAAAAAGTGGTTTGGACTTGGGAACAGGACTTTTATACCTCTTTTACTG
T
AACAAGTACCTCGGCCCGCTCTAGAACTAGTG
Sequence 387
TCCTGTATTGCCTTTTTAATCTTGCTTGTTTAAGNACNTTTCAGGGATTGTCATCATTG
A
TCATCTGTAAAATTGTCAAGNACTAAGGTCCTAAACCTTAATC
Sequence 388
CCTTCCCNCCCNGCGAGNCCGCNGGGGGAGATAAAAATATCACCAACATAATATANCACGG
ACTAACCCCTAAACCTTCTGCNTAATGAATTAACNAGAAATANGGGGGGGCAAGGAGNGCC
ANAGCTAANACCCCCTNAACCAGACGAGCTACNTAAGAACAGGTA
Sequence 389
CACGCCTGTAATCTCAGCACTTTGGGAGGCTGAAGCNGGGCCGGATCACGAGGTCAGGAG
TTTCAGACCACCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAANNGG
GTGTGGTGGCGGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGNGAAGAATCGTTTG
AACCTGGAGGCAGAGGTTGCAGCGAGCCAAGATCACGCCATTGCACTCCAGCCTGGGTGA
CAGGGCAAGACTCTGTCTCCAAAAAAAAAGAAAAAAGGAAAAAAGCCTTTCTTGATGCTG
TTCCCCATTTCTCCACTAAAACGCCTGCTTTTCTTAACTCCACACCGAACCAACCTGA
AA
TATTTTGGCNAGAATGCCAACAAGAATTGAAAGAAAAGATGCTTTACAAAAATAACAATA
TAAAAAGCAAATTATATTATCCCTTTTATCTCCATTCTTACATTAAAAAAAAAAAAATCG
GCCGCTCTAGAACTAGTGGGATCCCCCCGGGCTGCAGGGAATTTCGATATCAAAGCTTAT
CGATACCCGTCCGACCTCGAGGGGGGGCCCCGGTACCCCAGCTTTTTGGTCC
Sequence 390
AGTACNCGGGGCTTTTCTCAGGCGGNGGCATGGCGGGACAGGAGGATCCGGTGCANCGGN
AGATTCACCAGGACTGGGCTAACCGGGAGTCGGCCGCTCTAGGGGN
Sequence 391
CGCCGAGGTACGCGGGATGGGATTTCTGACCATTTGCCCTGCCTCTTGCAAAATAGGTCT
AATGGCAGGATGGTGTCATAATTAAGGCTACCAAGACTGCCCATTGTTCCAGGCTGGGCA
GTTCATAATGGGGGCAGACAATAGTGCAAAAAAATTTTACATTTTATCTTTAGAGTGTC
A
GGGTCAAATTGATTTCCATGGTTGAGGATGTAGCCAAGTGTGGAATCAGGTGGAATAGGT
GGAGAGTTGCCCATAGTGGTTTGGAAAAGAGAAGAGGACTTTGAAAAGTGGAGGGCTCAT
TAGGTGACCCAAATTTTACCTGGGGCATCCCCCCTTTAGGGCCCCAACTTAGTCTGTCAG
ACATCTCTGACCTTAGATGGGTGCTGGCACCACTTTGGAATGGTTCCCTCCATCACTGAG
GACCTGACTTAAAGTTTTTCTATCTCACTTAAAACAACCCTTTAACGCTCTCAACTTAG
G
CAATAATAAATTCCTTTTCATGAATTCCCTTCA
Sequence 392
AGCGCGGGGAGAGGCCGGTTTGCAGTATTGGGCGCTCTTCCGCTTTCCTCGCTCACTTGA
CTCGCTGCGCTCGGGTCGTTCGGCCTGCCGGCCGAGNCGGTNATTCAGCTTCACTCAAAA
GGGCGGTAATTACCGGTTTATTCCACCAGGAATCAAGGNNGGATAAACGCAGGGAAAAGA
ACATGTNTAGTCAAAANAGGCCAAGCNNAAAGGCCAAGGNAACCCGTTAAAAAAAGGCCCG
CGTTGCTTGGCGGTTTTTTTCCATAAGGGCTCC
Sequence 393
NATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGGACACAGGCACTCCTTTG
TCTGGTAGAGAGGAGGAGGGGAAATGGAGCTATTCCAGGATACAAGGGATGGCACTGAGG
GATGCATAAGTCCCCTGCCTCCCTTGTCTCAACATGTTCTCCTCTGCCAGCCCAGTCAGC

Table 1

TTGGGGAGCTAGGTATCAGAAACCTGAAGGATCCAGCCCGCTTTGTCCTACTAGTGTCTA
TAAGTCTCTGTCCTGAGATCCTGGGGCTCCTCCTATTTCTAGAAGGGATGAGGTGCCATC
AAAAATAACTTGGCTGGTGTAACAGTTTAGAGAAGGAAGTCACACCTGTAGCCTGGCTGG
CAGGCAGGTGGACATGAGGCTGAGAAGGGAAGCCAGATGTCAGAACATACTAGGCTAGCA
TGCCTG
C
Sequence 394
GTGGCGGCCGAGGTACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAA
AACTATCTCCCACTCTTTTGGCCCAGGCAATGTCAACGACTTCCACATTCCCTGGCCCAC
TTGCTGAGCAACCCCAGGTTCGGCTCTGTATAAGGACCCTCCCCTNCCAACCCCAACCCC
AGAGTGCAGTGCAAATCAACCAACAATTTACTGGTGGAATGGCAATCAAAGGAAACAGTT
AAACACCAAACAATTNCTTAAAGCCAAAAAATATTTTTCATGGAGTTGAACATTTTTCG
A
GTGTGTTTTTTTCAAGTGTAAAAGCAGTGACATTTTGTTCAAACAGAAGCAGCATCTAGG
AATTCTGGCACTTGGGGTTCTAAGGGGGTTACAGGTATGCCATCATGGATTCTTCTCC
C
Sequence 395
NGGGGCCGGGCCCCCGGNGGGGGTTANCCTTTCCATTTTTNANCAACCTTTTAAAAGCCCT
TGGGGAGGGNGGGGGTTTAANGGGGAATCCCTTTNAAAATTTTTTTAAATNTTNAAAAAGGG
CCCCCATTAAGNAATTTCCCAAGGTTTTTNAAGCCTTTTTTAAACCCCTNAAGNACCAGG
GNAAAAAGGTNGGAAAAAAGGGCCANTTTTTTTTTACCAAAGGGNGGGGGGGAGNGGAAGGG
CCAAANTGGGAAGGAAAAATTAAAANGGGCAAAACCAAGGAATTANATTACCGTTCCAAA
AAAGCNTGGGGAAACCAAGGGGGGGCAGGAAAATTCAAGNAAACCGTTGGTCCTTGGGCCT
TATTCAAGCCTTTTTTGGTTTTTTTTTGGACCTTACCTTAAAAGGGCCCCAAACCCCTT
T
TTTTTAATTTCCCTCCTTGGGAATNGGGGTTCCTGGCCAAGNACCCCAAAAGGTTTCCAA
GGGAAAATTTTTTAAGGGGCCCAAAAAAAAGGGGGAATTTTTCCCCCAAAAAAATNGGGGNATT
CCCCCCTTAATTAACCAATTCTTTCNAAAGGAAAAGGGAATTANCCAAGGGGGGTTTTGGG
AAGGNAAAAGGGAAAANGGCCCCCNNCCAAGNAAAGGGGNCCTTTTGGGTGGGAATTGGG
AAAAACCCCCAAAAAAAAAGGAAAAATTCCNTTTTTTTAAAAAAAAGGGAAAAANGGGGGGTTN
TTNCCTTTCNAAAAAAAATTGGCCCAATTTNGGTTCCCAAGGGTNAAGGNAATTTTTTTG
G
GGGTTNAAAACCTTTGGGGGGCCAANGGGGGGGGAAAAAAAAACCCTTTTGGGTTCCTTTGGG
GGGGNAAG
Sequence 396
TGGGGGCCGGGCCCCCGAANGGTTACCCCCGCGGGGGGGGGAGGCCTTTTNTTNCCCTTTG
GGCCCAGGGTNTTNCNTTTCCCCAAGNCAANGGAAACCCCCTTTCTTTTNCTTTGGGTTT
TTTGGAAAAAANGGAATGGGGTTCCCGGGCTTGGCNTTTTTTGGGGTTANGGGCCACCGC
TTCAAGTTCCTTGAAATGGTTCCCGGCNCATGCTTTCCCCGGGGCCCGGCTTCNTAAGNA
AACCTAAGTGGGGAATCCCCCGGGGGCCTTGCAAGGGAAATTCCGATAATCAAAAGCTTA
ATCCGGATAACCCCGGTCCGAACCCCTCGGAAAGGGGGGGGGGGGGGCCCCCNGGGGTAC
CCCCAAGCTTTTTTTGGTTTTTCCCCTTTTTAAAGTNGGANGGGGGGTTTTNAAAATTT
T
GGCCCGGCCCGCCTTTTGGGGCCGGTTAAAATCCAATTGGGGGTTCAANTAAGGGCCTTG
GGTTNTTTCCCCTTGGTGGGTGGGNAAAAAAATTTGGGTNTTAANTTCCCCGGCNTTCCAA
CCAAAANTTTNCNCCAACCAACCAAAACCCAATTTANCCGGAAAGGCCCCNGGGGGGGNAA
GGCCCAANTTAAAAAAAAGGGTTGGGTTAAAAAAAGGGCCCCCTTGGGGGGGGGGGGTTGG
GCCCCCNTNAAAAAATTGGGAAAGGGTTGGGAAAGGNCCCTTTAAAAAAACCCTTTCCAAAC
CAAATTTTTAAAAAAANTTTTNGGCCCGGGTTTTTTGGACCCGGCCCNTTTCNAACCCT
TT
GGGGCCCCCCCCGGGCCTTTTTTTTTTCCCCCAAAAGGGTTTNCCGGGGGGGGGGGGNAAAAA

Table 1

AA
Sequence 397
GTGGGGGGCCGGGGGCCCGGGAGGGGTACCCCGCCGGGGGGNGGCCTTTNTTTCCTTTGGCC
AGGTTNTCTTCCCNAACAAGGGGAACCCCTTNTTTCNTTGGGTATTTTGGAAAAAGGAAT
GGGTTCNGGGGCCTGGCTTTNTTGGGGTTAGGGGCACCGCCTCAAGTCCTGGAAATGGGTC
CCCGCCAATGGNGTGGCCNGGCCCCGCATCTTANGGAAACCTANGTGGGGAATCCCCCCC
GGGGGCTTGCAAAGGGAAATTTCNGAATATTCAAAAGCTTAATCGGAATNACCCCGGTCC
GNACCCCTCNGGAGGGGGGGGGGGGGCCCCCGGGGTAACCCCAANCNTTTTTTTTGGTTTC
CCCCTTTTTAAAGTNGGAAGGGGGGTTTTAAAATTTGGGCCNGCCCGCCTTTTGGGGCCG
GTTAAAATTCAATTNGGGGTTCCAATAAAGGCCTTGGTTTTTTCCCCTTGGGTGGGTTGG
AAAAAAATTTNGGNGTNATTNCCCGGCNTTTCAACCAAAANTTTGCCCCAACCCAACCAA
AANCNCAATTTAACCCGGNAANGNCCCCCGGGGGGGGGAAAGGCCCAATTTAAAAAAANGG
TTGGGTNNAAAAAAAANGGNCCCCTTGGGGGGGGGGGGGGTNGGCCCCCTTNAAAAATNGGGA
AAGGGTTGGGGAANGGCCCTTTAAAAAACCTTTCCAAACCCAANTTTTTAAAANTTTTTGG
GCCCGGTTTTTGGNCCCGGNCCNTTTCNAACCCTTTGGGCCCCCCCCGGGGCNTTTTTNTT
NCCCCAAAANGTTTCCTGGGGGGGGGGGAAAAAAA
Sequence 398
GCGGCCGGGTACAAAATTTAGAGGTTTCCCCTTTATCAACAAGAGACCCAGGTGCCAGCA
TGTTACTACCAGATCCAGTTCTTCTTAGGACAGTGTGGCTCAAAGGGATGAGACCTTCCA
GACACTGGTATCTGAGCATCTGTGGCCTGCCCCTGAGTTGTCAAGATAATTTCTTATCTC
TGAAGGAGTCCAGACAGGAATGCTTCCACTGCTGGGTGGGTGCTCGCCCCTCTTGCTCCT
TAAGCGCCCGGCTCACCCCCTTGCTAGCACAGGGTGTCTTACACAGTTTATGGGACTTTT
CTGTGAACTACCTGAGGGCAAGAACCATGTNCCACTCCCTGCTTGCTCCTCAAATATTTT
A
Sequence 399
CNGCCGAGGTACNCGGGGAGAGAGGAAAAGAACACAGATCTCGCATGGTTCAGATTTTTC
TTTTTAGGTCCAGGAGTAAGATATATCATACNGAAAATGAAAATTATAATTCTTCTTGG
A
TTCCTGGGAGCCACATTGTCAGCCCCACTTATCCCACAGCGTCTCATGTCTGCCAGCAAT
AGCAATTGAGCTTACTTCTTAATCTTTAATAATGGGTCAACTTTTGCCACTACAAACTT
C
AGGGGCCCACTTAATTCATGGANTCCACCTTTCTCTGGGAATTTTACAACAGCAGCAGCA
GGCTCAAATTCCAGGACTCTCCCAGTTCTCTTTATCAGCTCTAGACCAGTTTGCCTGGAA
CTGCTCCCAAAATCAGAATACCCTTAACCAGGGAAGAGGCCAGTTTTGGNCCCAAAGGGA
GCCCCAAGGCAAGGGCCAAGGTTNGAATCCCNTTAACNGNNTTTAAAAACAACCCGCCTT
TAAGAACACAAACCCAGGNCCCCCANGACACCGTTGAATGCCCCTTATTGTTATTTCTTC
CC
Sequence 400
GACAGACAGTGCTTGATGTTCATAAAAAATACAATGCCCTGGTAATGTCTGCATTCAACA
ATGACGCTGGCTTTGTGGCTGCTCTTGATAAGGCTTGTGGTCGCTTCATAAACAACAACG
CGGTTACCAAGATGGCCCAATCATCCAGTAAATCCCCTGAGTTGCTGGCTCGATACTGTG
ACTCCTTGTTGAAGAAAAGTTCCAAGAACCCAGAGGAGGCAAGAACTAGAAGACACACTC
AATCAAGTGATGGTTGTCTTCAAGTACCTGCCCGGGCGGTCGAGCGGCNCGCCCGGGCAG
GTACGCGGGGGCTAACCAGGCCAGTGACAGAAATGGATTCGAAATACCAGTGTGTGAAGC
TGAATGATGGTCACTTCATGCCTGTCCTGGGATTTGGCACCTATGCGCCTGCAGAGGTTC
CTAAAAAG
Sequence 401
CGGTGGCGGCCGGTTGCCTTGTATGTCACGAGCAATTAGGAGAGTCACGAGGATGAAATA
GATGAACCCGACCATGCAGTTAATCACCAACATCAACTACTAGCCAGACGGGATGAACCA

Table 1

CAGCGTCACACAATACAGTGTTCCTGTTGTAAGTGTAACAACACACTGCAGCTGGTAGTA
GAAGCCTCACGGGATACTCTGCGACAACTACAGCAGCTGTTTATGGACTCACTAGGATTT
GTGTGTCTCGTGGTGTGCAACTGCAAACCAGTAACCTGCTATGGCCAATTGTGAAGAGAT
GGGAGTCTCCCCGTATTGCCCAGGCCGGTCTCAAACTCCTGGGCTCAAGCAATCTTCCCC
GCCCACTTCCCGAAGCCCTAGGATTACGGGAGTGAGCCACCGCACCCAGCCAGAAAAACG
TTTAAAAATTTGGAAAACCTTACTTTTTTTAATGAGCATTTTTGCATCAAGGGGGTTAC
A
GGGACATTAGGCTTTTTTTTTT
Sequence 402
ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACATATCCTCTGTGGGAAAAA
CTGCTCTCAGAGTGTGCACTCTCCCCACAAGCCAGCGCTCAAACTGGAAAAAGTATCTCA
ATGTCCTGAATGTGGGAAAACCTTTAGCCGAAGTTCTTATCTTGTTCGGCATCAAAGAAT
CCACACAGGCGAGAAGCCTCACAAGTGCAGTGAGTGCGGGAAGGGCTTTAGTGAGCGCTC
CAACCTCACTGCCCACCTACGAACTCACACAGGGGAGAGGCCCTATCAGTGTGGGCAATG
TGGGAAAAGCTTCAACCAGAGTTCCAGCCTCATTGTCCACCAGAGGACCCATACCGGGGA
AAAGCCTTACCAGTGCATTGTCTGTGGAAAGAGATTCAACAACAGTTCCCAGTTCAGTGC
TCACCGGC
Sequence 403
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAAATTAAGTATTAAAATGAGGATTGAA
CTGGGGCAAACAGGTTATTGTGAAAACAGTCAATATGTAAGCTCCTTCAAGGGAAATCAA
CTACTGTTCCTCAAGATTAGAAGATGTNCACACTCTTTGCATTACCTCCCTAAAGGAGGA
AACACCCATTAATTTTCCCTTATGGAATCAATATGGAGTGGAAATATGAAATGAGGAGAT
GTTTTAGAAAGCAGGACANATCTACCTACCATTACTGGAATTAAAATGTATCCTCTGGGC
CCACTCCATTGATTCCGATCTGAGGTGAGGAGGACTAAAAGCAGCAGCAGGTTACAGAAA
GACTGAATAAGATGAAAGTATGCTACGTATGTCTAGCTGGGGAAGGGGGGATCTGGAAAA
A
Sequence 404
CCGCCCGGGCAGGTACGGACGCCCAGGGATCCGCGCCGAAGCTAGCACGCANCCTACCCA
ACAGTCTACACAGCNCGACCAAAGCCCCCGCGTACCCAGAGGAGTCGCTGGTGATNGGGG
AGCTCAACCCTGTTNAGTAGCTCTGCTCATCAAGTGTCTGGAGAAGGAGGTTGCGGCATT
GTGCAGATACACACCCCGNAGGAACATCCCTCCTTATTTTGTGGCTTTGGTGCCACAGGA
AGAAGAGTTGGATTGACCAGGAAAATTNAGGTGACTTCTCCANGGCTTTCCAGCTTGGTC
TTTTT
Sequence 405
CCGCGGTGGCGGCCGAGGTACGCGGGGGGCGGCGGCGGAGAGAGCTGGCTCAGGGCGTCC
GCTAGGCTCGGACGACCTGCTGAGCCTCCCAAACCGCTTCCATAAGGCTTTGCCTTTCCA
ACTTCAGCTACAGTGTTAGCTAAGTTTGGAAAGAAGGAAAAAAGAAAATCCCTGGGCCCC
TTTTCTTTTGTTCTTTGCCAAAGTCGTCGTTGTAGTCTTTTTGCCCAAGGCTGTTGTGT
T
TTTAGAGGTGCTATCTCCAGTTCCTTGCACTCCTGTTAACAAGCACCTCAGCGAGAGCAG
CAGCAGCGATAGCAGCCGCAGAAGAGCCAGCGGGGTCGCCTAGTGTCATGACCAGGGCGG
GAGATCACAACCGCCAGAGAGGATGCTGTGGATCCTTGGCCGACTACCTGACCTCTGCAA
AATTCCTTCTCTACCTTGGTCATTCTCTCTCTACTTGGGGAGATCGGATGTGGCACTT
TG
CGGGGTNTGTGTTTCTTGGTAAGAACTCNATGGAAACAGGCCTCCTT
Sequence 406
TCCCCGCGGTGGCGGCCGAGGTACAGTTCACAGTGCTTGATGATAATAAATGGTTATTTT
ACTGGTTCATGTATTTACTATATCATACTTTTTTTTCATTAGAGTGTGCTCCTTCTACTTA
TGTAAAAAAAAAGTTACCTCAGGGAGGTCCTTCCTGAGGTCTTCCAGCACACGGCATTGT
TATCATAGAAAATGACAGCTCCATGTGTGTTACTGGCCATTACCACCTTCCAGTGGGAAG

Table 1

GATGTGGAGGTGGAAAGCATACTGATGATTTTGTCCCCGTGGAGGCCTAAGCTAATGTGT
GTGTTTGTGTCTTAGCTTTCAACAAAAAAAAGTTTAAAAAGCAAAAAAAAAAAAAAAAAA
A

Sequence 407
GTGGCGGCCGGTGTGCTCATCGTAGCCTCGGGTCGGGGGATGCGTCTCCGCTTTAGCGCC
AAGATAGAACTTCCTCAGACCACCGCCGCCGCCCCCGCGTACCT

Sequence 408
GTACCTCCCTGGCTGAAGTCTCTACATAGCTCTCAGGAACCTTCGGAAAGGCATCCAACT
CTTTTACCAAACTTAAAGTTTTTTTCCGATTCAGTCGCCTCATCTTCAGGAAAACCTTC
C

TCTTCCTTCATATAGTCATGCTTGTGTTATGGTCCCAGCCTACCGCCATGTTTTACAGA
A

GCCCGGGTCGCCGGGGCTCCCGCGTACCTGCCCGGGCGGCCGCTCGAGGCAGGTACTGAA
TGACACATTACCTCCACACTCTCCCGGACTAGG·NGTCAACAGGGCCACAGGGTTGCTTT
CTGTCTTTGGTGGGGCAGGGGAGTTGACAGGGATGAGGGTCCAAGGAATTAAGCATGGAA
TGACAAGAAAACANGGGAAAGAGTTACCCTGTCACATAGTAGGTTAACTTTTTTAAGGGT
TTGCAAGTAAGAGGNNTTTCGACCCTTTCNCTTGGCTGAGCCANATCNCGGGAACTTGAG
AGCTTTTACTGGGATTTTCAATNNAAAAAAATTAACAACAATGTCAAACTNGGGTTTGGA
T

NATTGGNTTAAAGCCTTTTTAAGATTCTTTTTTAAATAACATTTTTCCCCGAAAAAAAAA
AAAAA

Sequence 409
TTTTNGGGGGGGAGTTAAATAAAATAAGCATGTCTNCATCCTTTATTCCTAAACATTTAC
T

TATGACAAATGTAANNACTGACAGAAATTTGAAAAATACCANGACACTTCTTAAATGATT
TCCCTTGGTTCAAAATTTACCCCTTCTTGGGTTTCTNTTGCTTTTCAAGGGTAATNTAA
A

CTCTTCTCTTTTTANGTTTGAACTATGCAAGTGCCAAAGGATTCCNCTGTAGTCTTTCC
A

AAGGGGGGGAAAGGGGGTNTATANAAAAAAAAAAAAACACCTT

Sequence 410
GGGCAGGTACTGTGCAGTAGTAACCCATAATTCTAAATGAGGATTATGGATTTTTCTGGA
AGATTCTTTTTTCCTGTGGAACATGATGAGAAATGTTTAGGAGAGGGGACATAGCCATTT
TTGTATGAAGACCAATTCAAGAAAAAAAATATATGTATGTGTGTGGGTGTATATGTGTGTA
TATATGTATAT

Sequence 411
GGTACGCGGGGTGCTGGGATNCAGGCACGAGCCAGTGCGCCCAGCTGCCTNTGTTTNTTT
TATTAGCTGNTCTGGACTGNGGGGGCTCCTTGGGCAGATGCTGTATTATGGGGATAAGCCA
CACACTTTNTGAACTGGCCCGGTCAGGGGGGACATANCCATTTCCTGTGCCCCCCCATCAA
NACCCACCTATTCTGAGNGTNNGCTCCTCCCCTGCTTGAGTNATGGCCACANATCTTGGC
TCGGNNCTCCTAAGCTGCATGNTGAATTCCTGGGACAACAAGACTGGCTTGTGGTTCCAT
TCTCCAGATCCTTGGGT

Sequence 412
GCCGGGCAGGTACTTAGAGTTTTCCAAGTATGTTCTAAGCACAGAAGTTTCTAAATGGGG
CCAAAATTCAGACTTGAGTATGTTCTTTGAATACCTTAAGAAGTTACAATTAGCCGGGCA
TGGTGGCCCGTGCCCGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCACTTCAA
CCCAGGAGGTGGAGGTTACAGTGAGCAGAGATCGTGCCACTGCACTCCAGCCTGGGTGAC
AAGAGAGACTTGTCTCCAAAAAAAAAAGTTACACCTAGGTGTGAATTTTGGCACAAAGGAG
TGACAAACTTATAGTTAAAAGCTGAATAACTTCAGTGTGGTATAAAACCGTGGTTTTTA
G

GCTATGTTTGTGATTGCTGAAAAGAATTCTAGTTTACCTCAAAATCCTTCTCTTTCCCC

Table 1

A

AATTAAGTGCCTGGCCAGCTGTCATAAATTACATATTCCTTTTGGG

Sequence 413

GCGAGGTACCTAGTCTANATGAGTTTGATGCTTACAGTCAAGGCTATTAGCAAATATTCA
GGAAAAGTAAAGCCTAAAGAAGAAAAGAGGGAATGAATAGTTTGTCTAGAGATAATAAAA
GGAAGGTGAATTTTTAAAAAGACAAAAATAANGCTAGAAAAGACTGAGTGGAGAAAGCCT
ACAGAATTTCAGAAAGCTAAAGAAATTGGAAATTAGATTGAATATAGATAGAAATGGGAG
GACAATGCAGCCAATGAAAGACTGTGGGGACTAATAAAGGGAGAGCCCTGTGGTTTGGAA
AGTGTCCCTTAATCAGCCTGCAGTGCTGCAAAACAGAACCCAGAG

Sequence 414

GGTGGCGGCAGGTACGCGGGATCCAAGATGAATGTGCAGAGAAAATAAAGAATCCAAAGT
CATAGTCATGAGGACAGAATAAAGACATTTTATGCCTTTTTGTTTTGTTTTGTTTTCCTT
TTTGTGGAGAACAGGGTCTCTCTATATTGCCCAGGCAGGTCTTGAACTCCTGGGCTCATA
CTGTCCTCCTGCTTCTGCCTCCCTAAGAGCTGGGATTACAGATGTGAGCCACCATGCCCG
GCCAGAATAAAGACATTTTAAAACTAAAAAAAAAAAAAAAAAAGAGTTTGCTTTGCATTAA
TCTTTTTTTTCTTTTTTTTTCGTTTTTATTTTTTAGTTTTTATTTTTTTTTGAGACGGAGTC
TCACTCTGTCACCCAGGCTGGAGAGCAATGGCATGGTCTCGGCTCACCGCAACCTCTGCC
TCCTGGGTTCAAGTGATTATCCTGCCTCAGCCTCCTAAAGTAGCTGGGATTACANGTGTG
AGCCACCACGCCTGGCCAGAATAAAAGACATTTTAAAACTTANGGAAAANAAAANAAAAN
NNTNGNNNCNNCCCCCCNNNAAAAAAAAAAAAAAAAA

Sequence 415

ACCGAAGACGAANGCCACTACATGCCCCCGCGTACCTGCCCGGGCGGGCCAAAGGCCAAC
AAGGGNAGTGGGGNCGGGCTGCANGAATTTCGATATCAAGCTTATNGATACANGTTGACC
TCNAG

Sequence 416

CCCCGCGGTGGCGGCCGAGGTACGCGGGGCTGCGGAGGACCGTGGGCACGCCAGGGTCGG
TGAAGGATCCCAAAATGGCTGGGCGAAAACTTGCTCTAAAAACCATTGACTGGGTAGCTT
TTGCAGAGATCATACCCCAGAACCAAAAGGCCATTGCTAGTTCCCTGAAATCCTGGAATG
AGACCCTCACCTCCAGGTTGGCTGCTTTACCTGAGAATCCACCAGCTATCGACTGGGCTT
ACTACAAGGCCAATGTGGCCAAGGCTGGCTTGGTGGATGACTTTGAGAAGAAGTTTAATG
CGCTGAAGGTTCCCGTGCCAGAGGATAAATATACTGCCCAGGTGGATGCCCGAAGAAAAA
GAAGATGTGAAATCTTGTGCTGAGTGGGGTGTCTCTCTCAAAGGCCAGGATTGTAGAATA
TGAGAAAGAGATGGGGAAAGATGAAGAACTTAATTCCATTTTGATCAGATGACCATTGAG
GGACTTGAATGAAGCTTTCCCAGAAACCCAATTAGACAAGAAAAAAGTNTTCCTATTGGG
CCTANCCACCCATTGAGAATTATTAAATTTGAGTNCAGGANGGAACTTCTGGCCCTTTGT
ATTACCCATTCTGGGCCTTTAAAATATTATTTTTTCCAAAAAAGGAAAAAAAAAAAAAAAA
AAG

Sequence 417

GGCGGNCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAGGGAGTTTTGCTCTTTTTGCCC
GGGCTGGAGTGCAATGGCACGATCTCGGGTCACTGCCACCTCTGCCTCCTGGGTTCAAGT
GATTCTCCTGCCTTAGCCTCTTGGGTAGCTGGGATTACAGGCGCCCACCACCATGCCTGC
CCAATTTTGTATTTTTAGTAGAGATGTGGTTTCACCATGTTGGTCAGACTGGTCTNGAA
C
TCCTGACCTCAAGTGATCCACCCNCCTTGGCCTCCCAAAGTGTTGGGATTACAGGTGTAA
GCCACCGTGCCCGGCCATCAGTTGTATTTNTATATAGTAGCANATGAACAATCAAAATGN
GATTAAANAAAATGCCNTTTTTTAATAGCCTTAAAAAAAAAAAAANTTNTTANTGAATAAAN
TTTAANCCAAAGGAGGGGNCAAACCTTTTCCNTGGGAAATTCCAAAACNCNTNTTTGGNA
NGAATTCAAAGNAGGNTGAAANCCCNNCCCCTTTTTNCGGNGTTNANAAAAAAANANATTT
TTTANNGGGGGGNCCCCNCCCAAANNATANTTCCNCNGTGGGGGGCCCTCTAAAAAAANAN

Table 1

TTTTTTTTTTTTTTTNTAAAAAAAAAAANNTTNTTTTTTTGGGNG

Sequence 418

CGCGGTGGCGGCCCGAGGTACGCGGGATTTTGAATGAATTCTCAACAAAATGTGCTAGCC
ACTGGGGACGCAAAACAAGTAAGATCCCTGTTGCAAGAAATTCATTTTATNGNGAGGGAG
GTTGGCATGGAGACTAAAATTCTCAGGAAAATGAGATCCGTGTTAGATTAGAAGTCCTGA
TGTGAAATGGGAGGACTCAGGAAGGAGGATCGTCTTTACCTGAGGATTTCTAGCCAGAGG
TCCCAGATGCCTGGGCTGAGAACCCAGCGATAAGGGGGCGTTCCCAAAGCAGACACAGGG
ATAAGAACAGAGGAGGCAGCAGCATTGCACAAGCCCCAGGCACAGTGGCAGTTAGGATGG
CTGGAGAGTAGGATAGTTCTATGGGTTGCCCAAAAAATGTGATGTGCTTCATGTTTTCTC
TGACTCATGGATCTGGTAGAGACCATAGACATGATATAGGACTAACTTGCCCATTTTTCA
CANAGAGGAAACCATCCTTATGACTTACCTTAAAGTTTTTTGTTCTGTTTTGAAAGGAA
A
CCATGTGCTTCATGAAACCTACAGTTGGCCAGAAGAATGNTCCTGCCCCGGCCGGCCGCT
CTAAAACTAGGGGGATCCCCCGGCTGCAAGGAATTCGATTTCAAAGCTTATNGATTCCCG
NCACCTCGAGGGGG

Sequence 419

CCGCGGTGGCGGCCCGAGGTACAGTATATTGACCTTAAAAATCAGTAAAGCAGTCATGGA
AATAACAGGTCGTGTATTATTCATGGGCACAAACTGACTCATGGCTGGGGAAGAAGCAGC
CACCTTAGACCAGATGGACAAGCCAGATACTGCAGAGAAGTTTCTGGGCTTTTCGGGGAG
CTCTAGATTCAATTCTGTAAAGTTATGATGCAGTTTTCTCCTTCCTCTCCTCTCACCTN
C
TNTGAGCACAGCTTTCAACAAAAACTTTGCATACCCCGCGTACCTGCCCGGGCGGCCGCT
CGAGGTACTTCTCTGAGCATTGGCCTCTGGCTGGGATTATGCTTCAACAGTCTTGAAATG
AGGTCCCTGGCTCCCTCTGTTACAAAGTCAGGGAATGTGAATTCAACCCGTGATATTCTT
TTGTAGGTCTCTTGGTATGTGTTTGCCTCAAAAGGAGGCTTCCCAACTAAAAATTCATAG
CAAAGAACTCCAAGGCTCCAAGAGATCCACCTTCTCATCATGCATCCACCTTCAATCATT
TCANGGGGCANGGAGTCCAAGGTGCCACAAAGAGNGGTCCTTCTGGGAAGATGGAGCATG
TACCTCGGGCCCTCTAGNACTAGTGGAT

Sequence 420

GAGGTACGCGGGGGTCGGCGCCATTTTGTCTCGGCAGCGGTGGCCCGTAGCTCCATCGCA
TTTTATGTTTCTGGCGAGAAGGGAACGGAGTTTTCATCAGGTAGATTGGTTTTTGT

Sequence 421

GGGGCGGCCGCCGCCTNCCCGTGAAAGACCTCCTGCTGGAAGACCTCCAGGATGGAGAAG
TGAGGCTGGGTGGCTCCCTGCGAGGGGCATTCAGCAACAATGAGAGAATTAAAAACTTCT
TCAGAGTCAGTTTCAAAAATGGATCCCAAAGTCAGACCCACTCGCTACAAGCCAATGACA
CTTTCAACAAACAGCAGNGGCTTAACTGTATTCGTCAAGCCAAAGAAACAGTTTTGTGTG
CTGCCGGGCAAGCTGGGGTGCTTGACTCCGAGGGATCGTTCCTAAATCCCACCACCGGGA
GCAGAGAGCTACAGGGAGAAACAAAACTTGAGCAGATGGACCAATCGGACAGTGAGTCAG
ACTGTAGTATGGACACNAGTGAGGTCAGCCTCGACTGTGAGCGCATGGAACAGACAGACT
CTTTCTGTGGAAACAGCAGGCACGGTGAAAGTAACCGTCTGACAGAAAGCATGTGCACTT
CNGGAAGCAGGCCTGCATCTTACCTGTACCTGCCC
N

Sequence 422

ACTTCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAACTGGGGAATTCTGGCCCTAC
GTGCATTCACAGGCAATGATGGGTTTGTGTGTATGGTGTCATGAGATCCTCTACCTCATA
ACAAAAGGACAGTGGGTAGACTAAGGCAGTAGCTCAAAGGGCTTTGCAAAATTTTAATAT
ATTAAAACAAGAGGCATCTGCTAGAAAACATTCTATTGTATACATACTGAAAACCCTATA
AGGTCCTGGATAATTTTTGTTTGATTATTCATTGAAGAAACATTTATTTTCCAATTGTGT
GAAGTTTTTGACTGTTAATAAAAGAATCTGTCAACCATCAAAAAAAAAAAAAAAAAAAAA
AGTACC

Table 1

T

Sequence 423

NCCCGCGGTGGCGGCCCGAGGTACGCGGGAGAAGGAGATTACCTCAACATAAGAACCGTA
TGTGAAAAGCCCACAGCTAACATCATACTCAATGGTGAAAGACTGAAAGCTTTTCCCCTA
AGCTCATGAAGAAGACAAGGAGGCTTGGTTTTGTGGCTTCTATTTAACATGGTAATGGGA
AGTTCTAGCCAAAGGAAGTAAGCAAAAAAAAAAAATCGAAATTAGACAGGGGGAAGTAAAA
TTATCTTTTTGCAGATGATATGACTTATATGTATTATAGAAAACCCTGGGCCAGGTGCA
A
TGGCTCTTGGCTGTAATCCTAGCACTTTGGGAGGCCGAGGTGGGTAGATTGCCTGAGCTC
ANAAGTTTGAGACCAGCCTGGGCAACACGGTGAAACCCCCCTCTACTAAAATCCAAAAAA
AAAAAAAAAAAAAATTAGCCCGGGCGTGGCGCATGCTAANGCANGGAGAATTGCGTGGAATC   .
TGGGANGGTGGANGNTGCANTGAGCTTGAAGATCTCCCCCTGNACTTCCAGCCTNGGGGG
ACAGANCCAAGACTNTTTTTNTTCCAAAAAAAAAAAAAACCGGGGGGGNGGACCCCTCAAGAA
TTCNCCCCNCCCCCCCCCGAANCCCTGGTTTGAAATTAATAAATGGGGTTCCGCCAAANA
AAGTNCCNGCTTNTTCAATCAACAGGCCAAAAATTCCTTGTTTTTAAANCCCTGCCCTT
T
AAAANTTTTAAAAAAGGAAACTTNGNATTCCCGTTTCTTTTTTATTGCCTCCAAAAAAAAA
AAAAAAA

Sequence 424

CCGCGGTGGCGGCCGAGGTACTGCCGAGCCGCTCCTCCCGCAGCTGTGCCGCCTCCTTGT
CCTCCTCCTCATTGTCACTGCCAAACAGGTCAATGTCATCATCCTCGTCATCCTCTGC .
TG
GTGTGGCTGGCTTCCAAGCTGGTGCCCGTGGGCTACGGTATCCGGAAGCTACAGATTCAG
TGTGTGGTGGAGGACGACAAGGTGGGGACAGACTTGCTGGAGGAGGAGATCACCAAGTTT
GAGGAGCACGTGCAGAGTGTCGATATCGCAGCTTTCAACAAGATCTGAAGCCTGAGTGTG
GGTACCTGCCCG

Sequence 425

CCTCCCGCGGTGGCGGCCGAGGTACTAAGTGGTTAAGGATGGAAAAGAGCTAACAAGTGA
CAACAAATACAAAATAAGCTTCTTCAACAAAGTATCCGGCCTTAAGATCATCAATGTAGC
GCCGAGTGACAGTGGGGTATACAGTTTTGAGGTGCAGAACCCTGTTGGCAAAGACAGCTG
CACAGCTTCATTGCAGGTTTCAGGTTGGTTGATTTCTTGGGCTTTTCCTTCATCATTAT
A
ATAATGTAGTTCCTGATTTTCATAAATGTATATGGGTTGTTACATCTTCTATAGGATAAC
ATGAGTCCGACATCTTCTGAATCAGCAAATTCAGAGGCAATACCATCTCAAGAAGCCACC

Sequence 426

CTNCCGCGGTGGCCGGCCGCCCGGGCAGGTACTGAATGTGGGAAAGCCTTTTGCCAGAAA
CCACACCTGACCAACCATCAGCGAACACATACAGGAGAAAAACCCTATGAATGTAAGCAA
TGTGGAAAAACATTCTGTGTGAAGTCAAACCTCACTGAACATCAGAGAACACACACAGGG
GAGAAGCCCTATGAATGTAATGCATGTGGGAAATCCTTCTGCCACAGATCAGCCCTCACT
GTGCATCAGAGAAGACACACAGGGGAGAAACCTTTTGGATGTAATGAATGTGGGAAAACC
TTCCGTCAGAAGTCGGCCCTAATTGTTCACCAGAGAACTCATATAAGACAGAAACCCTAT
GGGATGTAATCAATGTGGAAAATCTTCTGTGTGAAGTCAAAACTCATTGCACATCATAGA
ACACACACAGGGGAGAAACCCTATGA

Sequence 427

CCCGNGGTGGCGGCCGGGTACCTTACTTAGCAGAGCACTTTGCAAACATATTACTTATTA
GCAGAGCTCTTTGTAGACCTTCCACATCTGGCTGTCAGATCTTAAGGTTGTGAATTTAGG
CTCCAGTTATATTCACTGGAGAGCATAATCCCACACGGGTTATTTATAAATACAGAGCCT
CTGATTGGACGGTCTCCTGCCAAGAACTAGTAATACCCTTGTTTTAAAATCTTCACAAGG
TAAAACTTAAAAAGCCAACCAAACAAATTGCTCTCCATTCTACTTTTAATTGGGCCAAAC
AGCATATGCTACAGTAGTAACATGTTTTTTCGGAGAGTGTAAAAAACTCTGTTTACATTT

Table 1

G
CCTCCTCGTGGGTTGATCGAAAATGTATAAAACTGACTGCTTCTCGCCAGCCTCAGACAA
GAAAGAGTGAGCTGCTGGTACCTGCCCGGGCGGGCCGTCTAAAACTAGGNGGGAT
Sequence 428
GGCCAAATGCAGAAACGTCCCACATGCCCACCAGGAGCAAGCTTCAAAATGTTCAGCTTG
CGGGGCANTNNGCAGAGAAATNCCAGGGATGTTCCTGAAGGCCTNGATGATACCANTATC
CTCATTATAAGATGAATGCACGGGGCCCNTTGCGCTGGATACCGGCNAACCGGNTTCTNA
TTNTGCCTNTGNCAGCTCTCATTCGCTGAGAGGCATAGACCTTTTTGANGATCATTCCAA
NGCTATAAGTCNTCTTAAGGAGCAAAAACCAGCTTCCTTGGTCT.NTCTTGAAGNCCTTCA
ACTTTATCTTTCAACTACCAAAGGGAAGGTNCAGGAAACTTTCCTCAATAACCGANGGAC
CTTTAGGACATGAACCAGGTGNCTGGNTAGGGGCTGGAGGCCAGCCCAGGGCAAGAAACA
NAATGGCCGATANCCGTTTTTGGGGTTCCCGCGGTACCNTTGNCCCGGGNCGGGCCGGCT
TCTAANAAACCAAAGTGGGAANCCC
Sequence 429
CGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGTGATCTCAACTGCTTTT
A
GCAAGTTGTGAATATACTTGGGCTTTCTGTCTTTCCCCAAAAGCAATTTGGGATTATTT
T
CCTCCTTTTTTTTTCTGCATTTCATCATAAATACTGTCATATTCATACACAGTAGCATCTT
CTGCAAGGGCCTTCTGGATTTCCAGTTTGGTCTGTTTCATGGCCTGCTTCTTAGCAGC
TT
CCCTCTGAAGGCTTTCACTCACAGAGGTCTCATCATCATCATCAGAATCATTCCCAAACA
CTGATGGTTTTTGCAAAACAGGGTGCAACTGCTGTGTTTTCTTTGGCAAAATAAGCCCAT
ACTACCTGCCCG
Sequence 430
GTGGCGGCCGAGGTACAGACAAAACTACAGACTTAGTCTGGTGGACTGGACTAATTACTT
GAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAAATAAAACAAA
TAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGCTGTGTC
AATGGAGATGGCCTCTGCTGACCCAGATGAAGACCCAAGGCATAAGGTTGGGAAAACACC
TCATTTGACCTTGCCAGCTGACCTTCAAACCCTGCATTTGAACCGACCAACATTAAGTCC
AGAGAGTAAACTTGAATGGAATAACGACATTCCAGAAGTTAATCATTTGAATTCTGAACA
CTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCTGGAAACCGATTT
CAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAGGCTGCAGCCCATTCG
CAGGCACCCGAAAGAACTTCCCCAGTATGGTGGTCCTGGAAAGGAC
Sequence 431
GGTGGCGGCCGAGGTACCAAAACAACAGCCCTCCAAACAATGATGACCAGTGGAAAAACA
ATGGAGTCACCAAAACCTGGGACAGGCTCATGCTCCAGGACAATTGCTGTGGCGTAAATG
GTCCATCAGACTGGCAAAAATACACATCTGCCTTCCGGACTGAGAATAATGATGCTGACT
ATCCCTGGCCTCGTCAATGCTGTGTTATGAACAATCTTCGAGCGGCCGCCCGGGCAGGAC
GCGGGAGTTCAAGAAGCTGGTGGTCAAGGAGGAGGAGGTGGAGGTGGCAGTGGAGGAATT
GCAGAAGCTGGAAGTGGTCATATGAACTACATTCAAGTAACACCTCAGGAAAAAAAAGCT
ATAGAAAGGTTAAAGGCATTAGGATTTCCTGAAGGACTTGTGATACAAGCGTATTTTGCT
TGTGAGAAGAATGAGAATTTGGCTGCCAATTTTCTTCTACAGCAGAACTTTGATGAAGAT
TGA
Sequence 432
GCGGCCGAGGTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTC
TGCGTTGTTACCACTGCTTACTGCGTTCCCAGCATTTCTTTTCTCTTCTCGTTTCCTGT
A
GATTCCGGCTAATGGTTTCCCCTGGCATTTGACTTCGTGATGTGTAACTGAGTCTCTT
CC

Table 1

TGAAGGGGGAAACGCATTCCAGAGCATTTGTTCGGGCTCATGTAGGAATAGATCTTTGAC
TGCCCGGTAAATCCCGCGTACCTGCCCG

Sequence 433
GNGGTGGCGGCCGCCCGGGCAGGTACAAATCTACCTCCCCACCAAATGTCCTTAGAGGGC
CAAAGATGGCCTTTGTTTCTTCATGATAACATCGCCTTTCTTTTTTTTTTTTTGAGACAC
G
GTTTCATTCTGTCACCCAGGCTGGAGTGCAGTTGTGCATTCATGGCTCACCACAGCTTGA
ACCCCCAGGCTCAGGTGATCCTCTCACCTCAGCCTCCCCAGTAGCTGGGACTACAGGGGC
ACACCATCAAGCCCCGGGTAATTTTTGAAATTTTTATAGAGACAGGATTTTACCATGTT
T
CCCAGGCTGGTCTTGAATTCCTGGGCTCTAGTGATTCCTCTGCCTTGGCCTCCCAAAGTG
CTGGGATTACAGGCATGAGCCACCACACCCCACCTGTCTATTTTACAATTTTCCTTTGAG
CTCTTTTTTCCAGCAGTCATGAAGCTGGCAAATGGCAGAACTGGAGCTAGAAACTGCTGA
CTCCCTTTATCTTTTCCATAGCACCCCAAGC

Sequence 434
NCGCGGTGGCGGCCGAGGTACTTTTCTAAAAGCTCATCCACTCTATCATTTAGATATCCA
ATTTTCAGAATGTGCTCAACATTGGCCACTCCATCTGCCATTCTTAAGTCTCCTTGGG
AG
TCTCCCAGAAGAATTATGTTACTATTGTCTTTTAGTTGATTGAAATATTCTGTATTCCTC
AAGGCACCATCATGTTTGTTAAATACATGAATTAGTTCTCCTTTAAATCCTTTGAGCAC
C
CCCTATGAAAAATATAAATCTTTTGAACAGGCTTTAAAAATTCTATTTGTTGGATTTTCA
TATTTTGGAGCTCTTAATTGATGTCACTATTATTTCATCATATTTGTAAATACATCTTTG
ATACTAGAGATCTCAAAGCACTTAAGTCCATCACATTCACCATAGCTAAGAAGGGCTCGG
AGAAGTAAATGATTTTTTTAGATACTATTTTAAA

Sequence 435
CCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGGGGTTGCTCAAACCGAGTTCTGGAGAAC
GCCATCAGCTCGCTGCTTAAAATTAAACCACAGGTTCCATTATGGGTCGACTTGATGGGA
AAGTCATCATCCTGA

Sequence 436
GTGGCGGCCGAGGTACGCGGGGGAACACCACCCAGTGTGGAGCAGCCCAGCCAAGCACTG
TCAGGAATCCTGGGAAGCACCTCCAAGTGACTGCAGATCTGGAATAATAAGTGNGGGGTA
GATCTGCCCATAGAGCTCACTTTAGACCGGCCTATACTCCTACAAGGAATTGNGGTAGGG
ATCTTNTACTCATCCTTGGCACAATAAGAATGGCCAATGCCCTTTCTAGTTGTTTGGGGG
AAGGTCTTTGAAGGCACCATTTNCCCCCATCCCCCTGGGGGAAGAAATGGGGTCCCTAAG
GTAACGCCANGGTTTTTTGGGGGTTNAATTTGCAAAAATCCCCTTTTTTNGNGGGNTANNA
CACAAATGGGCTNGGCAATTTNTTTNTTTNCCCCAATTNGNTCAAAANGCCCAANAAAAT
TTTTTAACCGGGGTTGGGGGGGGGGCAAAATTTTTTTGGGCCANNTTGGCAATTCNCNGGG
ANAAAAAATTTCCCAANGGGGCCNGNNGTTCAANTTTCCTTNTAACCCCGTTTNAAACCT
TCNCCCCCCNGTTTNTTTTTTTGGANCCCTTAAAAAAAAACCATTTTTTTGG
GG

Sequence 437
GGCCGAGGTACCTTTTTAGAAGAGAAAAGAATCTTGAATTGTATATATTTATTTTGCTT
T
ACAGAAAAAAATGGTTTCGTAAATAATTTGCCTATTTTGGTTAACATAGCACATGGAGAT
AATCATCTGAAAGTTATAGGGCACTGCCACTGCTGAATCAAGAGCATGCCCAATATTTGA
GGTGGCTCTGATTTCCTGGCAGCTGAACTCGGGTAGTCCAGTGGCCTAGCTGGTCCTGCC
CG

Sequence 438
CGGGCAGGTACGCGGGGAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCC

Table 1

AGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGA
GGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAAGTGAGAGAGCAATGCGAGC
AGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGAGCCGTGTATCC
TCTCCGATCACATACAGAAGAGGATTGCACCGGAGGGAGCTCTTTGGACTTCCTTGGCAT
GCCGAGGGGACCCATTTGCGTGGGCCCACAAACNTCTTTAAACAACCTTGGAAATAAAAT
GTGTGGGACTTTAAATTTCACCCCAANGTTCTTTCANTNAATTCCTGGGGGGCATTCAAG
AAATAATTTTCTCTTTTATTGGGGTTNTTTGGGGAATNNTAACCCCTTCGGGGCCCGG
CT
TCTTAAGAAACCTTGNTGGGGGANTCCCCCNCGGGGNCTTGNCAAGGGAAATTTTTGGAT
ATTCTAAGGCCTTTAATTCNGATTACCCCGNTTCTAANCCTTNGAANGGGGGGGGGGNC
Sequence 439
CGAGGTACTCTGTGATTTCACCTAGATTTGGAGAAGGTGAGGGAGGAAAGGCTGTCCTNT
TTGATCCCATACCATGCAGGGGCAAATGGCTGCCAGCATAACAAAATAAGAAGGAAAGAA
AGAAAAGTGGGCCAGGCGCAGTGGCTCACTCCTGTAATCCTAGCACTTTGGGAGGCCGAG
GTGGGCAGATTACTTGAGGTCAGGAGTTCAAAACCAACCTGGCCATCATGGTTGAAACCC
CGCCCCACCAAAAATACAAAAAAATTAGTGGGGCGTGGATGGTGTATGCCCTGTAATCCCA
GTCTACTTTGGGAGGCTGAGGCCAGGGAGAAATCNGCTTTGAACCCAAGTAGGCAGNAGG
GGTNGNCATGTTGAGCACGAGTATCGTTGCCCACTTGCACTCCAACCTGGGCCGACAGNA
GTCAAGTACTCTGGGNNAAANAAAAANATAAACCAGGAAAAAAAAGNGAAGGNAAGGGAA
GGGGGGAAAAGAAA
Sequence 440
GGGGCGGCCGAGGTACGCGGGATGTCTAAAATATCTTGTAAAAAGTGTTAAAATAAACAA
ACCCAGTCAATTAAAAATTTTTGACTGTTATTGAGAAAACTCCAATGAGGGAAATAATAAG
ATCTATAAAGGTCTTAAGAAAAATATAATTTGAAAAAAACATGTGGCTGAGTGTGGTGGC
TCACGCCTATAATCCCAGCACTTTGGGTGGCCTAGGTGGGCAGATTGCTCGAGTCCAGGA
GTTTAAGACCAGCCTGGGCAACATGGCAAAACCCTGTCTCTACAAAAAATTAGCCAGGTG
TGGTGGGACACGCCT
Sequence 441
GCGGTGGCGGCCGAGGTACATTGTAGCTTTGAACTCAGTGTTTAAAAATTCAATCTGGTT
ACACACTCTATCTTCTAGATCCCTTGAGACACTGTCTTCCTTGAANAAGNNCCAGGTGAA
ATGGCATTTCAGCTGTGGAAGGATTTTCTCCAGGGAATTCTTGGTGACCTCACTCATGAC
TGCCCTCTGTGTCTCTGCTGTTCCGAAAAGCTGGTGACCAGGCTGATTTGTTCTTCAGAA
GTCTTCCTGTCTGCCCCCGCGTACTGTTCCTGCAGGTTAAGGCAGGACTGGAACTCCTCC
ACAGCTTGCACATAGTTTTCAGATTCAACACTAACTTCTCCGAGTTTAAGATGTGCCTGG
GCAGCATAAAGCTGTGCTTCTTTTGTTTCTTGCCTTTTAAAAATGATCTTTGCTAAATC
C
AGCATATCCCAGGCAAGCTCTAGGTTCCCAATCTCCTCCTCCTCATTTTCTTGAAGAGAC
TTGGTTTCAAGGACTGAATCATTTGGCAT
T
Sequence 442
TGGCGGCCCGCCCGGGCACGTACTTTTGCTGCTGAGGAATGGGAATCAAAAGAACGTAGT
CTCCTGGTAACCACCTCAGATCTCTATTATTAGGCTAGATGTNGNGCNNGTACTCCCCCA
GCTTCTTGCTCNNNACCCTGCACTGTAAGTTGCCCTTCTATTAGCAGCCAAGGAAAAGGG
AAACATGAGCTTATCCAGAACGGTGGCAGAGTCTCCTTGGCAATCAACCAACGTTGCTAT
GAAATATGCCTCACACTGTATAGCTCATTATAGGACGTCAGGTTTGTTGAAAAAAAGTGN
GGCAAGACATGATTAATGAATCAGAATCCTGTTTCATTGGGTGACTTGGATAAAAGACTT
TTTACTTTTANAAAAAAAAANTGTCAANAAANANGTTCCCTNGGCNCGGCTCTAAGAACT
AGTGGGATCCCCCGGGGCTGCAGGGAAATTCCGNATATTCAAAGCTTATCCGATACCCGG
NNGAACCCTCCGAGGGGGGGGGGCCCCGGGNAN
Sequence 443

Table 1

CCCGCGGTGGCGGCCGAGGTACATGAGAGACACTTTAAGCAGGCTCACAGGAATAGAGTG
AGTGCGGACTCAGATTGTTTAAGCTATCTCTGAACCCATTCCTACTGCGTTTAACTATT
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TATTGGTTTCTAACTACTACCACAGACACGGATACCTCACAGGTTCCATTATTACTCAC
A
GCGTTGTGGTCCGGGTTCATCGCCATCCTGCTCCACGCTGTCATAATCCTCACGCATCCG
CGCTCGGGACCCCTCTTCTATAAGGGACATACACGAGATCACCGAAAACTCCTCCTTTCT
CCCATTGTTCCTATGAGGTGGGTGGGGACTCCAAAACCCGTAGCTCCTGCCCTACTAGGC
CACTCTACCCCATT
Sequence 444
CCACCGCGGTGGCGGCCGAGGTACCCAGCCCCACCCAGGCAAACAGCTCCGACATGTTTC
GTAAGTGAGACAAGCCAGTGCAAGTTTTTTTTTTTTCCTTTNNTTTTGNGCTTACCTTCT
T
GCTTAATGGAATTGTTATGGCTAAGCACATAᴊAAGGCCAAAAAAGGAGTTTTTCAAACCC
AGCAAATCAAGTGCTTGGATTCTGAACTGCCAAAAGAAAACTGCACTTCCCCTCTTAAGT
AAAACCGAAATGAGTTTTCTTAGGTAAATGTATTCATCAAGCCCAGNATATAGAAAATAA
AACCCAGGTTANTGGTGNAGCCGTTTAGGTCACCTGCATCATTTTCCAGGGAAAGATTCA
AACCAAAAATACCAGTNCCCAGNCCAGGACTCACAATGTGTTGGANTAATATTATTATTA
AAAGCAAAAGGAGGCCCCNCCCCCACCAAAGCCCAAGCAGCTGGGNTGGAAAATAATCAA
GGCCTGGTCCCACNCCCGTNGGGTAATGCCCAAATTCCGGGGGGGAAAAATATACCTNCCC
TTTGGNAAAAAAACCTTGGGAAAGAAATTCTTACCCTTNGCCTTGGGGAAAAAAAA
Sequence 445
TCCCCGCGGTGGCGGCCGCCGGGCAGGTACTTTACTAAAATGACTGCATTCTTTGGATTC
CTTCAGTCTATGGTTCAAGTCACTAAAGATTCATTTTTGTTGAGTCCTTATGAGAAACA
G
NAGTATGAATCTTGACGGTTTCTGCCCGTCCTAATGGCAGAGCTCTCTGACTTGGGTGTA
TGCTACCAGGCTGGGTTCAAGTGAGAAGTTCTGGTCAGTCTTCTGTGGGTTGAAGGTTCA
ATATCAATTCTGTTTCAAAGCCTTTGTGATGCTATTTGAATCTTTGCTCGGTATATGCC
A
CCCAGTGGGTCAAGTCTGGGACCTAGGTGGTGAGCTATCCCATAAGTTCATTCTCAAACC
GTCTTTACTGCACTGTTTAGGGTCAGATACNCATTATATATACNACTTTGGGTGAGCT
CA
GGAGTTTATAAGCTTTATGGGCTTTGGTGTTTTGATTTATAAACAGGAGTTTATNGAAC
T
TTATGGGGTTTGCTTCCTCTTTCTGCCCAGGTTCCTTGGG
Sequence 446
GGTGGCGGCCGAGGTACGCGGGGAGACACAACTTCCTGGGCTTAGATATTTCAGAATATC
ACAACTAAACTCTTAAAAATTTCTGAAGGCTGGACACCGTGGCTCACACCTATAATCCCA
GCACTTTGGGAGGCTGAGGCAGGCAGATTGACTGAGCTCAGGAGTTCAAAACCAGCCTGG
GCAACATGGCGTAACCTCGTCTCTACAAAAAATGCAAACATTTGCTGGGCTTGGTGATGT
GTGCCTGCAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTAGAACCCATGAGG
TGTAGGCTGCAGTGAGTCATGTTTGCACCACTGCAGTCCAGCCTGGGTGACAGTGTGTAT
TAGTTTGTTTTCATGCTGCTGATAAAGACATACCTGAAACTGGGAACAGAAAGAGGTCTA
ATTGGNCTTACAG
Sequence 447
CGGCCGAGGTACGTTTTGTGACAGGCAATAAAATTTTAAGAATTCTTAAGTCTAAGGGAC
TTGCTCCTGATCTTCCTGAAGATCTCTACCATTTAATTAAGAAAGCAGTGNGCTGGNCGA
AAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCGTCTGATTCTAATAGNA
GAGCCCGGGCTTCACCNGTTTTGGGCTTCCGATATTAATAAGACCAAGCTGAGTCCTCCC
TCCCAATTGGAAATATGAATCATCTACAGCCTTCTGCCCTGGTCGCATAAAATTATGT
CT

Table 1

GGTGTTCTCAAGGCAATTAATAATGATTGTTTTAACACCAACAANAAAGAAAACTATTA
T
CACNAAAANTAAGGTNCCCTGCCCCGNGGCNGGNCCGCTTNCTANGAACTTAGGTGGGAT
CCNCCCCGGGNCTGCAAGGGAAATTANGNATTATCCAAAGCCTTATTCGAATAACCCGTC
CGAACCCTCANAAGGGGGGNGGCCCCCGGTATACNCCAAGCTTTTTTGGTTCCCCTTTTA
AGTGGAGGGGTTAAANTGGCCGCCGCTTGGGCGTAAAATAAATGGGACNAATAAGCCTGG
TTTTCCCTGNGGNGGANAAATTGGTTNTTCCCGCCTCACCAAATTCCCACCACNAAACAT
TACCGAAGCCCGGGGGAGCCAATAAAAAGTTGGTANAAAGCCCTGGGG
Sequence 448
CGGNGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTGTTAGTGTTTTCTGATGTCTTTT
CTAACAAATCTTTGCCTGCCCAAAAGTCTCAAAAACATTCTCACGTTTCTAGATTTTTA
G
CTTTAGCTTTTGTGTTTGGGACTATGATCCATATTTAGTGAATTTATTTTTGGGGGGGGC
A
GAGTCCATGTTGCCCAAACTGGTCTGGAACCACCACACCCAGCTAATTTTTTGTGAATTGC
GGGTACCAGCACACCGGCGCCGTCCTGGACTGCGCCTTCTACGATCCAACGCATGCCTGG
AGTGGAGGACTAGATCATCAATTGAAAATGCATGATTTGAACACTGATCAAGAAAATCTT
GTTGGGACCCATGATGCCCCTATCAGATGTGTTGAATACTGTCCAGAAGTGAATATGATG
GTCACTGG
Sequence 449
CGGCGGCCGAGGTACAAAAAGCAGGGGCCCAGCCCCAGCTGTTGGCTACATGAGTATTTA
GAGGAAGTAAGGTAGCAGGCAGTCCAGCCCTGATGTGGAGACACATGGGATTTTGGAAAT
CAGCTTCTGGAGGAATGCATGTCACAGGCGGGACTTTTTCANAGAGTGGTGCAGCGCCAG
ACATTTTGCACATAAGGCACCAAACAGCCCAGGACTGCCGAGACTCTGGCCGCCCGAAGG
AGCCTGCTTTGGTACCTGCCCGGGCGGCCGTCGATCTCCTTGTGTTCAAGCAACTTCTTG
CGGTAGTCCTGAAGCGCCTTATCTCTAGGGTCCGCCATGATGAGAACCCCGCGTACCTGC
CCG
Sequence 450
NGGTGGCGGCCGAGGTACTCCCTACGGCACTAGTCTACAGGGGGAAGGACGCTCTGTGCT
GGCAGCGGTGGCTCACATGGCCTGTCTGCACTGTAACCACAGGCTGGGATGTAGCCAGGA
CTTGGTCTCCTTCCCGCGTCAAGAGATAGAAAGACCAGTCCTTGTGAAAGACAAGTCTGA
ATGCTCCACTTTTTCAATTCTCTCTCCATTCTTCAGTAAGTCAACTTCAATGTCGGATG
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TGAGTAAACCTGAATCTTTGGAGTACCTGCCCG
Sequence 451
CGAGCGGCCCGCCCGGGCNGGTACAAATGCGTTTANGAAATGTTAGTATAAGGCTGATCT
GGACCCAAACTAAAACAACGTTAATCCTCTTCAAATCTAATTTAATATAGGGAATAAGAT
TATTGAAAAAAAATTTTTTTCCTGATTTTCTTTTTCCTGAAGGTTTTTTTTGTAGAAACCA
TGGTAAAAAGGGAAAAGAAACCTTTGACTGGCGGGGGCAGGGGGAATACAAAAAAAAAAT
CCCTTGATTTTTAAAATATACTTGAATATCAAACTCAGAAAGAGTTATTTTTGTGAAAGA
GGCAAAATTGGTCTTGAGCTGCTTCAGTCTATGTCTGAAGGTTTTACTGAAATTATGG
TC
CAGTTTTAGGAGAAAAATTCACAGAAAAGTCAGATTGTAGATTTTGAGAAGGAAACTCTG
AGGTGGTGATTTTCTCCAAGGTCATGGTTATGAAGCTCAATGAGGGCCTGAATTGCTTCT
TCCACAGATCCCAATTGAATGAGCGCCATTTTGCGATCTTTCTGAAAGAATTTAAAA
Sequence 452
GGGGCGGCCGCTAATGTNAGAAGTTAAGTNAGAACCTATATTGTACGAGGAACAAAAGCC
AATCAGTGTCCTTTTTTGTCTTTTTTTTACATAAACTTTTACTACAAAAATTNATATATGGA
TTTTGAATTTCCAGTCAAACCAAATTGTAAAACTGTTTCATTTGGTTCTATATTATGTAT

Table 1

ACATAATTTATCTATTATATATTTACATTAAAATATATGCATATATAATGGATTTAATTT
CCTTTNGGNACCCCCATATNTAGAAGNNTCTTCATAANTTAATAAATAATCTAGGGCCAG
CATTATGTTTGCTAGACCTGGNTTTGGCTCAATACTTAAAGTTAAAAGTTTCTGTCTTT
T
TTCTTGGACTTGAAACTGCCTANAGCGTCAGCCTCTCTGTTATTTNTNTCTATTTNCTT
T
TTCCCCCATCAGTCTTTTAGCCACTTGAAGCCAAAATTCTTAGTTTCTGTCCTAGTNGA
T
AAGAGTAAAAGGGGAAGGAG
Sequence 453
ACGGATACCCTGTTCCGCCTTTCTCCCTTCGGGAAAGCCGTGGCGCNTTTCTCATAGGCT
CACGGCTGNAAGGTAATCTCAGNTTCCGGTGTAAGGTTCGTTCGGCTCCAAGNCTGGGCC
TGTTGTGGCACCGAACCCCCCCGGTTTCAAGCNCCGAACCCGGCNTGCGGCCCTTATCCC
GGGTAACCTATACGTCTTTGAGGTCCCAACCCCGG
Sequence 454
NGAAGGCGGACGCCCGGNCAGGTACGCGGGGACCTTTNACGGGCGGGGGGAGCTGAGGCT
CCTGNCGNTATCTNTGATCCTTGCACCCTGGCAGGAAGNTGGTAGGGGGNACTNTAACGG
GAGGNCTNCACATATTGCAGAAAAGAAACCACTTTGGNGNGTAAGACTTGGAAGAAAGTA
ACCGGTCACTTTGGAAAACAGGGGTGGGGAAGAAGCTGCCTCTCTTTTGAACCTNTTCCN
AGGGACCAANTCTAACCCAGGTGAGGNNAACCNTGGTNGATGTAAAGCCGGTGGCTTTGG
AGGACAGAATCATCTAAGTGGGAANAAGATACACTAGGAAGGGNGCTGGGGGGGANTACCA
TCAAGAGGGAGGNGGGGATNACCTTCAGGCCGGGGGCTTNCGGNGGGGGATGAAAGAAGGA
ATGGGNCCGGACAGGTTTGNGGGTNGGAGGGTATGAAGGCTTGGCNAAATGGTGGGGAAT
TTTGGTAACNTTCGGGCCGGGTTTTTAGAANCTNAGGGGGGANTCCCCCGGGGCTTNGGA
AGGGGAAATTTTCGANTAATGCAAGGCTTAATANGAATTACNCGGGGGGACACTTCGGAG
GGGGGGGG
Sequence 455
CCCGCGGTGGCGGCCGCCCGGGCAGGTNCGCGGGGAGGATCTCTGTCTTTTGTTCCCTCA
CCTGTCTGCCTGTCTCCTCTCCTTTCCTGCCTGGGGGGGACTGTCCAGAAGACATCATCGT
CCAGTTCCTCTGCATTTGAACAGCTGTNCCCCCACCCCTCAATACCGTTTAGAGCAGAAG
CCAGCAAATACTAATCGGTCAGGGACACGATAGAAACTATTTTCGGCTTCATGGGCCACA
CAGGNCTTCATTGCAAGCTCCTCAAATNTGCTGTTTGTAGCTAAGGAAAGAANCCATTAT
ACCNTGTGTNAANCAAAAATGAAATATTGGCNTGTGTGCCAATAAAAAACCTTATTNACA
AACATTAATNGAGTNGGGCNTGGATATGACTTCACNANTACTGGTTAGTTTTGACAACCC
CCCTGGNTNCTAGNAGTTAAAAATCCCAAAAACTNCTTATTAGTCCCTCCC
Sequence 456
CGGCCGAGNACAACATGACATTTTTAACCAATCCAATCTAAAAATGTTGCCAGAATCCAC
CTGTGGCCCNGAATCGNGTNTTGGTTCCTCTTTCTACTCCNCTGCAGANGACCAAACCTG
TCCCGCTGCCACTTTCCTCACTGATATTGGGAGGAGGGCAAGGCCCAGCCGAAGTTCCAC
TAAAAATGCCCCAGGAGAATAGGCACCNGGCTGGCTTGCCAAAGGGTTTNGGGTTTTATT
GCTTTCTGTTTTTTCTTTTCCCCGACAGCACAAAGAANGTAAAGGGGCAGTTAATTGGAC
AGAGTGTTATTTTAAAACATCTCTAATTGTAAATGNAATGTGGTTGGTTTGGGTTTCTA
C
TGCAATTGGTGNGAAGCCATGCCGGNGGGGGAAAGAAGAAACNTGACCCCAAGGNTAATTG
AAAATNGGGAGNCCCCCTTTC
Sequence 457
NCGATATTACTGTGCGAGAGGTAAAGGATATAGTGGCTACGATTACNGCCTCTCT
Sequence 458
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGACAAAACTACAGACTTAGTCTGGTGGA
CTGGACTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGA

Table 1

GCAAAATAAAACAAATAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGC
TGAGCACGCTGTGTCAATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAA
GGTTGGGAAAACACCTCATTTGACCTTGCCAGCTGACCTTCAAACCCTGCATTTGAACCG
ACCAACATTAAGTCCAGAGAGTAAACTTGAATGGAATAACCGACATTCCAGAAGTTAATC
ATTTGAATTCTGAACACTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATC
ATCTGGAAACCGATTTTCAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAG
Sequence 459
GGCGGCCGCCGGGCNGGTACGCGGGTCGTGNGCTGGTTAGTGAAGGCTTTGTAGCTGAGC
AGTTTCTAAATAACACAGCCACTCAACTGACATACCATGGATTATGTGAACTAACTTCAA
CGGTTCAGGAAGGAGAACTTTGTGTGTTCTTTCGGAATAATCATTTTAGCACCATGACCA
AATACAAGGGTCAACTGTATTTGTTGGTAACGGACCAGGGGTTTCTTACTGAAGAGAAAG
TTGTTTGGGAAAGCCTACACAACGTAGATGGTGATGGAAATTTCTGTGACTCAGAATTTC
ATCTTCGACCTCCTTCAGATCCTGAAACTGTATACAAAGGACAACAAGATCAGATAGATC
AGGATTATCTTATGGCATTATCTCTACAACAAGAACAGCAGAGCCAAGAGATCAATTGGG
AACAAATCCCGGAAGGAATCAAGTGATTTGGAACTAGCAAAGAAACT
Sequence 460
GGCGGCCGGGTACGAATGTGCAAATTAAAGCATGGTAAACTGATATTTACATAAATATCA
AACCAACAATTAGTTTATACATTGTCAATGACCTTCTAAGATATGTCATGAGTGGATCC
A
AGAATATCTTTCCCCCAATGGAGAAGGTATTCAGAGGCTAAATTCCGACACTTTAAAATG
ACACACATCATAGGCTTTACCTGTTTGACCACTGCCTCAAATGTGTGAGATGTGATTT
TA
TGATCCCGCGTACCTGCCCGGGCGGCCGCTCGAATAGACTTCAGGGAAACAACACGTCCT
GAAAGAAACATGATTCCCCTCAAGCCACAAAGGATTTTCTCATCAAGTGTTTTCACCTCT
GCATTAGATTTGGACACAAGAAGAGGAGAGCATTTACTCAGGTAAAAATAGTTCTCTTAG
TCTCTTCCTCTAGTTACTAATTTTTTAATTTAAAAATACAATTAACTGATCTAGCTGATAA
AAGTCACAAGACAGAAATAAGCTAAGTTCTCTCTTNCTTTAGGGAACGCTGGTGGCAATT
CACCA
Sequence 461
GAGTTTGAGAAAGCTGCAGAGGAGGTTAGGCACCTTAAGACCAAGCCATCGGATGAGGAG
ATGCTGTTCATCTATGGCCACTACAAACAAGCTACTGNGGGCGACNATAAAAACAAGAAC
GGCCCCGGGGGATGTTGGACNTCACGGGGCAANGGCCAAGANTTGGANGCCTGGGAANGAG
CTGAAAGGGACTTCCAAGGAAAGNANGCCATGGAAAAGGCTNTACATCAACCAAAGTATG
NAAGAAGCCTAAAAGAAAAAAAATACNGGGANTAATGAGAGCACNTGGATTTTGGGNTAC
NTGTGCCCCATGTGTTTTATTCCTAAACTGGAGNACAATTGCCTNGNNTTTTTTTCTAAN
N
ACCCGNTGGAATGGTTGGGGAAATCTCTGGGGAAAAATAANCCAGNTAAAACCAGCTACC
TCAAGGGCNTGCTCACCCATACCG
Sequence 462
AGCCCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATATTGTTCCTGATTTGCCTGATGTG
TGGACGGATCACCAAGCGAGTGACACGAGAGCTCAAGGACAGGCTACAATACAGGTCAGA
GACAATGGCTTATAAAGGTTTAGTGTGGTCTCAGGATGTGACAGGCAGTCCAGCCTGACC
TTTCTGCACACTCCAGACAAACTTCCCAGACAAGCTCCTTTGTGCCTCTACGTGGAGAGG
GCGTGGAAAGTTATCACATTAAAAGATGGAGGATTTAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAGTACCTGCCCG
Sequence 463
GCGATNCCCCCTGGGAAGCTCCCTCGTGCGCTCNTCCTGNNCCGACCCTGCCGCTTACCC
GGATACCTGTCCGCCTATTCTCCCTTCGGGAAAGCCGTGGGCGCTTTCTTCATAAGCCTC
ACCGCTGTAGGNATCCTCAAGNTCGGGTGTAAGGNNCGTTCGCTCCAAGGCNGGGGCTGG
NGGNGCACNGAACCCCCCCGNNCAAGACCCGACCCGGTGGCGCCTTAAACCCGGAAAACT

Table 1

AATNCGNCNTGGAGGTCCCAAACCCCGGGGNAGGACACCGACTTATCCGGCCACCTGGGC
AGGCAGCCAACTGGGGTAAACAAGGGATTAAGCAG

Sequence 464

CCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTT
T
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAACNGCNGCCNCCNCCATGAAAGAGGG
GCCNCCACATNTTTATTGCATACNCAGGGGAATAACTTATTNTACAANGAACNCTCCTCC
ATTNGGAGACCATGCCCACTTACAGAATGCANCCGNAAATGCGGTAAATNTATTTACAGA
GGNTGGGGNGCAAGATGAGANAAGTTTCANCCCCAGGAATTTGAAGNGAGAATGATCTAC
AAATTNTCCTGACAAGGNGCAACCGGGCTTGNGCTAGNGNGGNCTGAAANAATTCCTGGC
AAANCGTAGGGGGAGATTAAATCTCGGAATTGACAGCAAGTTTGGGGACAGNGCAAAAAN
AGAGGGGTGACCCTGTGAAATTTGGTGCCTGGGGGAACTTCTTGANGCCCCAATGNGGGG
GCACCNCTTNGAGANGATNGGGNTAAATTTANGGGGGGATNTTTTAACCCCTNTCCNNCC
CCAACCAAAAAAGGG

Sequence 465

GGCGGCCGAACGCAGAGAAGGTNGANGATTGCACCATGCCGATTCGTCGAACTGTGAATT
CTACCCGGGAAACTCCTCCCAAAAGCAAGCTTGCTGAAGGGGAGGAAGAAAAGCCAGAAC
CAGACATAAGTTCAGAGGAATCTGTCTCCACTGTAGAAGAACAAGAGAATGAAACTCCAC
CTGCTACTTCNAGTGAGGCAGAGCAGCCAAAGGGGGAACCTGAGAATGAAGAGAAGGAAG
AAAATAAGTCTTCTGAGGAAACCAAAAAGGATGAGAAAGATCAGTCTAAAGGAANAAAAN
TTTTATNNNATTAAAAGTACCTCGGCCCGCTCTAGAACTAGTGGGATCCCCCGGGCT

Sequence 466

TGGCGGCCCGAGGTACGCGGGGAGGTCGGTGCGCGCTTCTCCCGAGGTGGAACGGGCGGC
AGTCAAGCGCCGGCGTTCTCTGCCGTCACCCTTTCCTTGC

Sequence 467

GCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAG
AG
TCTTGCTCCATCACCCATGCTAGAGTGCAGTGGAGTGATCTCGGCTCACTGCAACTTCCG
CCTTCTGGGTTCAAGCTATTCTCCTGCCTCAGCCTTCCAAGTAACTGGGATTACAGGCAC
ATGCCACCACGCCCAACTAATTTTGTATTTTTTAATANAGACAGGGTTTGACCATGTTAG
C
CAGGCTGGTCTTGAACTTCCATCAGGNGATCTGCCCTCCTCAGCCTCCCAAGTGCTGAGA
TTACAGGCATGAGCCACCGCGCCTGGCTGATTGNGTTCCTTTCTCACAGATTTTGTTT
CT
GTTTTTGTTTTCCTGAACACTCAGCTGGACTGCATTTCCCAGCTTCCCTTGCAGTTAA
GT
CACAAGTAGCGCTGTGACTGGGTTCTGCCCGGTAGGAAGGTAAGCAGAAGTGAATGTGTA
TCACTTCTAATGGTGTGGGNCTCCCNAAACCTTCTAAAGGGGTATGTTCCCCCTTTTTT
TT
T

Sequence 468

TTGGAGCTCCCCGCGGTGGCGNTCGGTGTGCTGNGCTCAGCTGCCTTCCNANGGAGGANC
NGATCGGCNAGTGCTCTGACTGCGTGGCCGACAANNGCTGNCGNAGAAAGAAATNAAANC
CCTGAAACATGACAGNGAGTGNTGNAAAGTGTGGAAATGCCTTCTTAAAGTTNATNAANG
TNAANTCAAANNACATTTTTTTTTTTCAAAAAANATAAATTTAGAACTAANTGNACCTT

Sequence 469

CGGAGGAGAATGGTATCACTCAGGCTCTCAGAGTGACACTGAAGCAAGACACTCATGGGG
TAGGACATGACCCTGCCAAGGAGTTCACAAACCACTGGTGGAATGAGCTCTTCAACAAGA
CTGCGGCCAACTTGGTAGTGGAAACTGGGCAGGATGGAGTACCTTCAGGATTGGCCTGTT
ATCTTCTTTAGAACTAAGTTCATCTTAAAAATTTAAGAAGGTGGACATTTCAACACCAT
C

Table 1

AAGTGCATTTAGGTGACATGTTTAAGTTAACTTGACTTCCTTGAATGACCTAGTTAGTA
A
ACTAGTCACTAGTAATTCGGTCACCAAGCAAATCAAGCCTGCAAGAAAGGAAGCCAATAT
TCAAAATGCCATGTTACCATCTAAACC
Sequence 470
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGATTTTATTGTCTACCTCTCTGGACTTG
CTCCCAGCATCCGGACCAAAACCATCAGTGCCACAGCCACGACAGAAGCCGAACCGGAAG
TTGACAACCTTCTGGTTTCAGATGCCACCCCAGACGGTTTCCAGTCTGTCCTGGACAGCT
GATGAAGGGGTCTTCGACAATTTTGTTCTCAAAATCAGAGATACCAAAAAGCAGTCTGAG
CCACTGGAAATAACCCTACTTGCCCCCGAACGTACCTGCCCG
Sequence 471
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGGGAAGA
CA
CAAAGATTCAGACCACAGCCTACAGGGAGAGAGGATTTCTGAGGATGGTGGTGCACTGTG
AGTCCACGCAGGCCTCCTGGGCATAGGATGGAGCAATTCTATCTCACCTCAGGCCTAGCA
CAAAGGGCTTCAGTAAACCACTGGAGTTTCCTTCATTAGGATTCCATCCCAGGATATCCA
GAGGACAAGAGGCTGGCCAACTGCAGGATTAGCCTATGCTCCCGTGCTGGATATAGGCTA
CACGCAAGAGAAAGCTTGGGTGGGATCTCCTGATCCCGCGTACCTGCCC
G
Sequence 472
GCCGGGCAGGTACTATGGGTGTAGTGNTACTATTACAGTTAATNCNTCCTTTGTAGTGCG
CTGNTAAATGCAGTGAGGATTGGAGCACTGTCCACTGAGTCTCTGTGC
Sequence 473
CAAAATAATTATAATGTATTAACTCATACTGCCTGTCTTTTATAGGGGAAAAAAATAAC
C
TNTTTTATTTTAAAGTTATAAGGGGGNTTACCTTNTAGNGTGCTTGGATGACAGGGAA
AT
TAGCCTACCCCATTTTGGTCTGGAACAGAAGACTTTCAAATTTAATATGGNCCAAGTGTC
TTNACTANTTAAGGCAAGATCATGCTTNTGTCAGTTNACCCCANTGNTTGGAATACCGTG
NACACCGATCGTGGCTCGNCTACAGCCTCCATGTNCCCAGGCTTCGAGCAGGT
Sequence 474
GGCGGCCGCCCGGGCAGGTACGCGGGGGAGCTGAGCCGGTGGGTGAAGCGGCGGCCACGG
CATCCTGTGCTGTGGGGGCTACGAGGAAAGATCTAATTATCATGGACCTGCGACAGTTTC
TTATGTGCCTGTCCCTGTGCACAGCCTTTGCCTTGAGCAAACCCACAGAAAAGAAGGACC
GTGTACTTCTAAAATTGCACTTTATGTTTTGTAGGCTTGGAGCTTCTTGATTATGGGTT
T
TTTCGTTACAAAATTCAACAACAGAATCAATACTTTGCATAAACATTATGGATGCTTTTT
CTGTTTGTACCTCGGCCGCTCTAAAACTAAGTGGATCCCCCNGGCTTGCAGGAATTTCGA
TATTAAAGCNTTATCGATACCGGCGAACTCGAAGGGGGGGGGNCCCGGGACCCANCTTTT
GGT
Sequence 475
TTGANGCCCTCCCCGCGGTGGCGACAGGGTTACATTGGTAAGGGTGACAGTTAGAAGGGG
AAGTCCTTTTAGTGAAATAGATGAGAGGTTTTAGATCTGCACAAACCTTTTTCATGGAAG
TCCAACTTTGCTCCTGGGTAGTTTAAAGGACGTAGTCCCATGTACCT
Sequence 476
NGGCTACACGCTAGGAACCTTGCAGCTTACAGTGACAGAGCTCCCATTCACGAGGCCACC
ACTCATCTCGATTTCTGGATCTCTAGGGAATGAGTAGAGCTCCACCTGGATTCCCTTT
TC
CAGTTTCTTATGTCCACAAGTCACTGTGCACAGATAAGAGTGTTCGTTCTCAAAACTCAC
AGGGCTCAGGGTCATGCGTGGAAATTGGGTCCCCTTCACTCCTCACCTTTCCCCGCTTCA
GAGGGCTGTCTATCTGGGTTCTCCAGGGAGAAAGATGGGGAATTCACAGCCCATGGACAC

85

Table 1

TACCATGTCAACAATGACTGAAGTCTTCCAATCTGAGCCAGGCAAATTCCNGGNGGGTCC
AGGGGGGGAGAATCTCAAACAGNTAAAATGGGTTTTCTCTTGGAACAAATTAAATTTCCCA
CCTCTTTTTTNTTGNTTTTTTCCCC
Sequence 477
NGGNGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCAAAA
A
TATTTATTAAAATGATTTTTTTAAGTTTGAACTTTATTGGAAGGAGTCCCTCTAATTCAC
ACTTTCATCCTAGATAAATGGGTAAGAACCACATATGGAATATAAAGCATTGATTTTTT
A
AAAACCACATAGTAGCACAGTTGAAAGAAATGCAATTCTCCAGGGTCTTAGAGAATTCAA
AGGNGGCATCTTAGGGNGGGTCCTAAGGAAACCCAAATTACCAGGTCTCATGGGTTTTCC
TTTTGGGTTCAAGGATTAGAAAGGAGTCAGNGGTTACCCACCTACCCTGGTTTTTTAGGA
GGGGTAGGAATATTGAAACCTTTCCTACTTAGTCCANCAGGTTTTACCTGGTTCAAGGGT
GGGNCCCCCAACCAAGGTTCTTTTTTTATCTTTCAAGCCCCCATTCTTTGGCCCTCTT
AA
GNGGGGGGTGG
Sequence 478
TCCCCGCGGTGGCGGCCGAGGTACCTGCATCAGGGATAAGAACCCATTCCCCTCCCTTGT
TCCGGTGTGCTCTCGCCATTGCACCATCCATGAGACGCACTCTTGTATAGAAGTAAAATT
GCCTTGCTGAGAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCG
Sequence 479
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGGTGTGGCCTGCATCTCAGCTGGCCGCCA
TCAGNGTAAATAGAGCTTAAAGTCATGGTTTGGCTGCATAAAAATTTTCTAACTTGGGT
T
NAATATTTGTAGNTGAAGTATCTGCTTTCATTTTTTTTCACGTTATAAATAAAAATACTAT
GCTGGNCGGGCGCGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAATGTGGGT
GGATCATGAGGTNAGGAGTTCAAGACCAGCCTAGCCAAGATGGTGAAACCCCGTCTCTAG
TAAAGATAAACAAAAAATTAGCTGGGC
Sequence 480
GCGGTGGCGGCCGCCCGGNCAGGTACAGATGCAAACGGAGGTGTAGACTGNGCAGCTGCC
AAAGTGGTGACAAGCAATCCAGAGGACCATGAAAGGATCTTAATGCAAGTCATGAACTTG
AATGTGCCGATGAGGCCTGGCATTCTTGTCCAGAGACAGAGTAAGGAAGTGTTGGCCACA
CCCTTAGAAAACAGAAGGGACATGGAGGCAGAAAAAAAAAAAAAAAAAAAAAAAACGTAC
CTN
Sequence 481
ATGTTTTGTGGCCAAGGTGAGGGCTGCAAGTGTTTTCTAAGGGTTGAAACATCANAATAA
AGGTATGGTGGCAAGTCCTCCTTCTGCTAGGCTGGCTGGCAAGGCCCTATGTCTTGACCT
AGGTGGTAGTTACAAGGGTATTTTATTTTGCCTTATAATAATTCACTAAACTATGTTATT
TGAGTNAGATTTTTATGTNGTGNGNCNTTTTAATTTACACAAAATTAAANCAAAAAGNA
A
CNAAANGTTGCNCTCNGNCTCGGNTTNTAAGTAAACCTAAGGTGGGA
Sequence 482
CTGAGAGATCCCCTCATAATTTCCCCAAAGCGTAACCATGTGTGAATAAATTTTGAGCTA
GTAGGGTTGCAGCCACGAGTAAGTCTTCCCTTGTTATTGTGTAGCCAGAATGCCGCAAAA
CTTCCATGCCTAAGCGAACTGTTGAGAGTACGTTTCGATTTCTGACTGTGTTAGCCTGGA
AGTGCTTGTCCCAACCTTGTTTCTGAGCATGAACGCCCGCAAGCCAACATGTTAGTTGAA
GCATCAGGGCGATTAGCAGCATGATATCAAAACGCTCTGAGCTGCTCGTTCGGCTATGGC
GTAGGCCTAGTCCGTAGGCAGGGACTTTTCAAGTCTCGGAAGGTTTCTTCAATCTGCATT
CGCTTCGAA
Sequence 483

Table I

GCGGTGGCGGCCGAGGTACTCTTCAAAATTGTCAAGGTCATGAAAGACAGCAAAAAGTGA
AGAATTCTTACAAACTAGAGGAGACAAAGATTGGAGAAGAAACAATGACTGGCNGGGCAC
GGTGGCTCATGCCTGTAATCCACTTTGGGAGCACTTTGGGAGGCCGAAGAGGACAGATCA
TCTTAGGTTGGGAGTTGGAGACGAGCCTGACCAACGTGGAGAAACCCCATCCCTACTAAA
AATACAGAATTAGCTGGGTGTGGTGGTGCATGCCTATAATCCCAGCTACTTGGAAGGCCT
CGGCAGGAGAATCACTTGAACCCGGGAGGCANAAGGNTTGTGGTGAGCCAAAATTGCGCC
ATTGCACTCCAGCCTGGGCAACAAGAAGCCGAAATTTCTGTCTCAAANAATAAANAACAA
AAAAAATAAGTACCTGCCCGGACCGGCCCGCTTCTANAACTAGTGGGATCCCCCCGGGCC
TGCAGGGAATTTCGATATTCAAGCTTATCGGATTCCGTNCGACCTTCGANGGGGGGGGGCC
CGGNTCCCCAAGCTTTTTGGTTC
Sequence 484
GATGTGAACAAATGTGTCATTGCTCTCCAAGAGAAAGGATGTGGATGGCCTGGACCGCAC
AGCTGGNGCAATTCGAGGCCGGGCAGCCCGGGTCATTCACGTAGTCACCTCAGAGATGGA
CATCGAGCGGCCGCCCGGGCAGGTCACAAGCTTTATTGGGCAACAGCAACGAGCCACGCT
GGCAAACAATGAAAGTAGAGTCGCTCAGAAACACGAAAGATCATATGTGTGTCATCACAG
CATCGAGAATTTAAATCATCTGGAAGTTCCTGCTAAATTAAAGCATACTGTGCCNNAGCT
CCCCTCTAATCAAAAAACGCTTGTCCTGGNGAAAAATTTGCATGNGGGNTTACAGAGAGA
GAGATCAACCAGGTGAGGAAATCACAAGACTCTTACATGAGTTTACAGTTAACCCCCCTG
CACCAAAAAAATAAATTAGCCATAATTTGGTT
Sequence 485
TCCCGNGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGAGGATACT
T
TCATTTTTATTTTATATCGTGAGGTATTGTTTGGATTGTTACAATGAACTTGCATTTCTT
TTGTAATGAAGAAAATAATACAGAGGAAATAACAACAACTAAACCTTTGGCCTGGGATTA
TCATCCGGGCTGGGAAATTCATGTTGGGATGGCAAGGTTTTTATTGATAACAAGGTTATT
TTTTGGGGTTTATTATTGCAAAAAAAAAAATTGTTCATTGGGAATTGCCCTCCTATTTGG
G
CTTGGGCACCTTGCCCTAAGGGCCACTTTTCACCAAGGGTATTTTCATCCCTTAAATCCC
TCACCAAACCAGGCCCTATTGGAAGGGGTAAATCAATTGGGGTCCCCAAGGTTTTACCAA
GGAAAGCCCTTTTGGGGGGGNGGGGGGGAAGAATTATTTGGGCTTTGGGATTATTACTTTCT
AATTTTGGCCCACCACCATTTTTTTTTTGGTTGGGGCAAAGGACCGGTTTCCGGTAATCCGG
GCTTGGGTGGATTTCACCTTGGGTCAAAAGGAAGCTTCTCATTGGGGCCAAGGGAGGTTT
CCCTAATTTGGTTGGCTTGGNAAAGGGAATTTCAAAATAATTCAAAAAATACTTAAGAAA
TTTTTTNCCCCCCA
Sequence 486
TGGCGGCCGCCCGGGCAGGTACGCGGGAGTGTGGATNGAACAGAAAATTGGAAATCATAG
TCAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACTTGACTGGGGTTTTTTCT
G
CTTAAAAAATTTCAATTCTCGTGGTAACAACCGCAGAGTAGAAGGAGAGGGTGACTTTACC
GAACTGACAGCCATTGGGGAGGCAGATGCNGGTGTGGAGGTGTGGGCTGAAGGTAGNNGA
CTGTTTGATTTTAAAAAGTGTGACTGTCAAGNTTGTATCTGTTGCTTTTNTCAATGATT
C
AANGNGATACAAAATGGGGCTTCTNTCANTCATTTAAAAAGGAAAAACGCCGACCATCCT
TTCTAAGGATTCTCTGTGGGAAAAATGGACTGTCAATTAAAATGGCGGGGTTTT
Sequence 487
CCCCAGGGTTCAGTCCTCAAGGGGCCATCCTGTCCCACCATGCAGTGCCCCTAGCTTAGA
GNCTCCCTCAATTCCCCCTGGCCACCACCCCCCACTCTGTGCCTGACCTTGAGGAGTCTT
TGTGTGCATTGCTGTGAANTAGCTCACTTGGTGATATGTCCTATATTGGCTAAATTGA
AA
CCTGGAATTGTGGGGGCAATCTATTAATAAGCTGCCTTAAAGTTCAGTAACTTACCCTTA

Table 1

GGGAGGGCCTGGGGGGAAAAGGGTTAGAATTTTGTATTCAGGGGTTTTTTTGGTGTACCC
TGCCCGGGGCCGGCCCGCTCTAAGAACTAGTGGGATCNCCCNCGGGCTGCAGGGAATTCG
ATNTCNAAGGCTTAATCGATACCCGTTCCGACCTCGAAGGGGGGGGGGCCCGGTACCCCAA
NCTTTTTGGTTCCCCTTTTAAGTGGAGGGGTTA
Sequence 488
CNCGNGGTGGCGGCCGAGGNACTTTGTTTTTTTTTTNTTTTTTTTTGAGGGTGGCTTTAT
TT
TCAATATTTGTCTTATTAATATTTTTCTTATTTTATAATGCAATTACAACNGNTTTAGGA
GACAAAACAATATAAACAAAAGAATGTTAAATAGGTTTTTTTTAAAAAATAAGCTTGGTT
GGCTTTGCAANGGAAAGTCCATAATAANTCTTATTCCCCCCCAAATATTAAGTTTTATT
A
CTTTNGCCACNTAGAGACCCAAAAAATAGCTTATTGGGGAAAAAAATTANGTTATTTAAA
AATANGCCTTAAAAACCACCAAGGAAAAACCCTTACCAGGGCNTATTAAAAATTAAACCA
ATTAAAAAATTACCAAGGGTTTAAAACTTTTTAAATGGGNGGGATNGGCCTTTAAAAACC
AAA
Sequence 489
NGCCGACCGAAACCTGGTGAAGCCCTTTGGGCGATTGGTGATCACCCCTAGATCCGTGAA
AGCTGGCTGCCCCCCCATCCGGGCAAGCAGGGCCAAGGTGGCATCTTNACATTCCTGGAA
CCCACCCAGTAACAGCAGCAGGTATTTCTTCTGGGTAAATGAAGAGCCTTTCGAAAAAAC
TTTCTTGCCCTCAAAGTATTTACCATAAATTCTCTTTAAAAGTGGACATGGTTCAAGAA
T
CAAGNGGGCTCAAGAAGTTTNGAAAGTAAAAGNAGGTCATTTTCCTTAAGTTTCAAGCTT
TTCAAGTTTTGNTATAACTTTTCAAGCCCTCTGGCCCCTTTTTCAAAAAGAATTTTCTT
G
GGAGGAGGTCCAAATTTTTTTTTCTTTTNGTTTNCCAATACNTTTCTTTTTTT
Sequence 490
NCCGCGGTGGCGGCCGAGGTACCTGATTTTTATTTCNAGTTTTCATCCGAATCCACTGGGG
AATGGGACGATTTTGCTTTTGTTTCTTGGCCAGGAATCGCTTAATCCTGAAAGTCTTG
TG
AGAAGACATGGCGAGCAGCGGAGTCAAGAACACACCACGATGGCGGAGAAAGGAAGAGGA
GGCCCCGCGTCCTGCCCG
Sequence 491
ACTCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAAAAATAAAAAGGAGGCTGGTGGGAG
AACTGCTTGAGCCCCAGAGTTTGAGGTTACAGTGAGCTATGATCACATCACTGCATCCCA
GGCCTGGGCGATGGAGCGAAACTGTCTCTTAAAAAATGGCAGGGAGTTGGGGAGCTGGGC
AGGTGCAGTGGCTCATGTCTGTAATCCAATACCTCTGGGAGGCCCAGATGGGAGGGATC
ACTTTGAGCCCCAGGAGTTTGAGACCNGCCCTGGGTTACACAGGGAGACCCCCGCTNAAA
ATTTTTAAAAAANTAGTCATTNCTTAGTGGGTGCNTTCCCTGTNGTNCCCCACTTCTTT
G
GANGGTTTNNGGNCCAAGGATTTCTTTTNGCCCCTGGANGGACAAAGGCTTTCANTGAGC
CTTTTTNATTTTTACCCCTTGGCTTTTAAACCTTGGGCCATATNAATTAGAANCCCTTN
T
CTTTTAAAAAAAAAAAAAAAAANGGGGGGGNGGGGCNCNCCCCCTNTTTTTTTTTTTTGGCCCA
ANCNCCCCNNATTTTTTTTTTT
N
Sequence 492
TCCCGCGGTGGCGGCCGAGGTACATGAGAGATAATGTTATGACAAGAATAGTTTCTGCAA
CATTAAGTATGGGTCAAAAAAAGAAGAAATGGGCCAGGCGCGGTGGCTCATCCCTTTGGG
AGGCTGAGGCAGGTGTATCACAAGGTCAGGAGTTCGAGACCAGCCTGACCAATATGGTGA
AAACCCATCTCTACTAAAAAAAACACAAAACTTAGCCAGGCATGGTGGTGCACGCCTGTA
ATCCCAGATACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTG

Table 1

CAGTGAGCCCGAGATCACGCCACTGCATTCCAGCCTGGGCAACAGAGCAAGACTCCATCT
CCCAAAAAACAAAGAAATGACTTTAGACAAATGGCTTGAATGAAATTACAAAGAGGAGGT
GCATTAAAAAATCCCAGCAGTAAAANCTTTTGAAGAATTAAAATGACAGGCTAAAAATAA
ATAATAAATGTTCTTTTT
Sequence 493
CCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGTGGCGGCGTTGGGTTGAGCGGGCT
TTTTGGAAGTTTGTGGCGGAGTTCTGTGATATGAGCAACAATGGACCAGAAGATTTTATC
TCTAGCAGCAGAAAAAACAGCAGACAAACTGCAAGAATTTCTTGGGCAGGGCCTGGGGAA
TGCTTTTTTATCTCATATTAGTGCCTGTGATGGCATCTTTCATCTAACACGTGCTTTTG
A
AGATGATGATATCACGCACGTTGAAGGAAGTGTAGATCCTATTCGAGATATAGAAATAAT
ACATGAAGAGCTTCAGCTTAAAGATGAGGAAATGATTGGGCCCATTATAGATAANCTAGA
AAAGGTGNCTGTGAGAGGAGGAGATAAAAAACTAA
Sequence 494
CGCGGTGGCGGCCGAGGTACTCATGGTTGCTGTAAATTAAGGCAGCCGTTCTGCAGGGTT
TTGCTTAGCCAGGCTCCTCTGAGATCTGGCTATTCTGTCTTGTGGATTTTCAGTCCCC
GC
GTACCTGCCCGGGCGGTTCG
Sequence 495
AGATCTCAAGATCTGGACTTCTGTTGAAAAATTTTCCCGTGAGGNTNACTTATGTCTG
TA
AAGATGGGAAAAAAATACAAGAACATTGTTCTACTAAAAGGATTAGAGGTCATCAATGAT
TATCATTTTAGAATGGTTAAGTCCTTACTGAGCAACGATTTAAAACTTAATTTAAAAATG
AGAGAAGAGTATGACAAAATTCAGATTGCTGNCTTGATGGAAGAAAAGTTCCGAGGTGAT
NCTGNTTTGGGCCAANCTAATAAAAAATTTTCGAAGAATNNCCCCCCNCTNGNAANCNCC
CNGNCTTGAAANCNTTTTAAAAAAAAAAAGAAAANGGTTTAAAANNGTAAAAGGGGNCCCC
CNCCCTTTTTTTAAAAAAAAGNNGAAAAAAAGGGGNGGGGGGG
T
Sequence 496
CGCGGTGGCGGGCCGGCCGGGCAGGTACCGTGAAAAGGGCACTTCTCCTTGAGAAGGCCT
GACAGTGTCGTTAATGTCCTGCTGGCGCATGGTGAAAATTTCAGGGCAACAGTAAAGCAC
CCTCTTTAATTTCCCTTCTCCAAGCCCAAGCTTTTGCAGGTAACTGGAGCGCTTCCTC
AT
TTGCATAATAGGCAGTTTCAATAACTGGGGAC
Sequence 497
CCGCGGGTGGGGCCGGCCGAGGGTACNNNGGAGGCCTCATAANGGCNGGGNATCNTCGAG
GNTGGTATNGNACTGNTNANAAAGCCNNCATGGTGGTANCNCACCAAAANCTCACAAGAA
CAATTGNNGCNGCGAAACAGGCAACAGANTCTGNCATTATATAATAAGGGCGTGGTACGG
TTGGGGAACCCCGNANGANTCNNTATGGTCCTTGNTTNGCAAGCNNTGCATTTTAAATCA
GACGACCGTNAATTTGTTANCCCCAANCCTTNTTANAATAAATCGGCAATCGCGCAATAT
CTCATCATTNANCNACTGTGGACGACTTGACAATCTTAGTGGCTTNATGGACTTATTGCA
AAACTCGAGAAAGAACAAACCTAGGGGTGCGCCCTGACCTTCGGAATAATTCGTAAGCTA
TATGTGAGAAACTAGCAACAGGGCGTTTCATTTATGNGNAANGGGACGCGAANTGGANGA
TAATTATGTAANAAGNGGGCCCCTACGANTTTGGCCCCTAGACGCCCAGGGAAACCGCGG
GGCNCCATGCATNACNCANACTTANGGNAGGGGTANTTCTCCNCACACNCNTCNTTTTCG
ATTTGGANAATANGCTGGGAATNAATCCTACATGACCTGTCATTTTCGGAGTTATCGCNG
GCCGGTACNGNNCCCCCCGGGGGGGGGGGGGGGGNCCCCCGGGGNTTANCCCCCCAAGCT
TTTTTTTGGTTTCCCCCTTTTTNAGGTTGGAAGGGGGGGGTTTNAAATTTTGNCCGGCC
GC
CTTTTGGGGCCCGGTTAAAAT

Table 1

Sequence 498
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGGGCCTTCCACTTCAGCTGACT
GAATTTAGGCAGTTCTGGCCACTTCAGTTTCCGCACCCAGGCCTCCTGACCCATGGTATC
TACGATGAGATCC
Sequence 499
GTGGCGGCCGAGGTACCTCAATTGATGATTTCTGGTATGACCTAGCAAATACACTGCTTT
CACTGAAATTTCAGTCTTGCAATCTGCTTTGGGTTCCCCAATCTAAGACAGAAACATACT
CATTTTCCCATCACTGGACTTCCAGGTTGTTTTCAATTTTTCACTGTTACAAACAAGGT
G
GCAACATTTATCTACAAACCTCTTGGATATTACACCGTAGGNAAGCTTTCTGGGTTATT
T
CCACCTAGTGAAACCTTGCTCAAGTTTGAAGGGGGTANTGTTGGGATNCTTTCATCTT
TT
TAATTAAAATTATTTACCAACCATGTTGAAAAAGCCCCGACCAATGGTCAAGGGACTGNG
CAAAGGAGGTGCCCACCAATGTTGAATGGGGGNTGGTGGGAAATGGGCAANGCTTCACTG
NTANACAAGGGTGGCTTGGGGGGGACCTCAAGTTTTGGGGGGTTCTTTGGGAGNAAAGCCAC
TTTAGNTTTATTAGCCAAGGAANTGTTCTTCATAAAAATTGGGTNTTCTTGGATTTAGG
A
AGACCAANGAAGTTAGGTTNGGGGGGAAAT
Sequence 500
CGAGCCGGGGAGCCATTNANAGTTGTTAAAAGCCTNGGGGGTGCCCTAAATGAGTGAGCCT
AACCTCACATTTAATTTGCCGTTTGCGCCTCAACTTGCGCCCGCTTTTCCAGNTCGGGGA
AAAACCTTGTCCNTTGCNCAGCTTGCATTAAATGGAATCGGNCCCAACNGCCGCCGGGGG
GAGGAGNGCTGGATTTTGCCGTTATTTGGGGCGGCTTNTTTCCCGGCTNTCCTTCCGCTT
CAACTTGNACTT
Sequence 501
ACATACTAGCNNGGGTAGCATAAAAGNTGTTAAAGCCTGGGGGTGCCTAATGAGTGGAGC
TTAAACTTCACAATTAAATTGCCGNTTGCTGCTCCACCTGCACCTGCTTTNCCAAGAT
CT
GGGGANAACACNTGNCGTGCCCAGGCCTGNNATTAAATGCAATTCNANNNCAACCGCCGC
NGGTGGGAGNAGGGACGGTNATTGCCGTTAATATGGGGGGCCGCTACTTTTTCCCGC
Sequence 502
NACAAACATTACGAGCCGGGTAGTCATAANAGCTGTAAAGCCTGGGGGTGCCNTAATGAG
Sequence 503
GCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTATGAATTATTTATTTTCTT
TCTCAGAAAAGGATGCGCCTCCACTTAGCAAGGCTGGGCAGGATGTGGNTTNTGNATCTG
CCCACAGACGGGGTGGTTCTAGACGGCCGCTCTNNAAC
Sequence 504
ACATACTTANCCCGGNAGCATTAAAGTGTAAAGCTCTGGGNNTGCCTAATGAGGTGAGCT
AACTCACATTAATTTGCGTTGCTGCTCACTGCCCCGCTTTCCAGTCGGGAAAACNCTTGG
TCNGTGCCCANGCATGCATNTAAATGNANATCGGCCCAA
Sequence 505
CACAACATACGAGCCCGGGAGCATAAAGTGTATAAGCNCTGGGGTGCCTAAN
Sequence 506
CGGTGGCGGCCGCCCGGGCAGGTACTCGTCTTGGTGAGAGCGTGAGCTGCTGAGATTTGG
GAGTCTGCGCTAGGCCCGCTTGGAGTTCTGAGCCGATGGAAGAGTTCACTCATGTTTGCA
CCCGCGGTTGATGCGTGCTTTTCGCAAGAACAAGACTTTCGGCTATGGAAGTCCCCATGT
TGATGGATCCTGAGGCTTGAAAAAAAAACTGAAAGAGAATAAAAATATCTTTAGAGTTCGGA
ATTATTGAGAAAAATCAAANACTCCCNAGTTTTGATGACCTGNGAAGGAATATTTCNGAG
GGACNCCANGCCCTTTGGGGNAAGGANTCCTTGACTCTATCTTTTCAAAGGGAATGNAAA

Table 1

ATTCCTAGTAACAGGCCCTNTAAAGACTNAANACCAAACTTTGGACTTCTTGCTTGGATT
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TTAAACTTGGNACCTTTTCCTTAAATAATATTACCTTTCTNATTCAAAAGGTGGGAAAA
N
GGGAAAATTTCC

Sequence 507
GGCGGCGCCGGGCAGGTACGCGGAAATCCCCTAACTTCCTTGCTATCTTCCCATNCCATA
TTTAGGTTAGATNGAGAAGTGTGTATGTGTGTGTGTGTGTGTTGCTCNGCACAGTNGA
TGAACTGTAAACATAAATTGAAGATATTGGAAAANTACATNAANTTATGGACCAACATGA
CAATTTTCATTAGGACTTCCTATTCANAGAGTATCAGTTTNACANNTTGGGTATTAGNT
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NTACAAGTTNTAAGCATGTCTTNTANGNCTATGCTTTGGAATACCAGCTAATAACCAAT
C
AACAAGNCCAGNAGCCTTAANGTGGTATTTTTTTGGTTGACCCTAAAAAAACATGGAACCT
NAANGGGTTTCTNCAAAAANTTGCCTTAACCAAATGGAAANTAGGTGGGGGGAAG

Sequence 508
TATCCGCTTCACAATTCCACACAACNATACGAAGCNCNGTTAGCATTAAAGTGTAANAGC
CCTGGGGTTGCCCTAATGAGTTGAGGCTAACCTCACATTAATTTGCNTTTGCCGCTTNAC
NTGGCCCCGCATTTTCCAGTTCGGGGGAAAACCNTGATCGTTGGCNCAGGCNTGCCATTT
ANATNGGAATTCGNGCCCAACCNCNCCGGTTGTAGGAGGGNCGGGTTTTGCGGNAATTTG
GGNGCGCTTCTTTCCCGCTT

Sequence 509
CCNANGTACACTCCCACCACCACCNCATGGTCTCTTTCATATNNCTCAANNNTCAACNTG
NTCCTGNGGCTTCATAATTNTCCTNTTNCATCTTTTTCACTTCNNANGCAAACACCGC
CT
CNNCTNANGCTNTNNANTCAATNCANTTNNCCTTAATNNAAATCACAAANTNTCCTCC
AT
TACNCANNAANNTNTNNNCATTCANNNCCACAATCCNGGTNNTGGTCTNNCTNNNCCACA
TCANCAAAAATCACATCCACCATTNCNATCCCNCNTACCTTCCCNNNCCNCCCCTCTAAA
ACTANTNNATCCCCCNNNCTNCAANAATTCNATATCAANCTTATCNATACCCTCNACC
TC
NAANNNNNNCCCNTACCCAACTTTTNTTCCCTT

Sequence 510
CGGCCGCCCGGGCAGGTACTCTCTGAGCCAAGGACATTCTCATTTAAACAGTTTAAANAG
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AAGCGGANAGGGACNCTAANATCAGCAAATTCNCCAGTTTGGATCCTTGTCCTTTTCCGC
CCTTTTCCCCCCATTAAATCCANAACCCGTCACATGATAATTAANAAAANGGTTCAGTTC
CTCCTCCTCAAACCACTTCCNGTAAGAGGATCCCCCNCNTACCTCNGCCCCTCTAAAACT
AGTGGATCCCCCGGCCTGCANGAATTCNATATCAACCTTATCCATACCCNTCACCCTCA
AGGGGGGGCCCCGGTACCCAACTTTTTTGTTC

Sequence 511
GGGGGAGGGCAGNAAANCAAACCACAGCNCACNGCANGGGCACACANCACAATCCCCAGC
AAAAAAAAAAAAATNNNTNNTNCCAAACANAAAGAGCCTGGCCAGGGGGCCCANACGGGCC
NNAAAGCCCNGGAACCAATTTTTTTNTGGGGGCGGGGGCCCCCCAAAGGGCGGGAAAAACA
GCCACGACCCACGGCNCCAAGCNCGAACAGAGAGCNGGGGGAGACGCNGCCAAAGCAAA
ACGGCGGCCAAANCNNAGGGAGCAANNNGGGGCGAAAAGNNNAACGGAACCANNANGAAA
NAAAANCAAAANAAAACCGGACCANA

Sequence 512
AGCANCACCGCGGNGGCGTTTGCGGGAGAAACNGNGGACCCCCCGGGCTGCAGGAANNCG

Table 1

ANANNCNATTTAGGGNGACNNAAACCCC
Sequence 513
NAGNCACCGACGAGACCAGATTANACNTNGGGGGCNGNAAAACCCCAGCCCCCCCCGGNC
ACAGCCCNAAAGGCCAACCCTTTTTGGAGGNGCNNGGGGGANGCAAACNGAAAAAANAGCNG
GAAAAAGNAGGAGNNGAAGCCAAACAGCCAAANNCNGCCANNAGGAAGNGNGNAAGGGTT
TTGCNANTTTTTTNANGGGGGGGGNANCACACCCCCNGAANAAAGNCCGGGCNGNCGNCC
CNGAACGAGGGGGGGGGGGGGGGGGCNGCAAGAANNGGGNGANCAAAGCNNNANCGANAC
CGGNGACCNNGNAGGGGG
Sequence 514
ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTCCGAAATCTTACCTTCAGT
CTTCTCTGCCACCCAGTCATTTATATGCTTCCTGCACTCTTCAGTGTCTTCAGCAAAG
GA
CAACTCCTCCAGCTCTGCCTGATAGAACTTCTGACAGTATTCTTTAAAGTCTGGAAGGAA
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AGGAAGTGAAACCACAGAGCTTCAAAAAAAGAGCGGGACAGGGACAAGCGTATCTAAGAG
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CGACAACTTTGAAAACGAACCCATCCTCTATGGTCGGAGCTACACTTGGCTGTGCTATGA
AGTGAAAATAAAGAGGGGCCGCTCAAATCTCCTTTGGGACACAGGGGGTCTTTTCGAGGC
CAGGTGTATTTTCGAGCCTCAGTACCTCGGGCCGGTTCTAGAACTAGGGGGATCCCCCC
Sequence 515
TTCGCCCACCGGAATGATCACCAAGACACACAAAGTAGACCTTGGGCTCCCAGAGAAGAA
AAAGAAGAAGAAAGTGGTCAAAGAACCAGAGACTCGATACTCAGTTTTAAACAATGATGA
TTACTTTGCTGATGTTTCTCCTTTAAGAGCTACATCCCCCTCTAAGAGTGTGGCCCAT
GG
GCAGGCACCTGAGATGCCTCTAGTGAAGAAAAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCG
GGCGGCCGCTCGACGTGGTCGCGGCCGAGGTACAACTGCAGTAAGAGGGACGGTTAATTC
ACAGCTTCCAGCTCTTGGCGCCAGAGTCCGATGCACTCCTGCAGATAACGGTCATTTCCA
TTTCCGGGAGAACCTCTTTCGAAAAACAACCCGGATGAGACTATCTGGCAAATTGCAGCC
CTTGGCGGGCTTT
Sequence 516
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ATCTCAGATCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTTTCCTGCTTCATCTT
CC
CAGGTAGCTGGGATTACAGGCATGTGCCACAACGCCTGGCTAATTTTGTATTTTTAGTAG
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CGCCTCGGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGCCCAGCTATACTG
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GAACATAAAGTTATCATGGTGTTGGGTAAATTAGCGAAATTCAACCCCTTCCTAAGGTTT
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GTGGATTTCCCCCTTAATTAGGGATGCATGGTTGATTAAACCTCNAGATACAGCTTTT
TT
GCAGTAATGGGGGGGNTGGGT
Sequence 517
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TTCAACGAGAAGGATTTGGACGTCAGAGTATGTCAGAAAAACGCACAAAGCAATTTTCAG
ATGCCAGTCAATTGGATTTCGTTAAAACACCGAAAATCAAAAAGCATGGATTTAGTAGCT
GACGAGACTAAACTCAATACAGTGGATGACTAGAAAGCAGGTTCTCCCAGCAGAGATGTG
GGTCCTTCCCTGGGTCTGAAGAAGTCAAGCTCATTGGAGAGTCTGCAGACCGCAGTTGCC
GAGGTGACTTTGAATGGGGATATTCCTTTCCATCGTCCA
Sequence 518

Table 1

AAACCCCACCCCCCAGGGGGAAGGGGNNGAAGGGAGGGGCTTGGAGGGCNGAGGGGGAAGC
CCCCGGAAAANGACNNCCCCCAACCAGGGGGANAANAGACCCGGNAGGGACAGGCNAAGGA
GAGGGAACAGGGGAACCANCACTTTTTNTNTTTTTGGGGGGGCACNNGGGCNGGGGACCCCCC
NACAAAAAAAAANANCCCCCCGCCAGGANGGGGGGGGGGGGGNNAAAGGGNAAAAAAAAAAACA
AGACCCAAAGAAAAAAAAC
Sequence 519
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AAAAANCAAAAAAAAAAAGTACCT
Sequence 520
GGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATGTTGAATAAATGTTTTTTTTCC
CTTTTAATTTTTCTGCTTCCCTAGTGCATAGAATTGAACTGCTTAGGGAGTTTGAGGCT
G
CAGTGAGCTATGGTCATGTTACTGCGCTCCAGCCTGAGTGATGGAGTGAGAACCTGCCTC
AATTAAAAAAAAAAAAAAAGAAAGAAAAAACAGTGCAGTGGGCTCATGCCTGTCATCCCAN
CAGTTTTTGGAAGCCAAGGCAAGAGGATTCCCAGGAGTTCAAGACCAGCCTAGGCAACCT
TAGCAAGACCTTGGTATCTTCCCAAAAACCTTTAAAAATTAGGTTGTGTGTGGTGNTGCC
TGGCTGAGATGAGAGGATTTGCTNGAATCCAGGAANGTGGAGGCTGNAGTTGAGCTATGA
TTNGGGCCNCAGCANTTCCAGGCCTGGGGNACNCCAGGGGATACCCTGGTCTTTAAAAAA
AAAAAAAAAA
Sequence 521
CCGGGCAGGACGCGGGCGGCTCTTAGCGGTGGATCACTCGGCTCGTGCGTCGATGAAGAA
CGCAGCTAGCTGCGAGAATTAATGTGAATTGCAGGACACATTGATCATCGACACTTCGAA
CGCACTTGCGGCCCCGGGTTCCTCCCGGGGCTACCGCCTGTCTGAGCCGTCGCTTCCAAA
AAAAAAAAANAAAAAAAAAAAAGGTCCCT
Sequence 522
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CCTTCGCCTTCCACCAAGACTGTAAGTTTCCTGAGGCCTCCCCAGCTTCCTGCATGCTTC
CTGTGCAGCCTGCAGAACTGTAAGTCAATTAAACCTCTTTTCTTTATAAATTACCCAGT
C
TCAGGTAGTTCTTCACAGCAATGTGAGAACAGACTAACAACAATCAACTCATGGCTTTAA
CACAAAAAAAAATAGGTAAGTTCAAAATTAACATATTACCACATCCAACTTCTTTATTCTT
GAGAAAACAAAAAAGTCCAAAATCAAAGGAAAGCACCCGTTTTAAACCCTCATATCTTTC
TCAGGGCTCACTGCAGTCTGGCCATATCTCAAGCAGGTC
Sequence 523
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AGGGATGCAACGGGGCAAAAACTGAACTGTTCAGGCTTCAGATTGTAACTGACGATCTGA
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AGGGACGGACAAAGAGCTGAGTGATTTACTGGATTTCAGTGCGATGTTTTCACCTCCTGT
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AGAAGACAGAAGTAGCTCAGGGTCCTGGGGGAATGGAGGACATCCAAGCCCGTCCAGGA
Sequence 524
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CAGGAGATGTGGGCCGTGCCAAAGAGATGGATGAGACTGTTGCTGAGTTCATCAAGAGGA
CCATCTTGAAAATCCCCATGAATGAACTGACAACAATCCTGAAGGCCTGGGATTTTTTGT
CTGAAAATCAACTGCAGACTGTAAATTTCCGACAGAGAAAGGAATCTGTAGTTCAGCACT
TGATCCATCTGTGTGAGGAAAGCGTGCAAGTATCAGTGATGCTGCCCTGTTAGACATCA
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Table 1

TTCAAGTGATTCTCCAACCTCAGCCTCCCGAGTAGCTGGGACTATAGCAGTGCACCACCC
ATATATGCAATTTC
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Sequence 525
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GGGCCACACNCNAAAAAANCGACCCGCAANNNGCACCGACAAACANCGGNGNGCNAAAACA
NAACNNGAACANCCCGAGGAAACCGCCCNATTTTTTTTTTGGGGGGGNCCAANGAGGGGC
CCGNCGCCACAAAAAAAAAAACCAAGGCCCCNGGGGGGGGGGGGGGGGAGCCCAANANNGGGG
NGGGGGCNN
Sequence 526
AACTTAATGTCTTCCTTTTTTTTTTTTTCACTGGCTTTTTCATANATCGAGACATGTAAGCA
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TATTTATAGACAGCTCTAACATGATAACCCTCACTATGTGGAGAACATTGACAGAGTAAC
ATTTTTTNGGGGGNAAGAAGAATCCTACAGGGTCATGNTCCCTTCTCCTGTGGAGTGGGGG
GGNAGAAGGGGTATGGCCCCAGGGNNGGCCATATTACTGACCCTCTACAGAGAGGGCAAA
GGAACTGCCAGTATGGNATTGCAGGATAAAGGCAG
Sequence 527
AGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGG
ATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAG
AACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTT
TTTCCACTATTCACACTCTGTGGCGTAACCTTCTTGAATATAACCCCAAATGTCACCCA
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TCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGAGACAGTCTGATCAG
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TTT
Sequence 528
AAGGANAATTTTTTGGGGGGGNCAAAAAAAACCCCANCCCCCCCACAACCANGCCNAACTNA
ATCTTNGGNAAAAGAGGGAAANAGGCCCCAAAAAGGACAAAAGGGNNCANNCANAAAAAC
AAANNNCCAAAAAANCCGGCCAANAANANNNCAAAANNNNCCCCCAATTTTNTTTTTTTGG
GGGGGGGAAAANGGGAAGNNACCCCAANGNACGCAAAAACNACCCAAACAGGGGGGGG
Sequence 529
CCGCGGTGGCGGCCGAGGTACATTGTATACTGCAGTGTCGTCTACATGGCATTGGACAGG
ACATAATGTAAAACATAAAGTGCAATTGTTACACTTACATATGATAGTGGAATGGCAAC
CGTGACCAATTTTTGGCTCAAGTTAAAATACCAAAAAC
Sequence 530
CGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTGGAAACCCATTTGGATTAATTAGA
GGTCTGTCTGAAGGAGTTGAAGCTTTATTCTATGAACCCTTCCAGGGTGCTGTTCAAGGC
CCTGAAGAATTTGCAGAGGGGTTAGTGATTGGAGTGAGAAGCCTCTTTGGACACACAGTA
GGTGGTGCAGCAGGAGTTGTATCTCGAATCACCGGTTCTGTTGGGAAAGGTTTGGCAGCA
ATTACAATGGACAAGGAATATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCTGCCC
GGGCGGCCCGNTCTAGAACTAGTGGATCCCCCCG
Sequence 531
ACATTACNAAAAGGAGAGGNGGCCCAGNNNAAACACNCNGAANCCANCCNNGCCCNGAGN
AACAAANCACNGGAGAACAAAAACGAAAAACAGCAGGNCCCNCNNNNAAANCCAANNCAN
ACAAAAANGNCAAAGNAGAACCAAAAGCCANGNGNCCCGCCAANAAAGCCNCCCCAAAAG
CAACAAAGAGGNCNGCCCAAACCNCCNAAAAAAACAAACCCCCAAGANGAAAAAAAACCA
AAACCCCNAANGNAAANGAAACAANCAACCGGGGGCCCCCCAA
Sequence 532
TTTTTTATTCAATTTGCGATNGACAGNNNTAGNTTNAAATGTTNGTAACACTCTTAGAN

Table 1

N
NNCTGGTTTGTTCATTTGACATNGGGGCTGCACCAATTTTTATTACAAAAATCAAAAAA
G
TAAAAATTCTTACAATATTTGCAGAGTATAACCACTAGTTGCCTAGACAAAAGCTAATT
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CTACAAAATCAAAAACTTAATGCAGTTTTATTAAGAGAGTCAAAATTCTCTCAGTTAAC
T
GGATATACATAGTGGTATATATCTTAAAGCAGAAAACCCCAAAAAACAAAAACAAGGAAA
AAAGAAAATACATGTCAACAGTCAGGTAAATATTTTGACCTGACAGGTTCTACAAATAGG
GGATTTTCACTACATATAAAGGAATCTGTTACATGGGGGGTAAAACTTCCAGAGACCAAGT
AGGAAGNGGTGGAATAAAAAACCAATAAATNCAAACGCCACCCCAGGCTGG
Sequence 533
CCAGCTGCTNGCCTGCAAAGANGAGCCTCCTNNGGGGGGGGGGNAAAACCCCNCCCNANCC
NGGANCTTGGCCTTCACANTNNCGATGGGGGGGCACTGGGCGCCACCTCANGGGAGAAGGG
CTTGCCGGGAAGGGNTNNCACGAAGAACTGCATTNNGACCTGGNAGCGGAAACCAGGATC
CTGCCAATNTNTNNACCACGGGGCACCCACAGGGACACAAACAAGCNCACCCAACAAAGC
CAACCGCCCCNNCCCGNGGACCNGCCCG
Sequence 534
CCCGCGGTGGCTCTTGGGGCTAACCTCTCTGCAGATGAAAAAGCAGCTGAAAGGAGTTTT
TGGCGNCACCAATAACCCTAAAACTGAAGCCTGATTACTGGAGTGACAAACTACNTGAAA
GAAGCAGAAGCCGTTTGCTTATTATCGCCGGACACACACTGCCAATGAGCGGCGGCGGCG
TGGTGAAATGAGGGATCTCTTTGAGAAATTAAAGATCACNTTTGGGATTACNTCATTC
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CCAAGGTTTCCAAAAGTCTCATTCTTACTCGAGCCTTCAGNGAAATTCAGGGACTAACAG
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TACGGAAAGGATCGNCTCTTTCAGGTAAGACAGAAGAAGTGGGCCTGAAGAAGCTAGAGG
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ACCTGCCCGGGCCGGCCGCTCTAAAACCAGGGGGATCCCCCGGGCTGNAGGAATCNAAAT
CAAGCCTAATCGAAACCGNNACCCNCGANGGGG
Sequence 535
NGGGCAAAGGGAAGNAACAGACACACNCTNNTGGGGGNGGATNAAACCCGGGACCAGAGG
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GGAACNGAGAGAAAGAANCNGGGGCTGGCNNAAGAAAANANAGACANNCNCACAAAAGCC
NAGTNCATNTTTNNTTNCCGNNGGGACCGNNCACCCGCAGAAANANNNCACAANAGGCCG
CCGGNCAAACGGGGGGGGAGCACGGACNGTCAGGNCNCNGGGAAGGGGGCAGCGCAACCCG
CAGGGCNNCNCCCCCCCNGGCCNNNGGAGAACCAGGGCCCNNCNCAGGGGCCCNAGGGAC
CGCCAGGCNGGNNCAGCCAGGAAGGCCAAAANCAAGAGGGAGAAGGAGAAAGGNGNAAAA
AAGAAAAAGGGGAGGNGG
Sequence 536
GGGGANCCCGCGGNGGCANATTGGGGGGGGAACACACAGCAAAGANACGNNACAGCCTGAG
AGCTTTCCTTGGGGGGGGCTTAAAACCCCCCGNCCGNCCATCTATCCATCCATCTGCTCAT
CCNTNCCTCCATCTGCGCAACAAACGCNAGAGAANCAATCCTTGGGGCAGATACTGGGGC
TGCCCTCAAGGAGCTNNNATAGAGGNCAGGGGGACCTTTGNCGCTNTTTNNCTAGGGGANC
Sequence 537
GGNCCCCCCGGGCTGCAGGAANNCGANATNTNCTTTAGGGNGACCAAAACCCCC
Sequence 538
GGCACCCCGCGGNGGCCCTNGGGGGGGACAACNCCGCGCCCGCCAGNAACAGGCCACAGCC
CAGAGCTCNNTCGGGGGCNNAAAAACCCGGACAAGCNGCANGCGGGGGGGACAGGNCTGCG
GGNCNTGGAAACACTGGACNGGATGGCACANGAACCAGAACTCCGCTCCGNTTGGCTGCC
CAAGGANCCCACCAACNCATNCTAANCAGCGANCACNGAGGAAACGCNTTTTANNCCGAG

Table 1

GNACNANNNCANAGAACAGGCCNACCGCAAGGGCANACCAAGAAAGGGGGGCGNAAGGAN
AGNNAGGGGGNAACAANGNACCANAGGNCNNCAAANGNCNGACANNCANCNNNACCCNAC
CNCNAAANGCCCNNCCNTNNCACAANANCNNNCCNGANNGCNGNGNAANAGAAAAACAAA
CAAAGACANGGAANNACCGGGCANANNAGCAGAACCAAACCGGAAAANGCANGGAGGGNN
CAAAAACACCACCNACAGGAAGGAANAACCCAGAGGAAAAAGGCCGAAAGAAAGAAACCG
AAAANANAAGACCNGGGCCGAAAAAGCNNACCCAGGAGGAACCCACNNNCACGAAANCAGA
ANNNCCCCCNNCCAACCANNAAACAGGGGGAAAAAAAAAAAAANCNG

Sequence 539

GCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTCTTTTTTATAGTTTT
TTTGTTTTTGTGATTTTTTTTTTTTTGGTTTTTGTTGTTTTGTGTTTTTTTTCCTTTTTTT
TTTGGTTCTTAGAAAATCTGAGACACGTGAGGCCAGACAAAGCAAGGCCGGGGCTGATGG
CCTGGCTGCCTGGTGGTTGATGGTTTTGCTCCCCCTACCTTTTTTTTTTGAGTTTATTCT
G
ATTGATTTTTTTTCTTGGTTTCTGGATAAACCACCCTCTGGGGACAGGATAATAAAACA
T
GTAATATTTTTAAGAAGGAAAAAAAAAAAAAAAAAAAA

Sequence 540

ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTATTTGCTAAAAAAATGCT
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TTTTGGTGGCTGCTGACTGATCAGCGTGGTGGTTGCTGAAGGTTGGAGTGGTTGTGGCAA
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TGGGAGGCTGAGGTGGGAGAATCTTTTGAGGCCAGGAGTTTAAGACCGGCCTGGGCAACA
TGGTGAGACCGTGTGTCTGCAGAAAAATGAAAGAAATTGGCTGAGTGTGGGGGTGCATG
CCTATACTACCATCTACTAGGGAGGGTAGGATGGAAGGGTTGCTTGAGCCCAGGAATTCA
AGGNTGGGCCACTGCACTCCACCCTGGATGGCAGAGTGAGATCCTGCCCTCAAATTTTAA
ATNA

Sequence 541

TTTTTTTTTTTTTTTTTTTTTTGTTAAAAGACACAAGTAGTGATATATCAACATCTGTTTAACT
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TTTTCCTGATTTCCACTTTCAGTTTCCATTCGTTCGCTATCTTCTGGTAGCCACAGCTC
A
GCTCCAATCTGCGAAATACGGCACTCTCTTTATTGACTACTGCTTCTCTCGGCCCCCGCG
CGGCCCCGGGAGTACCTGCCCGGGCGGCCGCT

Sequence 542

GCCGCCCGGGCNGGNACAAAATGTTAAAGACGTTGTTTGTATNTGTAAGGCTGGTGTATT
CAGAGAGCATNATCTCTTATTCCTCACTTTCCACCCCCGTATTTTGTAATGACCATGAT
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AATGTTTNTACTTTTTGTNTAATGGGGTGGGGTGGAGTGGGGGCTATCTGAGAGTCANCC
TGAGGTCTTTAGAGGACCANCTATTGTATCACCTTGGATACTTGAAGTTT

Sequence 543

CAAANACTTTGGCCANANTAAAATNGNTGGAACTANAGGTTTCTTTTTAAAAAAAGGAAG
GGTTAAAGAAGCCAAACGGTNGCTTTTNGGGGGAANGCCANGAAAGAAAANAAGGGGGGA
GNAAAAAAGGCCATGNCCATTCNTNTGCCCCTTGGNAATGGAAGCCCCANGGGGGGGNAC
ACCAAGCNAAANNAAGAAAAGGCCCCACCTTNATTCTTCAATTTTTAAAATTCCTTTTA
A
CCAGAACATTCTTCTTTTGGCAACAAGNGGTCTTCCCCTTNGGGATTGGTCGGAAANAAA
TCACCCATTGGAAGANTGAGAGAGTNCACTGGGAAAAGCGGCCCACCTTATTCAGTCCCC
TCCCCTTTCTTGGCGTNTGGCAACCAAAAGNTTNTTCCTGGCGGGGCGTTGGGGACCCCG
TNTTTCAAACCAAGTAAGGAAGGGGCCTTTTAATTTTTTGGGGACCTTTATTAATGGCTT
N

Table 1

AGAAAAANGCAATNGGTAAGNGGCCTTTCNTTGNGGGNGAATNAAGGGGCCCCACGGAAA
AGCTTTTTCCCCTTGGAATTGTACCCCGGCCGGNACCTTTTTCCNAANGCCCCCCTTNNC
CCTTTANAAGGACCCCCCAAAGGTTGGNTNGGGCCCCCCC
Sequence 544
TCCGCGGTGGCGGCCGAGGTACCAATACTTACTTACAAATTTAATACTGCTTCAAGGTAT
TTAATCTAAAATTTTACCAACTTTGATTTGTCTGGTTAGGATATTTTGTTTTAGTGGATA
TGCTTTAATTCGGATCAATTACTGCAGTAAATCTCATCCCTAAGCATGAAATGTTGTCA
A
CAAATACCCAGTTCCATTTAGTTATCAATTAGCCCAAATAAGAGATACAAAGTATAACAG
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AGAGTGCTGTGTTTGTTGCTATATCCCCTCCAACACCTAAGGCAATGCATTTCACATC
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GCTGAGAGCAGATAACCTCAATACCTGGGAACTAGAAAAT
Sequence 545
AGTGAGGGGTTAATTGCCGCCGCCTTGGGCGTAATTCATGGTCATAAGCNTGTTTCCTGT
GTGAAATTTGTTATCCGCTTCACAAATTCCACACAACATTACNGAAGCCCGGGAAGCCAT
AAAAAGTTGTNAAAAAGCCCTGGGGGGGGNGCCCCTAAATGGAGGTGGAGGCTTAAACCTT
CAACCATTTT
Sequence 546
GCCGGGCAGGTACCTGATGCAGGGAATTGAAGCCAGACCCAAAACGGGCAACCCAATAGG
ATGGCCATCTGCCCCATTAATGCCAGCTTGTCCAAGTGTAATTATTAACAGTGCCCCCTT
TCACTCTCCAAAGAGTNCCTTGTNCAAACAGNTTAATTGTGGAAGTCGCCTTCAAGATGA
CTGGGCGGGTAAAGGAAAGTGGGAGTGAGGGAAGCAGGGTAGGTGGAGGGTGTGAAAGGG
AGAGGGCCTCATCTCAGGGTGGCTTGGACCTGCACCAGCATCGGCCTGCATGAAATGTGC
TCCTACTCTTGCCCAGGCTGAGTATCAAAGAGAAGCAAGAAATCTAGATAAAAATNCAAA
TCCAGAAACA
Sequence 547
GCGGCCGAGGTACAGGTAAGCCCTGGCTGCCTCCACCCACTCCCAGGGAGACCAAAAGCC
TTCATACATCTCAAGTTGGGGGACAAAAAAGGGGGAAGGGGGGGGCACGAAGGCTCATCAT
TCAAAATAAAACAAAATNACAAAAAGTTATTTAAAGGGCGAAANGATTTTAAAAAAAAAA
ATTTTTTGGCAATTTACCAATAAATTTTTTACCACCGAAAAAGCCAAANTGGCCTTANT
A
CACCCCTTCNCCCCNTGNTGGTGGGGACCTTTTGGGGGAAGGAAGGGNACCTTGGGGGNC
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TAAGTGGAATNGGGGCTAAAGGGGGGAACCTTTTCCCCTTGTTAAAACCAAAACCGCCAA
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ACCCAAAATTGGGTTGGCNAAATTCCAAAAAAGGTTCCCNTCNGGGCCCCCACCCAATTT
TGGTGGAAAAACCTTTTTTGGGGGGGGGGGAATNGCCTTTCCGGCCTTCCCCAAAACNCNG
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TCCCCCTGGGAGGTTCCAAAAGGCCCCAAAAAAAAAAAAAAAAAAAAA
Sequence 548
GGCGCCGGGCAGGTCCCTTTGTAATATCCTTTATAATAAACCAGTAAATGCTGTTTCCCT
GAGTTCTGTGACCTGCTCTGGCAAATTAATCAAACCCAAGAAGGGGGTTGTGGGAACCCC
AATTTATAGCTATTCAGTCAGAAAAAAACAAGGTAAGACAATCTTGGGGCTTGCGACTGG
CATTGGAAGTGGGGGACAGTTGTGCGGGGCTCAGCCTTCAACCTGTGGGATCTGACGCTA
TCTCTGGGTAGATGAAGTAGAATTGAACTGGGGGACACCCAGCTTGGTGTCCACTGCAGA
ATGAATTGCTTGCTTGATGTCTAGGGAGGCCGCAGAATTATAGCAGGGAGGTGAAAAGCA
CTTCTTATATAGCAGTGGCAAGAGAAAATGAGAAGGAGCAAAAGCTGAAACTCCTGATAA
ACCAATCAAGATCTCATGAGGCTCATTAACTATAACAAGAATAGCATGGGAAAGACTGG

Table 1

Sequence 549
NACCCTCTCAGCCNCCCTGTAATTGCGCNAACTNTGGAAACGCTGCAACGATTGTCGAGT
CGTATAGCGTCTATGTACATATAGCATNTTCNATAGTCATTGGTGTAGAGATAGAAAATG
CTTCGTACATGTCAATGGGAGAATGGGTGGTACCACTACACCGGAACTATCCCTAAGTCC
ATCCGCCTGGGGCGAAAGGAAGGAAAAAAAGA
Sequence 550
NTATCTTGTTGCCTCATGNGGGCTACACCNACGCTAGNNAGCCCAATGAGACGTTACGAG
CGCGCAAGTNAGAAACNAGATTTCATAGAGCGCTTGTTGGGAGAGGGACATTCGCAAACC
GCGCGTTTAAGTTACTCGTAGATATTGAGTANNTAAGGNCGTTGGGGAAACGCAACCAAA
TACTCCTAGAGCCTTTGCCGNAACAAGNTACTACANTTGTTCNGGGGGGAACGAAGGTGCC
CCGGNTCAACCCNTTGGCCCCCAAANAGCCCCAAGNCTTCCNTTGTTNGGGTATGGCAAA
NNNCTTAACNGAACCACATTGGGCCAANGGNNCGCNANTGGNCCCCNTGGTTTTTATCNN
NCANTAACCCNANCNAAATGGGCGNCNTCCATAGGNAAACCTTGTTCCCNTAGCCCCTTT
NGATATTTCCTCGGCATTTTNTGGCCCCNTTTTCGCTTTNTNTAANCGCCANTTACCT
NT
AGCNCCCTTTTAGGCAACATCCTTTAAAAACGGNGCGGAGCGGTGTCCCCCCAAGGGCCT
TNCCCCCCCAAAANGCCCCTTTTGGTGTCGAATTTGGCAAGCCCTTTTTGGNAGGGAACNA
AAAGGGGGGGGTTGGGGANAACTCCGGCCCCNACCGCCCCTTTGGNCCCTTGGGTAAAAC
TCCAAATNGGGGGGGANGGCAACNAAAGGCCCCCTTCNTTGTNGNGNCANTNTTTGGGGNA
AAGAAGNACCCCAAGGNAAGTGNNCCCACCGGGGGGGTTNANAAANAAAACCCCCCAAAGC
CACCCAAGNGGAACTTACCCCTTANAAACTTTTTGGNATTANGTTNTAACNAAAANNNACC
CGNCCAAAATTTAAANAAAANANAAGGGGCGGATTTAATTTTTTTAAAATTCCNTTGNCCCA
TTNGGGGGTGGAAACATNTAAAACAAATNTTAAAA
Sequence 551
AGTGGACTNTGTGACCTTGAAAAAGTCATTTAACATCTCTGAACCCTACTTTCTAAGTC
T
CTACAAGTAATATATAGTGGGTGAGGTGTTCTTTCTTTGTTCTGNTACTNGGATGTGA
AA
CTCTCCNTTTGGAGATGAAACCATGGCGTAAGTAATATAAAGACTTTTCCCTGTAGTT
AT
CTTACAGACTGGAGAGAGTGCTAGTGAATGCTTTTGTCTTCAATGCCCATCTCTTGGAAA
TATTGAAGGTGGAGTAGCAACCGGGCATTATATTATCTCTTGGAAAAGGACCTCAGCAAT
GGAGAATATCCCCATCATCACAACTGTCATCACTCTGCCGCACGTGATTGTGGAGAATAT
CCCTCTCCNTGTGAATGCCAGAATGAGATTCATTTACAA
Sequence 552
GGCCGGCCGCCCGGGCAGGTACTACAATGATTCTGAAGCACAGTGTATTCAGACAGATAC
AGTGAACCAAGTGCAATATGTAAGGATGAAAGAAGAAGAGATGACAAAGAAATCCAAGTA
AATGCCTTGTCTTTGCAAATGTTTTTATNTTAAAATCATTAAGGGAAGGGAACTACTTT
G
CCTTTAAATGNTTATCAAAAGAGTTTTCTAACCAAGGNGTAATACCCTTANTTCTTAAC
A
TTTNTTTTTCTTTATGTGNTAGTTGTTTTCATGCTACCTTGTGTAGGGGAAAACCTTTAT
TTACAAGACNCATATTTANAAAAGGGCTANATTTTTAAAATACTCAANATTAATATTAAA
AAGGTTGGCTCCTNGAATTANNAGCCAAGNAAAATTANTATTTTACCAGTTTTTCAATT
T
CCCAACNANGAAAATAGGCCATTTCCCATAAACCCCAACCTCCCNANAAATGNAACCCCA
AAGGGGCCAATTATTTATTACGTTATTTTTTGGGGAAGGGGGAAANTCCAANNGGGGGGT
T
Sequence 553
CGGGTGGCGGCCGAGGTACCCATCTCTGCCCATCACCGCTGGAATTTTGATGACCTATTG
GAAAAGATCTGGGACTATCTGAAACTAGTGAGAATTTACACCAAACCCAAAGGCCAGTTA

Table 1

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CCAGATTACACATCCCCAGTGGTGCTTCCTTACTTCGAGCGGGCCGCCCCGGGCAGGGTA
CTTCACACCAAACACTAGCTCAAGCACTGACGTTATTCTACAGGACTATGAACCTTCATA
TCCACATTTACAGTCCGGACAGATAAAGGAAAACAACCCAAATCCAGGAGGCAATATAAA
AGGAAGAGAACAAAACACACATTCATACACTCACACTTAAAAATAGGGGAAGACCAACAG
GGGAACTTTTCGTTCTCTTCCTGGGATGTCTACTTAAAAATCCCATGTGGGTACCT
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Sequence 554
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NCGGGTGGCGGCCGAGGTACTCTTGAGATTGCTTTAAATTTTGTATTGAAACAACAATAC
ATTTTGCACTGTAGTAATGGGAGCACTAACTCTTACAACAGTTAGTGAATCGTTTTAAA
G
AATCAGTTCAGTGTAGACATTTTGAAAAGATTGTTTCCTGTGCTCTACGATAGCTTAGT
G
CAATGTGCACTTCTGTTTTACTTGCCATTTTCCTGCTCTGTTTTCTCTGTGACATGAAG
C
AACAGAAACTGAGATCAAAGTTAAGATTATATCCTGTTTGTAGTATCAGATATTTTTCT
G
TGTACATTTACATTCAAGTTTGATAACACTGGTGGTTTCATTTCAATACAAATTATGCTA
GAGAACTGACATTTTCANACATGGTCATATATATGCTATTTGAATTCCTTTATCTTGATA
CCAGATCTTGGATTGTGAATCTCTTGATGATAGATGTGCAGCTAATTTTGTCCCGAAA
CT
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Sequence 555
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GGGTGGCGGCCGCCCGGGCAGGTACAAGACCATGACACCGCCCAAAACACTTCCTGCAGA
TGTTGTCGTTGGAAAACTGTCGTCTTACAGAAGCCAGTTGCAAGGACCTTGCTGCTGTCT
TGGTTGTCAGCAAGAAGCTGACACACCTGTGCTTGGCCAAGAACCCCCATTGGGGGATAC
AGGGGTGAAGTTTCTGTGTGAGGGCTTGAGTTACCCTGATTGTAAACTGCAGACCTTGGT
GTTACAGCAATGCAGCATAACCAAGCTTGGCTGTAGATATCTCTCAGAGGCGCTCCAAGA
AGCCTGCAGCCTCACAAACCTGGACTTGAGTATCAACCAGATAGCTCGTGGGATTGGTGG
GATTCTCTGTCAGGGCATTAGAGAATCCAAACTGTAACCTAAAACACCTACGGTTGAAGA
CCTATGAAACTAATTTTGGAAATCAAGAAACTTTTTGANNGNAAGTGAAAGGAAAA
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Sequence 556
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GAGAGCCCGGGTGGCGGCCGAGGTACGCGGGGGGGGAGTGGCACTCGCAGCTGCAGCAAA
TCTCAAAATAAAGAGGCAACGGCCTTTCTCTTCCTCTCCATCTCTCTATAGCACACCTT
T
TATTTCTTTTCTTCTTTTTTTAAGCCTCACGAAAGATTTTACTTGTAGATCAACTTTCAA
AATGTAGGAAGTCAGAATGGGTGACATCATCAGAAAAATATGTGGAGCTGATCACAAGAA
GTGAAGAACCCAGAGCACNGAAAGCGGTTGTGACTCCTGGGCCCAGGGAGTTGACAGCGT
CTGGGCTTCAGAGGAGCCAGCCGCCTCCGAGTTGTCTTGGAAGTGAGGCTCTGCTGTAGT
CCTGTTCTTCTGGCTCTAAGATCTGAATGTTGTGACCACTAATTTGCTNTTTCCTGGA
GG
GTAACCCCAGTTTGGTCCACAAGGGCTT
G
```
Sequence 557
```
GAGCCCGCGGTGGCGGCCGAGGTACTGGATGTCAGGTCTGCGAAACTTCTTAGATTTTGA
CCTCAGTCCATAAACCACACTATCACCTCGGCCATCATATGTGTCTACTGTGGGGACAAC
TGGAGTGAAAACTTCGGTTGCTGGCAGGTCCGTGGGAAAATCAGTGACCAGTTCATCAGA
TTCATCAGAATGGTGAGACTCATCAGACTGGTGAGAATCATCAGTGTCATCTACATTCGA
GCGGCCGCCCGGGCAGGTACCGCGGGGGGAGCGGGCCCTACCGTGTGCGCAGAAAGAGGA
GGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACTCAACTGGTTC
GTTGCTTTCCAGGGCCTGCTGATTTTTGGAAATGTGATTATT
```
Sequence 558
```
CCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTGAGACGGAG
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Table 1

T
CTCCCTCTGTTGCCCAGTCTGGAGTGCACGTGGCATGATCTTGGCTCACTGCAACCTCCA
TCTCCTGGGCTCAAGCGATTCTCCTGACTCAGCCTCCCAAGTAGCCTGGGATTACAGGNT
GCCTGCCACCATGTCCCGGCTAATTTTTGTATTTTTAGTNAAANACGGGGTTTCACCA
TA
TTGGTCAGGCTGCTCTCGAAATCCTGACCTCGTAATCCGCCCGCCTCGGCCTCCCAAAGT
GCTGGGATTACAGGCCCGAGCCACCGNACCTGGCCTGTATTCCCGCGTACCTGCCCGGGC
NGGCCNCTNTTAGAACTAGGNGGATCCCCCGGGCTGCAAAGAATTTCGATATTAAAGCTT
AATNCNANTNCCGTCGACCTCTAGGGGGGGCCCCGG
Sequence 559
CGGGTGGCGGCGCCGGGCAGGTACGCGGGGGGTGCCTGGCTCCGTTTCCTGCTTTTGGTT
CTTACAGTAGTCGGCGTAGGCCTTAGGTGGGTTCGTGCGCCTTCTACCTCGCTGTTTCGG
TTTTCCTGGCTCCTCGGCCCTTTTCTCCCCTGTTGCAGCTGGGAGCGGACGAAGCCGCGA
AGCTGGGATTTTTTACTGTCTCCTGAAGAATTTAACACAAACATGGATATCAGACCAAAT
CATACAATTTATATCAACAATATGAATGACAAAATTAAAAAGGAAGAATTGAAGAGATCC
CTATATGCCCTGTTTTCTCAGTTTGGTCATGTGGTGGACATTGTGGCTTTA
AA
Sequence 560
GCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGATCGGCA
A
GCGACGCTCATACANGGCNTAGCCCCGGGAGGAACCCGGGGCCGCAAGTGCGTTCGAAGT
GTCNATGATCAATGTGTCCTGCAAT
Sequence 561
CATGTGGGAAGCGCTGTGAAGAGTTGTTGCCTTNCAAGATATACTCCAAATTCCCAGTTC
CAGCCCGTGTCATTAAAACTCCGCTGGCGTGAAAGATGACATCCTTAGCCCAGCAGCTGC
AACGACTCCGCCCTCCCTNAAAAGGGGGATNCCAGCCTTTTAATNTANAGATGAANTTTG
CCTTCCTTTGNTATTTT
Sequence 562
NNNAGCCGGGTATTCANCCTCTACTTCAAAGGCGGGTAATNACCGGTTTATCCACAGAAA
TCANGGGGGAATTAACCGNCAGGAAAAAAGANACCATTGTTGTATGCCAAAATAGGGCNC
ATGCTAAAAATTGCNCATGTGGAAACCCCGTTTAAAAAAAAAG
Sequence 563
CGATAAGCTTGATATCCGAATTCCTTGCAGCCCCGGGGGGGGGATTCCCACTTAAGTTTTC
TTAAGAAGCCGGGCCCCGCCCCCGGGGGGCCAAGGGTTACCCCCCGGGGGGGGGCCCGGGN
AAAAGTTTGGGAAAAAAAAAAAAAAAAGGGTTTTTTTTTTTAAGGTNGGGGCNTTTTGGNA
AGGGGTNTTTTTCCCCCCCCCAAAAGGGAAANACNCGGGGNNNCCCCNGNCCANAACCCG
GGGGGGG
Sequence 564
AGGTACCAAGTAGGATAATTACTACTGCCAACACACACATGCACGCATGCACACACACAC
ACAGATGTATGCACGCACACACACTCTCACTCCTAGACTGCTAAAAGCAAAAAAAAAAAA
AAAAAAAAAAAAAAGTCCCTGCC
Sequence 565
NGACCTCGGCACTNAGCANCGNCACTACTTAGGGGGNGTTAAAACCCCCCCCCCCCCCN
GNAGAAACCNCNGCGCCATGAGNTNTCAAGNGGAGGAAGAAGCGACCCGCGCANGCTGAA
GCGCAAAAGAAGAAAGANGAGGCAGAGGGCCAAGNAAACCGNNAGCNNGNNGCACCGNGG
AGGCNTTNTNGNNTTTGNNGGGNGGAANGCNNGACGCCCNNGGAAGNANGAACNAAGAAG
CG
Sequence 566
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGGGGGACTGGAGGACCTGTCTGG
TTATTATACAGACGCATAACTGGAGGTGGGATCCACACAGCTCAGAACAGCTGGATCTTG

Table 1

CTCAGTCTCTGCCAGGGGAAGATTCCTTGGAGGAGGCCCTGCAGCGACATGGAGGGAGCT
GCTTTGCTGAGAGTCTCTGTCCTCTGCATCTGGATGAGTGCACTTTTCCTTTGTGTGG
GA
GTGAGGGCAGAGGAAGCTGGAGCGAGGGTGCAACAAAACGTTCCAAGTGGGACAGATACT
GGAGATCCTCAAAGTAAGCCCCTCGGTGACTGGGCTGCTGGCACCATGGACCCAGAGAGC
AGTATCTTTATTGAGGATGCCATTAAGTATTTCAAGGAAAAAGTGAGCACACAGAATCTG
CTACTCCTGCTGAC
T
Sequence 567

GTTTTGGGGGAACACCGCGGNGGCGNTTTNGGGGTANACCGGGCCACNCACCANCNNCAA
GGNCGAGGNNNNTNNNTTNGGGGGGGTTTAAAACCCCNCCCCCCNCGGGCNNNGNAGGCCG
NCANNANTTTTTTAGNNNGGGGGGGGGGGGNNGCCCNCCGAAAANCCCGGACCTGNCCGGGC
GGGCGTTNNAGAACNAGNGGANNCNNNGGGCNGGAGGAANNNGNNANNAAGTTTTTTTTT
TTTTNGGGGGGGNNNGGGGGGGGGGCCCCNTAAAAAAAAAAAAAGGNCCCCNAGNGGGG
Sequence 568

GCGGNGGCGGTTTTCGGNCGAGCCCTCTCTTGNCCATCTTCTCCCGCTGCTGAAATTTCT
NTTGCGGGCGCTGNAANCCCAGGACCCCNCCCCCCGCGTACGCTGGATAGCCTCNTGGCC
AGAAAGAGAGAGTAGCCGCCGAGCACAGCTAAGGCCACGGAGCGAGACATCTCGGCCCGA
ATGCTGGCAGCTTCAGGAATCCCCGCGNACCTGCCCNNTGCGGTCTGTTCGN
Sequence 569

ACAAAAACCCAAACCCCAGACAGCAGNAATGNCAGAAGANCCANGGAGAACAGCAGAANC
TNACACCGCNGCNCTCTGAAGGCTGAGAACACAAGNCAAANACATNNAACTNAAAAACAA
CCGCTGAGAGAACACGGGGAAAAATNTNCANTTTAGAGANGNCCACAAAAAAGGACACGC
AAAGGGGAAGGGCAAGGCGGNGAGACAACGACGNNANNCNNGGGAAGACNGGGGAGGGGG
NGGAGAAGAGCCNNGGNNGCCAGAANNCCGGNCGGAGGNCACGAGGCGGNGACCCACAAG
GGACCNGCCCGGGCGGNCGGNCNAGAACNAGGGGAACCCC
Sequence 570

GCGGGNGGGCCGGGTTTTTTNGGGGGGGGGCAAACCCGCCNGGGANGGAAGGAAGGAAAAA
ANGGGGAAGGCCAAGGGNCCGATTTTTTTTNGGGGGGGGGGGNNNAAAAAACCCCCGGGGGNG
GGGGGGAAACGGGGGGGNNNNAAAAAAANGGGGGGGGGGNAAATTTGTTAAAGGGGCNNAAA
AAANGGGGGGGNAAANCCNCAAGGGGGNGGGGGGGNNCNNNGGGGGGGGGGGGGGGAAAAAACC
NNAAAAAANNNNGGGGGGGGGGGNANAANNNNNNGGGNNNCCCCCNGGGGGGAAAAAAAAAAC
CCCCCCCCCCCCNGGGGGNGGNAANTTTTTTTGGGGGGGGGGGGGGGNNNNAAAAAAAAAAA
CCGGGGGGGGGGGGGGGGGGGAAAAANCCCCCCNAAAAAAAAAAAAAAAAAAACNACNCCCCC
CCCCCCNNGGNGGGGGGGGGGGGGGN
Sequence 571

CGGTGGCGTTTAGGGACCAAACGATAGCNGTTCTGTTTAAGTAGGGACCTCTCATGGTNT
NCAGGCTNTGACAACCGAGAATCAAACTGGAGAACATTCCGAAGCCGTTCTTATAAGNGT
CTCCATCTCTACCTGGGCTGAAATGGAATGTGCAAATGTAGCCCAGCCTGGTCCTTGGGT
GTTGCCAGTTGATTGATGACTGGGAGCCAAAGTGGCATTTNCTTNGACCTAAACGGGCGA
TGATGAAATAAATCGAGCGGCCGCCCGGGCAGGNACATCTGTGAATGTGAATGCCAAAGC
GAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGAAATGGGACATTTGAGTGTGGCGCG
TGCAGGTGCAATGAAGGGCG
T
Sequence 572

TGNAANNCCCCCGCCACGGAAAAGGNGGCCCCNGAGCCAGAGCTCCAGCAGCCCNGGGAG
GGCGGGGCCCGAGGCANGGANAAGNGGGAAGGAAAACGAAGAACAGGAGCAGAANNGAAG
AAANACAAAGNGAAANGGGGCCAGNCAGCATGTCAGAGACNGACCACAAAGCCCCCACNN
CCACNGAAAAAAAAGGNGGGAAAACACCGGAANNAAAGGAAGACCCAAGCAACNNGGNNN
CNGGCAANGAAAGCAGCAAAANAGAAAANGAGGCCAAACCAANGGCAANAAACACCG

Table 1

Sequence 573
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AGGACANAAAGGAAAACANAAAAGANGCAAGGGGACACGACACANANGAAAGGNGAAGGG
CAACGNCGACCAAACGGGGGNAGAAGACAAAAAACCAAAA
Sequence 574
NGGGNGGGGTTNTTTGGGGGGGGGNAAACCCACAAANAATACNGGGAAGGGNGGNGGNNGG
GGNNGGAATTNTTTTNGGGGGGGGGNGGTAAAAANCCCAAANCCCNAAAAGGGGGGGGGGGG
GNAAAGGGGNAAAAAAATTTTTTTNGAAAGGGGGGGGGGGGGGGGGGGAANNCCCCGGGGAA
AANNAANGGGGGGNGNGGGGGGGGGGGNNNNNNAANNANNNNANGGGGGGGGGGGGGGGGGNN
NNAAANGGGGGGGGGNNNNNNNNNNNAAANTTTTTTAAANTTTTTTTTTTTGGGGGGGGGGG
GGGGGGAAAAAANCCCCNNNGGGGGGNGGGGGGGNNNNNGGGGGGNNNNCNNNCNNNNNNG
GGGGGGGGGGGGG
Sequence 575
GGAAAANCACACGCCAGGAACCNNGCAGCNNACAGNGACAGAAATTNGGGGGGGNCGANAA
ACCCCACNCACCCCGANNNCNGGANCNCNAGGGGAANGAGTTTNAGCNCCACCGGGNGGCC
CTCCCCCCAGAAACNNANGNCCACAAGNCACTGGGCACAGANAAGAGNGNNCGGNCNCAA
AACNCACAGGGCNCAGGGTTNGCGTGNTTTTGGGGGGGGGGGANGGGNNACCCCCCCCGAA
AAGAGGGCNGGNNANCCGGGNNCNNCNGGAGAAAGANGGGGGANNCACAGNCCANGACACN
ACANGGNAACANAACNGAGNNNNCAANNNGAGCAGNAANNCGGGGGNC
Sequence 576
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTAGGAGCCTCTCTCCCTAC
TGCTGCTACACAAGACCCTGAGACTGACCTGCAGGACGAAACCATGAAGAGCCTGATCCT
TCTTGCCATCC
Sequence 577
CAGGTACAGAGACCTCCTTACTTACCCCCCTTCTCCTTCGGCTGGAGCTCGGCGAGCGAG
AGGCGGCGCTGGCGTTGGAGAGCGACGGCGGCCCCCGCGTAAGCAGTGGTAACAACGCAG
AGTAACGCGGGAATGAAGAATCTTAGGCGGGTGCACCCAGTTTCCACCATGATTAAGGGT
CTTTACGGAATAAAGGATGATGTCTTCCTTAGTGTTCCTTGCATTTTGGGACAGAATGGA
ATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAGAGGCCCGTTTGAAGAAGAGT
GCAGATACACTTTGGGGGATCCAAAAGGAGCTGCAATTTTAAAGTCTTCTGATGTCATAT
CATTTCACTGTCTAGGCTACAAC
Sequence 578
GCGATTGGAGCTCCCCGCGGTGGCCCGCCCGGGCAGGTACCTCACAACGAGTTCAGTCAG
TAGCAGAAGGATCTTCTCTCTTGTTCCTGATGATTTCAAGGTCCTCACAGTCCTGATA
AT
CTGGTTCTTCCCGAAACTCCCAAATATCTATGGAGAGCTGTTCTAGCTTTTGCACAGGGA
ACCAGTGGACAGAGGTATCATTAAACATGTCCATGTATTGNGAAGTCTGAGGAAACTCAA
GCTCCTCCAGTCCTTTTAAAATCTTTGCAATGTAGGGATAATTTTTCTGCAGAATCCTT
G
CCAACAACCTCTCCTCAAGTCCTTTGAAACTGTTCCCAATGATGACCATCTTAGAAAGGG
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Sequence 579
ATTGGAGCTCCACCCGCGGTGGCGGCCGAGGTACTTTGGACAGTGAGGGTTCGATCCCAA
TTTTAGGGGTAGGGTTGGGGGTGGGAGTGGGAGTGTGGGTTGCCAGGAGGAAGAATGAGT
CTACTTTNGANACAATTAAGTCATGGNCCTCTCTTTTTTTTNTTTTTTTTTTTTTTTTTGGCT
ACNTAGACNTCTTTCTCATGTATTGTTACTAGAACAACTTNTATAGGGTTTTATGGTTN
G
GGGAAAACATTNNTAAAAAATGGACTNATCTCTATTATACAGANNTATAATATAAAAATG
ATTTAAAGGCTATATTTTTCAGCATGTAGGTAGCTNCNCTGTCANCCTGTTGAAGAANN
CT

Table 1

TTCCTATTTAAGCTTATAGGATGAAAATATATAATTAAAG
Sequence 580
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCATCCAAATGCTTCCCTGGTCTTGATGAT
CTCTTCCAGAGTCGATCTGAGTGGCCTTTTCTGCACCCTCCCCTTCTTTCTCTTTGAA
TG
GAATTAAACCCAATTTGGAAACAACATTGACCCAGTCAAAAGCTTCTAATGGTTTCTTT
T
TCTTCCTCCAGTTTTAGTTTGCTTTTATTAAAAAAAGAAAATAGTGCATGGCCATAGCT
C
CTTCAGTTCTCTTATTGCAGACTAACCATCAGGATGGTATCAAAGCACAAATACTTTGGA
GGGGAATGCGTTGAACTGGGGCAAGTACCTGCCC
G
Sequence 581
CGTTGCGCTCACTGCCCGCCTTTCCAAGTCGNGGGNAAACCTGGTCCGTGCCAGGNTGCAT
TAAATGAAATCGGCCCAACCGCCGCCGGGGNAGNAGGGCCGGTTTTGCCGTTATTGGGGG
CGCCTCTTTTCGCTTTTCTCGCTTCACTTGACTTCGCTGGCGCNTCGGGTTNCGGTTT
CG
GGCTTNGCNGGTCGNAGGCCGGGTANTTCAAGTCNTNAACTTCAAAAA
Sequence 582
NTNGAGCTCCCCGCGGTGGCGGCCGAGGTACCAAATTGTTAAATACTCGNAGGCCTTTAG
GAACCTGTGACTGANTNCATAAATANCAGANCCTATATTGTGATGNTGGTNAAAGGACAN
GTGCTCANCTTCCAATTACA
Sequence 583
ACCCTCCTGGAACCGNAATAAGTTNNTGGGGGGGGTNAAACCCNGGNCCACNGAATNNNC
GGACCACANGANCNAAACTNAAGGNCTAGCTCANAGAAAGCAAGNGNCAAGCNGGGCANT
AGCTGCTGCTTCCCCTGGNGGAACATNGCCTGCTNCCTCATAANCCATNNCCAGACAAGC
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NGGGGGGGGCTNCCAGGGGAGANGAAANGGGAAGNCGGGCNGCAGCAACNCNGGNCAAAAA
AAACACCAANNNCNGGGGGCNCAANGGCACNAANCAGAACGGCNCGCCCNNNGGGANCCAC
AGCNAAGAACCGGCC
Sequence 584
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CAAGAAAGCATTTTCACCTCCTGCGCTTTCCTTCCTGTGTGCTTGTGGTTGGTTCTTT
CT
TCTCAGGCTTTNTNATTCTGATGCTGAGATAGTTCTGTTCACTTAGCAACTTGGGACA
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GACACAGGGTTTGTTCTGTACAAGCAGGTTATCCAAGAGGCATCCATACCCTGGGTTTTC
CTCCAACCATAAGGAAAATTGATGCAGCTGTTTCTGACAAGGAAAAGAAGAAAACATACT
TCTTTGCAGCGGACAAATACTGGA
Sequence 585
AGGTACCTGGGCCACCAAACACAGCTGGACTCAATATATGGGGAAGGTAAGTGTCCTCAG
TTTTTGGAGAGAGATTACCCTCTTCCAAAAGAGTGCTTGATTCTGGTAGTCCAAGCTGTC
TCCGTCTGGTGGCACCCCAATTTCCCCTGCCTAGACCCACCTCCTTTCCTCAGCCCCCTT
CGCCTGCCGCTGAAAAGTGAGAGCGGGCTCTTGCGTCCCCCGCGTACCTGCCCG
Sequence 586
GGGGGGGNNAAACCCNGAAGANGCGGNNNACGCCNNNCAGAGCCACANNATTTTTGGNCGA
AANAGGGGNCCAGNNCCGAGGAAGGNGGAGGAGGNCNGNAGGNACCNNGGGCGGNNAGA
ACNAGGGGANCCCCCGGGCNGGAGGAATTTTNNATTTTTTTTAGGGGGGGNGGGGGGNNCCC
CCGGGGGGGGGACCGGGACCCAGNNNCCNGNNNNGGGGGGGGG

Table 1

Sequence 587
ATTGGAGCTCCCCGCGGTGGCGGTCGGGTCAGCTTTAAAGCATCATAATGACTAATTATA
GGTGAATAATTTTACAGACAGTCTATATTCTAGGAGGCAGCTGTAGGCGTTTTAATTGGA
AATAAGCATTCTGAGATAATGATAATAGCAGTGTAGAAAAATGAAGCTAAAAAAATTCAA
AGTGTTGAGAATCCTCCTGTCCTTCTGGGATTTTTATTTTAATCATCTCCTCCACAGAG
A
ACAAGCAGNACTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGTTATTTTATGCACAAAGAGCC
ATCGTGGTTTTTTATTAGGTAGATGCCCTGGATAATCCTTTCAAGGAAGATCACTTAGT
C
CAACTTAATGAAACCAATATCCTTCGCATAC
Sequence 588
GAACACCGAAGAGCCAGANTNTTTAAGGNCAGAGAAANCCCCAGANNGCCGAGGNACGGG
ANAAGAACCGGGAAGGGAANGAAGGACAGGGAAGAGACCAANGACCGGAACCCNCCCNCA
GACTANGAACAAGCAGAGGCAGAAGCCAGGCACCNGGNCNANGAANCAGACCAAAACAAG
GATGNNAAGCNGNCNAAGGAGGAGAACCGCCGACAAGNANGACANAAAAGACGGCAGCCA
GGNNACAGAANNNGGGGAGGCCNNAGNACCCCGGCCGNNCCAGAACCAGAGGAACCCCCG
GGCNGGAGGAANNCGANANCAAGCNNAANGAAACCGGCGACCCCGAGGG
Sequence 589
GCAGAACAGACTTGCAGCCGACCAATTTTTGGGGGGGATNAAAACCNAAANCCCGGANTNC
ACCTTTCCACTTTTTGAGGACANTGGCCAGGGGCNCTGGGCTACCCGATGACAAAGCAAA
NCAGCACAGCATCCCGAACNAGGGGGAAGAGAGGGGGCGGACANTGGCANAGGAAGGAGAA
CCCGAAGTGTNCCACAGGCNCAACNCTANNCCCNGGGGGGCGAANNCAAAACCGGCCGGG
NAANNCGNAAACACTGGAGGAACGNAAANCNCGGGGAAGCAGNCCCNGGCGAAG
Sequence 590
GCGGNGGTTTTTGGGGGGGCAACACGCGGGACNGCANGCCACNGNCNAGAGCNNGTTTTTT
TGGGGGGGAGAAAAACCCCGCCCCCCGAACGCCGANCACCNCNGAGACCCACCTTGNCTCA
NAAACAAAAGGCCCANGCCCGGACCACNGCCCCGGACCNGGGACAANCNGGACNANNNCN
GGGNNNAANNGNGGCCGAGNGGAACAACCATATAANAAATTNCCNCGGGNGGGGGGGGAGC
CGAAGAANNAACNAAAAAAAAAAAANCCCNNANANGGGGGGGGGGGGGGANGNACCCNGCCCGG
GCGGCCGNNCNAGAACNAGGGGANCCCCCGGGCGGCAGGAANNCGANANCAAGCCNANCG
ANACCGNCGACCNCGAGGGGG
Sequence 591
CGCCCGGCAGGTACTCAGGTTTTATCTCTGCACTCCAAGTAGGATGAAANGATAAGAGCA
AAGGCTCATGTTTGCCAAGTCTGTCCTTTTGTAACAAAAAACCCAGCAGCTTTATCAAGC
AGAATTCCACCTGTATTTCTTAACTTGCCAGAGCTGAGTCTCATGGCCACCCTTAGCAGG
AGTTGGGGAGGTATTTTTAACAAGGCACATTATCATCTCCCCCACCCAAAGTGGAGCTAT
TGCTAATGAAAAAGATACAATGAGATGTTTATGAAATTATCTGTAGCTATTAATGTCAG
G
TTTTTGAAATTTACTGACCTGGAAGAATACTCATAATGCAATGTCAAGTGAGAAGCAGGA
CAAAGA
A
Sequence 592
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C
AATTAAAAAAAATTTTTTTTTTTGTAAAGACTGGATTTTGCCATGTTGTCCAGGCTGGTCT
G
GGATTCCTGGCCTCAAGCAATTCTTCCTCCTCGGCCTCCCTAAGTGCTGGGATTACAGGC
ATGAGCCACCATACCTGGCCACTTCTTCATTCTTGTTGGCTTTGCGTNCCCGATTTAA
AA
TTGGNGAGAAGTTCCTTCGGCTGGGCTGAGGACCCGNGGTCATGGGTGGATCTCATGGAG
AGAGGGCNAGGACAG

Table 1

Sequence 593
GTGNATTGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACATAACTCCCGCAGGATCT
CAGGGCCTGCCGCCCCATTATGATGATGTCGAGGTTTTCATCCTGCAGCTGGAGGGAGAG
AAACACTGGCGCCTCTACCACCCCACTGTGCCCCTGGCACGAGAGTACC
T
Sequence 594
CGAGGTACAGGTGCGATTCTGGATGACAAAAGAAGATGCTTACTTCACAGAAATTCGAAA
TTTCATTGGGAACAGCAACCATGGCAGCCAATCTCCCAGGAATGTGGAGGAGAGAATGAA
TGGCAGTCATTTTAAAGATGAAAAGGCTTTGTCGAGCGGCCGCCCGGGCAGGTACTTTNT
TTTTTTTTTTTTTTTTTTTTTTAAGGAGCTTTTATTGTTTTAGTAATCTTAACATAACTTAA
AATAAGAGAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCAC
ATTTCTTGGGTCTGTTTCTCTATCTCTAAGGGCAGTCTCAAAACCCCAGC
Sequence 595
TCACGGGTGGCGGCCGCCCGGGCAGGACATGGCCACCAAGTAAGAATGGTTGGTGACAAC
GACAGAAGGCTAAAACAGGAAGGTAATCTTGTGCACCTGACAAATAGAAAGAATAAAGGA
TCAAAATTGAAGGCANGCTATAANAGTATCAAAGAAATTTCTTAAAAACCAAANAGTGAT
TTTGGAAGCACAAAAACTTACNGTTAACTGCTTNCCCAAATGTTCAATGATTGTGGCCCA
AAGAACANTTTGNGGCATTNCTAAANTTTAGAAAAAATTGCNNATNTGCNAAAAAATTTT
TANAATNGGGANACACNACCTACCATTTTTTTTTTTCTAAATCCNAAATTTCTCCCCCCC
C
TCCTTCCCAGAAANAGAGAAATTTTGNTNAAACCTTCAATNT
Sequence 596
TGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATTTAAGAAAAGAACAAGGTTAAC
TAACTAAAAGCAGGAACTCACTTATTTTTTGCTCCCTAGCCAATTAAAAATAAGTTCAT
T
AAAAGCACTTGAAATTATATATTTAACCTGAAAAAAAAAGTTGCTAAAATTCCAATATAAA
TGTAAATATCTTTAACTTGCTTAACCCAGCTATCCCCAAAACAGTGTAAGTGGGGCAAAA
TGTTCAAAAGAAAAATCATCCAGTGCACGTAAGATGGGGCACCCAAGAAGGCTAAGCCTT
CCTTGNGCCGCGTACCCTCGGGCCGCTCTAGAACTAGTG
Sequence 597
CCGCGGTGGCGGCCGCCCGGGCAGGACTTTNTTTTTTTTTTTTTTTTTTTTTTTGAGTTAC
TC
TGATGTTTATTTTAATGCATCTTAGTCCACACAGTTGGTATAAAATCAGAAAATGCAAA
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CAAAAACAAAAGGTCTGGAGTCTTAGCATCAGAAGGGCACCATATATACATCTACAGTTG
GNGGCCAATACAAGTCATTGCCAGACAGTCCTTGGAGGCACAGAACAGCCCAGACCCAGC
CAAGCTCTAGGAACTTCACGGGTCCCAAGGGGTNTAGACCNCTTGTTCTNGATGCTCCGA
ACCCGTAAAAAAAAATGTGGGGAAGTTGATGAAGGCTTTTATGATTTACTCATTATCCCC
GCGTACCTNTGGC
Sequence 598
TCACGCGTCCGGGGAGGTAGTAGAAAGGCGCTGGGTGTTCTAAAATAAGGCTCTCCTGGC
CCACGGCTGACTGTCTTCCTTGTGTCTCTACAGTGGACCGTGACTCTGGACCCAGACACG
GNCTACCCCAGCCTGATCCTCTCTGATAATCTGCGGCAAGTGCGGTACAGTTACCTCCAA
CAGGACCTGCCTGACAACCCCGAGAGGTTCAATCTGTTTCCCTGTGTCTTGGGCTCTCCA
TGCTTCATCGCCGGGAGACATTATTGGGAGGTAGAGGTGGGAGATAAAGCCAAGTGGACC
ATAGGTGTCTGTGAAGACTCAGTGTGCAGAAAAGGTGGAGTAACCTCAGCCCCCCAGAAT
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CA
ATGACTGGCCTACCCCCCCGNGGNCCCCCGGTTCCACCGGGGTGGGGGGAT
Sequence 599

Table 1

ATAGAGGTTCTGACTCCTCAGGAGCAAAAAACATAACCTGAAGAGGGAGGAAGTGGATTT
GGGGTTCACCATTTCTTGGGGCACACTTGATTGAAAACTGANACTTCTGAAGAGAAGGCC
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ATCCAGGCCCAGGAATCCATAACACTGGAGGATGTGGCTGTGGACTTCACTTGGGAGGAG
TGGCAACTCCTGGGCGCTGCTCAGAAGGACCTGTACCGGGACGTGATGTTGGAGAACTAC
AGCAACCTGGTGGCAGTGGGGTATCAAGCCAGCANACCCGGATGCACTCTTTNAGTTGGA
ACAAGGNGAA
Sequence 600
AGGTGACACAATGGCCGAAGGCTCCATGGCGGCTGGCTTCTTCCAGCCCTTCATGTCACC
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CCCTGGCTCCCAAGCCCCTCCTNCCTGGCGCCATGGAGCCCTCCCCACGAGCCCAGGGGC
ATCCGAGCATGGGCGGNCCAATGCAGAGGGTGACGCCTCCTCGTGGCATGGCCAGCGTGG
GGCCCCAGAGCTATGGAGGTGGCATGCGACCCCCCACCCAACTCCCTCGCCGGNCCAGGCC
TGCCTGCCATGAACATGGGCCCAAGGAGTTCGTGGCCCGTGGG
Sequence 601
AGCNCTNAGCTCGACGCGAAAAAAAAATAAATAAAAATTAAAAAAATCTGTGCAATAATTT
TAAAATGTGCTCCCAGGAATAGACACAAATGTTTTGAGTATCTTTTAAGCTGCATTTTC
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TTTAGTGATGCATTTGTCAATTGCACTGAATTTAAATCTGAAAGTCAGAGGTGATTATT
G
ATAGTACTTTTGTATTTTGATATGGACAGTTTATTCATTTGCATACAGTTATTGACTTTT
TCCCAGCTGATTAAAAGATAGTCAAGAAATTCTGCAATATAGCTGCCAAAATAGACAGCT
ACATTTTTATGATATTGTCATCTTTTCTGNTTTTTTTTTTCTTTTTTTTTCTTTAGCTATTT
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Sequence 602
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CTGAACCAGGTGGCAAGACAACAGTCTCACTTTTGCCATGANTGCACGGNGGGACNCGGA
TTCGCCGGAATNTGNACTCCAGCTCTCCAGAGGATGNAAAAGGCTANTGGGCAAAGTTTT
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Sequence 603
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G
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GCAGAGATGTGTGGGAGNCTAGGAAAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTTGTTGC
CACTNGTGNTATTGGGACCCGTGTTAGNATTTGTATGCCAAGAATTTTTCTTGAAAAT
GG
AAAATGNTTTTGNTTTTAGNACCGNAGNATTCAATACNCCGGTTAAAAGGCANGGNAAAT
TNGACCAAAAAGTCTTTGGCTTTTTTTTTCTTGGGTAATTGNTTTCCTAAAANGNTGGTTA
T
NTTGGTGGANCTTTTTTTTAACCTGGTTTAATAANTTTAAAATNTGGCCCCAAATTAATT
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NAGGTTTAAAAAAATNATTAAGGNAATTTA
A
Sequence 604
CCCGCGTCCGAGACAATACAAAGTTACATTTTTGGACCATATTAAAACTGCAAGAAGACA

Table 1

GGGGTCTTACTGAAGATCTTTTAGAAAACTTAAATCCTGTCACAGGATATTTAGACATG
T
GTAGAATGTAGCTCAATTTTTTAAAAAGTAACTGACCTAGAGGGTGAAAGTTGAAACTGA
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GGCAGNATCTTGTTGTANTGTATATAAACGCTAACACCAGGAGTTTTTTAAAAACCANAA
ATTTAAATTTATTTTTANGCTTTTAATTGGAAAGGNTTTGGTTTTTTNTTTTTCCTTTCC
GAAACCCTGGGAGTTATTCAATTAATTTAATTAAAAACAGGGTNAGTTTTTTNAANACC
C
NAAGAAANTTAAGGCCAAGTTNGCCCCCCTTTTTCTTTTTTTTTGNTAACCATTACCTT
G
GNATTTTGGGGAACC

Sequence 605
CTCCCCGCGGTGGCGGCCGAGGTACCCAAATACCACTTCAGGAAATCTGGCCAGATCACC
TGAATCCAAATGTTCTATTAATTCAATACACGTTATCAAGTCAAATCCAAGCAAACGAGA
GTCTCTCTCCACAACGGAGCCATGATACAATGTGATGGTCAAATTCAGATCCCGAGGTTT
CAGAAAATCCCCCAGGAAAGGAGCTAACGAATCCCCTCTCCATCGTAATTTATCCTCATT
AATATCTACTCCAACAAGCAATTCAATGCATGGATTGACTTTTAGCAGCCTTAAGAGTGA
AGTATCACCACATCCCAGGTCTGCAACCTTCTTAGGCTCATGTTGATCCACTAAATTTT
T
AACGAACTGGTACCTGCCCG

Sequence 606
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CCACCGGTGCAGGTCTNTCCGNTCATCAAGCT

Sequence 607
CGGCCGATGAGAAGAAGAAGGGGCCCAAAGTCACCGTCAAGGTGTATTTTGACCTACGAA
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CAGTGGATAATTTTTGTGGCCTTAGCTACAGGAGNAGAAAGGATTTGGCTACAAAAACAGN
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TCTGGANTACNCCGTCCGGACCCTTCGAAGGGGGGGGGGGGCCCCCGGGTNACCNCAAGCC
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Sequence 608
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CAACATACTGCCAAGGAAATCTGATGTGGAAAGGAAAATAGAAATAGTGCAGTTTGCTAG
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TAGTTTTGCCATCCCATATGCCATTGATGTACCTGCCCGGGCGGCCGCTCTAGAACTAG

Sequence 609
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CATTGGCGACCTGGACTCTGAACTCAGGTTTATTCTAAACCCAGTGAGAGGTGAGGGGGA
GTGATGAAAGGGGATCAGCTGTATTTGTGTGTGTGTGTGTGTGAGCACCTGACAAATCTA
TGAAACCCGAGTGAAAGGAGAAATGTTAGATTCTTTATTATTTTATTATATTTATATGGA

Table 1

AAGCTCGACTCTCCCTTTGGTAAGTCCGAAGCA
Sequence 610
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TTTTTAATATGTTTTGATAACTTTAATAACTTCAGGGTGATGTCTGTATAATTTTTAAAG
TGCAGCTCTCTCTAACAAATGTGCCCTACAACTCCTGATTAAACCGGCGTCTTGAAGGTT
CAAAAAAAAAAAAAAAAAAAAAAAANGTACCTGCCCG
Sequence 611
GTGGCGGTCGAGGTACTTANGAGAAATTGGCATGCTTTGCTAATNTTTATGCAGAGGTAA
CCATGTTGANNACATATGTANTGTTGAGAGGNATGTCTAATTTTATGGTCNTAGGAAAAA
TTAAAAGAAAACTGCTGCTTTCCTGAAGTCTGAAATANAAATGTTTACAACTTGACNAGG
ATCCATTTGGTGGCTAGNCTCGCCTTCCAGGGNGGNAAAGAGAATATGCCAGTTCTGTNG
TATGGACTNTTCACANAAGCTAAGGNAGGGGNAGTTCCTTTCTTGGTGGNGACAAGTTCC
TGCNCACTTAATTTTTCCCNTCCTGNCTTCNAAACCTGGGAAA
A
Sequence 612
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ATCCACTCTCAAGCTTCTCATGCAGTGCGTATTGTATTTTCTGCATAAGAAAGGGCTGCC
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G
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GGCTAAAAGCTTCAATATTTTACAAAATATTAATTAATGNAAATTGGTCCCAATTATTAA
GAAACTTTTTTTNCATTT
Sequence 613
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AACNCCACGNCNGGGGGCCAANGGCCNCNGCNGGGNANNNACNNNACGAGAGGCCCACCNN
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Sequence 614
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CATTCACAAGCGTTGNTGGTGGGGGTGNGNATNGTGTGNGCTAAGGGNCAATGGGCNGAA
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TTACAANCAGGGTGCCCCANAAAAAAGGNACACCACTANTCAATACCCNCCAATACAAAA
AGAAAACCAATNTTCTTCCNCCANTACCTAAAAAAGGAAACCCGGGGTAAAC
Sequence 615
CGGTGGCGGCCGCCGGNCAGGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTAATTTTCCATGTAT
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Table 1

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Sequence 616
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TNTCTACTTTCACATCAAGTTTGAAGAATGCATTTCTCTTGNGGTATTCTGTTTTTTGAA
CTTACTTCATTGGAGAAGCCCCTTGATTTTTCTTCCTTTATACCAGATCTGGCTTCACG
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AAGCTGCATTTAGGTACCTGCCCGGGCCGGNCG
Sequence 617
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CCCAACCGTGCAANTTGATGGTACCCCAAGCCCAAGCGACTGGNAAGATGTCTTTGGNAA
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AGGTGGCAACCGGGACTTGGGCCGTTCAANACCCGTGGACCGTTCAANATTCCCCAACCA
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NTTTTTAANAAAAAAA
Sequence 618
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Sequence 619
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AAGATAGGCTGCAGGAAATGTAACCTATGAAATTTTCTCAAATTAGCTTTCAAACACACA
CAAAAAATTGCATTTGTTTGAGGAGCAGAATGTAACTTATATTAAAGAATAAACTACTA
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Sequence 620
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GATGGAAAGAGAAGAAATTAACTTAATTCTAAGAGCCAAATTTACTCAGAAGGTTTAGAA
ACACCAAAATTAACAGCCAGTTTTCTTGATTTTCTTCTTGAAGAAGAGATTGGTGTTGC
T

Table 1

ATGGTGAGATATACTATGGCCTTGAGAGGCAGTTTCAACTTGAAAAGAAGATGCAGGTTG
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ATTCTCAAAGTTCTTTTTGGTTTGCAACCCTTTTTTTAGTAACCTGCAGAGGTATAAAC
T
GATTGTGCACACCCCCTGGTATTCCCCCAGCCATGGGCATGGTCCCAGAATATAAAGTAT
GATGGAAGGGCTTCCAGG
Sequence 621
GGTGGCGGCCGAGGTTAAGGACGCCTGCCCATGACAGAGCCTCAGGAAATCGCGATGACA
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AACCCTGTACCTGCCCG
Sequence 622
CCCGCGGTGGCGGCCGAGGTACATTTATTTAACATAAAAGGACAATAAGTTTACTTTGTA
TCTGAACTCAAAACAAAGTAGTTGTATATTTTAACATTCAAAATTGGGATTTCCCAATG
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GACACATCATGAATGCAAACCCCTCCAGCCCATCAGACGCCAGGCTGCCTACTGGTAATC
TGTGTATAGTATATAAACATGTAAAAATAGGTTGTATTTTACTCTATGTATGATGCTAAT
CAATGAACACTTTATTTATTTTACAGAGAAAACTTATCTGTGAACTTTACTATATATCTG
NTATTTTACCTTTATTTTTTTTTTTAAATAAAAAAGGGGTTT
Sequence 623
CCGCGGTGGCGGCCGCCCGGGCAGGTACAGCCATTGCTCTTTGAGTTTGGTCTGGCTAGC
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Sequence 624
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Sequence 625
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ATCTAAATTTCTGCCAATGAGGACCAATCGATTTGTTCTCTCAGTGTCATCCTTCCAGC
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CACTGGAGTCTCCTCNATCATAGAGCTCATCCCGCGTACCTCGGC
Sequence 626
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CAGATGTATTGCTGTCCTTGAATATTAGCCCATTTGAAAACGCCTGGGAAGTTCAGCCAT
CAGTATGTCAGTACCTCGGC
Sequence 627
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TGTTTGTGACCTGTTTTAAATGAACCAAACCAAATCATACTTTTTCTTTGAATTTAGCAA
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Table 1

NNNNGGGGTNCTCCCTGATAAAGGGGGAATTTCCNTGCCCGTCCACGGGGGGGTTGNCCCT
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ACCCTTTTTTTTTAAAANGGGGGGGNNTNNNCCCCCCGGGGGGGGGGGGGGGGANTTNCCCGGG
GGGNTTNTTTTTTTTTTTTTTTNNAAAAAAAAAGGGGGGGGGGGGNCCCCC
Sequence 628
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AGGGAAGTGTTTATTTCGCGTCCGCTTCTGTTCCTCCGCGCCCCTGTGCTGCTCCGACTC
ACATACTCGTCCAGAACCGGCCTCAGCCTCTCCGCGCAGAAGTGCCGGAGCCATGGCGGT
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CNTATNGATAC
Sequence 629
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GTGGGATCTGCAATTGCAGCTACTGTCGGAAGC
Sequence 630
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G
GCAGAGCAGATTCGTTTAAAACTTTGTTTTTCTTAAAAGCTTACAGTGTTTGGCTAATT
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TTTAAACTGTGTGAGATATTAACCAGCCCGCCCTGTTATAAAATCAGGAAATCCAAACAG
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AATAAAGAAATAAAGGAAGTAAAAAGAAAGGAAAGAAAAAAAGG
Sequence 631
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GCTAAGAGCTCAGACACTCTGGCGGGGGCACATGTAAAGATTCATCGTTGCAACGAATCT
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TTTGTCTTGGGCCCTGTAGGGACTACACTTCACCTCCACAGTTGTGACAATGTTAAAGTC
ATTGCTGTTTGCCATCGTTTGTCCATCTCTTCTACAACAGGTTGCATCTTT
Sequence 632
AGGTACCACACTCAGGGCAGTTTCCAGCTCCTCTCACAAACAGTAAATCTACACAACTTT
CACAGAGAGTGTGTCCGCACACATTCACCATCAGCTTCAAGGAGGGGTTCCGATATTTGG
TGGTCTTACACCGAGGGCAACCCTGATCGTCCATGGCGGTTTCCCTCCTACAGACTCTCG
CAGGCGCCTGTTTCAGCCAGAGCCACCTACAAGCCCCCTCCCCGCGTACCACCACACTGT
CCCAAATTACCTCTTCATTACCCAAATCAAAGAATCTTTCTGTTTTCCCAATCCTCAAA
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GGAATGAAGAAAAACCAAAGAGCAAACTCAAAAGATGATTTTTTACCATAAACCTCAAATG
TGGCTTAACAAGTACCTGCCCGGGCGG

Table 1

Sequence 633
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AGTGGCTGCAAGAACTGGGATTCCCTCTCCTTCTCTCTCTTCCCCTCTCCCCCGCGTACC
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Sequence 634
GAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGAAAACCACTTCCAGAGTCTAAAG
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CAAGGTCTCTGTCTGTAGTTACTGGGATTATCCAGATACACTATCAATGATACAAATTC
A
TAGGAGTATTAATGCATTTCTTTAAACACAACTTGATTAAGAAGCAAATATGTTAAGCA
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A
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CATCTGTAGAGGTAAAATTTCTATATTACCAAGCTCCAGAGGAATATGATATTTTACAGG
CACAATTTTCTGGCTGTAGTCCCTGGGGCATTTCATTTGCTGGCCTCCA
Sequence 635
NCTCCCGCGGTGGCGGCCGAGGTACAGATGATGAAGCTTCCAGAGCTTATCTGTCTCTTA
GACAGAACTCACATAAACACACAAATACAAGAGGTTATTTTCAAGACACACACTTGCAAG
TAATCTTTCTATAGAAATGGCCACAGCATTATAATATTCAAAATATGGAAGATTGCAGT
C
TGAGGATTTTTANGAAAAAAAAATCAAAGGACTTGCCAAAAGGATAACTACATAACAGAT
ATGACAATCTACAGGACAAAAAGACAACATGTCACCAAATATTGTTCATACAACAGCGTT
AATGGAAAACAGTAAAACACCTTTTAGCAGTGTGCATGTTAAGTCTTTTAGTAAGATTA
T
CTGTAATGAGGTTTGAAAGTAAATCACTTAGTAGACAAAGTAAACCACCACAGAACCAGG
AATAGCACCCATCACTGCTGCTTTGTCACTCCAGAAAGCTGAAAGTCAACCCGAACAATG
AAAAAAAGTCAAAGAAGCATTTCCCTTTGAATTCAGTCCTAAAAATATGAATGCCTTATA
ATTAATTTCAAAATAAGTATCTTACAAGTGTTTCATGAAACATTGGTTTT
Sequence 636
GTGGCGGNCGAGGTCTAAAGGGCAAGGTTCACCACTACAAAAAGGAAGTTGTCTAAAAGC
AAGAATTCAATTAACNGCTGGGTAAGAAAAGTCAAAACACTAATGAGTTGTCCATGAAGC
CAACTGCTAAGAACGCGCTCAACTATACCGCCGACATTGAAGACACTACGCACGAAGCCT
TACTTGGCGAGTCTGAATTTCTATTAACTAAGGGCAGAGTGAGGGAGAACAAAGAGCCTA
CTTCCGTAACATTTTAGTATCCAGATAGTACCTGCCCGGGCCGGCCGCTCTAGAACCTAG
TGGGATCCCCCGGGCTGCAGGGAATTTCNTATATCAAAGCNTTATCGATACCCGTCCGAC
CTTNGAGGGGGGGGGGCCCCGGTACCCCAGCTTTTTGTTTCCCTNTTAAGNGAGGGGTTAA
ATNTGCCGCCGCTTGGGCNTAATCATTGGGNCATAGGCTTGTNTTCCCTGNGGTGAAAAA
TTGNTTAATNCCGCTTCACAANTTTCACCACCAAACCAATACGGAAGNCCGGGGAAGCAA
TAAAAGGTNNTAAAAGGCCTTGGG
Sequence 637
AGCTCCCCGCGGTGGCGGCCGAGGTACAGGAAAGGGAAGCACAGTTTGGAACAACAGCAG
AGATATATGCCTATCGAGAAGAACAGGATTTTGGAATTGAGATAGTGAAAGTGAAAGCAA
TTGGAAGACAAAGGTTCAAAGTCCTTGAGCTAAGAACACAGTCAGATGGAATCCAGCAAG
CTAAAGTGCAAATTCTTCCCGAATGTGTGTTGCCTTCAACCATGTCTGCAGTTCAATTA
G
AATCCCTCAATAAGTGCCAGATATTTCCTTCAAAACCTGTCTCAAGAGAAGACCAATGTT
CATATAAATGGTGGCAGAAATACCAGAAGAGAAAGTTTCATTGTGCAAATCTAACTTCAT
GGCCTCGCTGGGCTGTATTCCTTATATGATGCTGAGACCTTAATGGACAGAATCAAGAAA

Table 1

CAGCTACGTGAATGGGGATGAAAATCTAAAAGATGATTCTCTTCCTTCAAATCCAATAGA
TTTTTCTTACCAGAGTAGCTGGCTTGNCTTCCTAATGATGATGNATTGAGAATTCAGCT
T
CTTT
Sequence 638
CGGTGGCGGCCGCCCGGGCAGGTACGCGGGAGAAAACTAAACCTTCATTTACTGTGAACA
TCTTCTGACTGTGGCTTCCAGATGCTAGTTTACAGAACAACCACACAGCAAGACCAAGCT
TATGCTGAGTTGACGGAACAATGAGTAAACATAAGGATATTACTGTGACTTTGAAATTCT
GAAATTGTTCTTTCTTAACTTTTGCATTAAAATCACATTTATTTTATAAAATAATGAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Sequence 639
CCCCGCGGTGGCGGCCGCCCCGCNCGGGTACATGGCCCTTAATNCCATNAGATTTGTAGA
TCTTAACCACGGCAGGTCACCGAGGCCTCGGAANTCCCTTTNAGCTCCAGCTTTACCCAC
ATCAGCTGCTAGACGGGTACCT
Sequence 640
AGACGATTGAGCTNCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGGGCTGTCTCACCGG
TGAGACCTGGAAGCGGGCGAGTCTCGTGCTGTGTCGGACCTGCAGTCCCTGGCCTTCCGC
CACCATGGAGTACCT
Sequence 641
CCCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGTCTTCAGAAACCAGGCTGCTTTCAGG
AACATTGCTGTGGATTCCCAGCTTTCAGACAACACATGACTAAGACAGAATGAGACCACT
CTAGTTGCCTCATGGGAAACTCGGGAAAAGACTGCAAAAACAACATTGTTTCTCCCTTTG
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AGCAAGATGGCTGAACTCAATACTCATGTGAATGTCAAGGAAAAGATCTATGCAGTTAGA
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A
Sequence 642
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TATTAAATGGAGATGATTCCATCTTGTCTACAGACACTGAAATACCTGGCTAAAAGCCGC
CTTTCCTCTGCGCTGCTACCAGCCCTGTCACAGGTCCCGGCGCTCTACCTCCCCGCGTAC
CTGCCC
G
Sequence 643
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AGCGCCAAAAGTGATTTTATACCAAGGGNCCATNCATACAAATAAACAAAATCCTATCCT
CTTCTTTCTATATNNTNTTTCTTACATTTCTTATACAAATAACAGAATGCTTCATTTTAT
TCACTTCAATAGGACAAAGTCCTTAAAGAAAGACTGAAAAGAGCTGATAATCAAAATCCC
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GGAAAACATTCTCAGTAAATTGAGCATTTGAGTCTACAAATGTCTTGAAGCACTCTGGCA
AGTTACATGTATCCCATGTTGCTTTTGGNTTCCCATCTCTTCTTTGCTTCAAACCCCCA
T
GCAAGNTTTTTNTTTTTTCGGGCAGNCTGTGAATTTTCAACCTCCTTTTT
Sequence 644
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GTGCATTGTTAGAGGTGCACCGGGAAGGGAGCTTGGTTTCGGACCCCAGGACATCCTGTC
CGCAAGCAGCTGCTACTTCTTGGGCTTCTCTAGAATATTGAGGAATTTCCCCCGTGTCAT
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Table 1

CATCAAATTAGCCGTGGTGAGACTCCCCAGTTCTTTCAACATGTCGATGTCATCACGTTC
TATCTCAGCCATCCATTTGGGTGGAGAACTAGTAATAGGACTTTTGAAGGAAGCTGCAAA
TTCAGCAACACCTGGTAATTGTTCTGGCCAAAGATCTGGTGAGGCACGGTCAAGTTTTTC
AAAACTTAGCAAAGATGCTTCCAGATCTGTCCCCGTCTGTGGGAGACGCCATCTTTCAAC
CCATGTCACGTCCCCGCGTACCTGCCCGGGCGGCCGCTCGAGCCAGGAACCGTAAAAAG
Sequence 645
CCGCGGTGGCCGGCCGCCCGGGCAGGTACTTCAGGGAGGCCTATATATTGGCACCCAAGG
AATGCCAGGACTGCCACCTGCTGCTCCAGCGTTAGCCTCACTCGTGTGCTTACTCACTTT
GACTGCCTTTTTGTCTATTTCTGGGAGGTTGGTAGAATGAAAGGGATGCTCCAAGGCAAG
CAGATGGCCTGTCCACCTCCTATATATTGACAGTGCCAATGAGTGTAGAGTCTTGCTACA
AGAAACAAAGTCATGAGAAATGCCAGGCTTCCTGTTACACCCAAAGACTGCTGGCCCTCC
TACTCTATCCTTTAGACCAGAAACTTTTTCTTCTAAGCACTTGCCTACCGGGAAGGTT
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GGAGTCTTGTTTTACCGTACC
T
Sequence 646
TCNCGCGGTGGCGGCCGAGGTACCGGCCAAGCCTGGTCCCCTTCTTGTTGGGCACTGTGT
ATGGGCGGAGAAAATCCANCTTGTTCTTGCTGATGACGCAAAGGTCAATGTTGCTTCCGG
AGCCCAGGTTCACTGAAGATTGCCANNTGCCGATGGCTTCGCTCACCANGATTCTNGGCT
TNCTNCTCCTCCATTGTCTGGCCTAAACTTTATCTTCAAATACAGACCATTGCTTGCTC
A
ANNGAGACCAAGAAACCCATNNGGTGACCACTAAGGGCAACTTATCAGNTTTGATTNCAT
GAAGGGATAGGATGTCTTGTATTAGGGTNGGAGAGTCCCAGGTAAATCTATGCTACTNCC
CCCCTTAANAAACCTNAGNNTCTNGCAACCCAATTNTAAACNNTTTGNATACNCTTGAAAA
AAGGCATTCTGNCTTTTNAGCNATCCGATTTGGCCTGTNCACAAACTCTGGGGGAAAGAC
TGGTCCAGTTGNNAGAAGGGGAGTTGGGAGCNTCCAGGTTTGGAAAAGNAAA
Sequence 647
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TACACAATATGTCAAAATATTAAAGCTTTTTTTTTAAATTGGGAACNCTCAGGATATTGG
G
ATAATTAATTAGGCAATGATNCAAAGATGTTTTGTTTTAAAATTCANAACCCNCCAAAG
G
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C
CNTNAAAAAAAAAGGGGGGCCNNCCCCCCNTTGGGAAAANNNTTTTTTTTTTTTTNNNNGCC
CCCCCCNNTNTTTTTTTTNCNGGGGGGGGTTTTTAANAAANGGGGGGGNAAAAAAAAANNGNGN
GTCCCCCCCCTCNNNNAAAAAAAAAAAAAAANANGGGGGGGGGGG
Sequence 648
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NATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCNGGGGGAANNCCCCNTTNTNNGGNNTTT
CCCCCNNNGGCNCCNANANGTNAANCCNNCNNANCCNNGGGGGNNGGGGGNCCNCNNNNCCC
NNNNGNGNNNNAANNNGGNTNNGNGGGNGGGGGNAAAAAAGGGGGGGGCCNANGGGGNCCCC
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NAAAAAAANANGGGGNCCCCCCCNGGGGGGGGGGGGNNAATNTAANANAAAANTTTTNNTNCC
CCCCCCCCCCCCNGGGGGGG
Sequence 649
TTGACTCCCGCGGTGGCGGCCGAGGTACACGATAGGAAGAATGTATATTCTGTGGTTGTT
GGGTGGAGTGAATGTCTATGAGGCCCCTGACTTCTTTCATTCAGGAACACAGATTCAGAG

Table 1

CTTCTGCTGTGCAGTAGGGGGCATCAATAGTTCATTTTCTTTTTATTGTCTGCTACCAT
T
CCATTGTATGGATTCAACCTAGTCTGTTTATTCATTCTCCCAGGCTTTCCACCAGGCC
AT
CTCTTTCACTTCGGGGGCACCTTTCCCAGGGAGATGAAGAGACACAGGTTGGCCTCTGCT
GGGACTCCACATGTCTCCCCGCGTACCTGCCCG
Sequence 650
TTGACTCCCGCGGTGGCGGCCGAGGTACTGAGTGGGGAAGAAGGTAAGAAACACGTTGAT
TAACACCCTGTGTTCTGGCAGGTGGGATCAGCAATATGTAATCCAACTCACCTCCATGTT
CAAGGATGTCCCTCTGACTGCAGAAGAGGTGGAATTTGTGGTGGAAAAAGCATTGAGCAT
GTTCTCCAAGATGAATCTTCAAGAAATACCACCTTTGGTCTATCAGCTTCTGGTTCTCT
C
CTCCAAGGGAAGCAGAAAGAGTGTTTTGGAAGGAATCATAGCCTTCTTCAGTGCACTAGA
TAAGCAGCACAATGAGGAACAGAGTGGTGACGAGCTATTGGATGTTGTCACTGTGCCATC
AGGTGAACTTCGTCATGTGGAAGGCACCATTATTCTACACATTGTGTTTGCCATCAAA
TT
GGACTATGAACTAGGCAGAGAACTCGTGAAACACTTAAAGGTAGGACAGCAAGGAGATTC
CAATAATAACTTAAGTCCCTT
Sequence 651
GACTCCCGCGGTGGCGGCCGAGGTACTGCGTTATGCAGAGGTGTCCAGCCCCCTTCCTCT
TCCTGGAAATTAACATTGGCTCCACCTTCCAGCAATTGCTGGACCAGGTCAACATCTTCG
TTTTGAACAGCTTTAATCAGCAAGTGATTGTCTTCCACTGCAGCCCTTCTACCGCTGGAG
GACGTGGGTCCCTCCTGGGGGTTGTTATGATCCCTGCTCTCCATGACGGTAAATGCCACC
TGCTACCACTTTTAGCCTTTTCCTTGAGAAAATGCAAATTTATCTCCTAGCACTTAATC
A
AAGAAGCTTTGAGTGTAAATTGGGATTCTCTGGCAACAGAGCAGCAGTATGAAGAAGGAA
CAATGTTCTCAGTCTTCTGACATTCCACCTGCTCAACTCAAGACGTCTCAATTATTCCT
T
TGGCAGCCGCAAAGCCTGGAAGACTGCTTGCAGCCCGAGCAGTTTCCTCCTGCTGCCCCC
GCGTACCAGTGAGGAAGGA
Sequence 652
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CTCCTGGAGCTGCAGGCGGCGGGAGGGGCTACAAATGCTTGACTCAGTGATGCAGAACCT
TTCAGAGTTAGCTGGAAGCCACAGCCCTGCCTCTTGATGCAGCCTGGATCCAGCCGGTGT
GAAGAGGAGACCCCTTCCCTCTTGTGGGGTTTGGATCCTGTGTTTCTAGCCTTTGCAAAA
CTCTACATCAGGGATATCCTGGACATGAAGGAGTCCCGCCAGGTGCCAGGTGTATTTTTG
TACCT
Sequence 653
TCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTGTGAACTGAGGAATTATAGATAAACCTT
AGGTCAAATCATTTCGCAATTGCATTGGTGGTATTGAAAAATGATGAGATTTCTCTGACA
GAGAGCTTTGTCCTAGTTTTTGTTCTTCATAGGTCAAAACTGGCAATATTCTCTTGTCT
G
CAAGATAAAGTGTTTGTGCTTCTATCACCATATGCATGAACATGTAAGAATCAGATACAA
TTTCTGCTTCATCAGTTTCACATGTTCATGTTGTCACTGAAAAAATGCATCTACTGTTT
A
TAGCTCCCAAGGAGACCCCAAATCCTTTTTTTTCTTTTGAGATGGAGTCTTGCTCTTGTT
G
CCCAGGCTGGAGAGCAGTAGCGCGATCTCAGCTCACTGCAACCCCCACCTCCTGGGTTCA
AGGTGATTCTCCTGCCTCAGCCTCCCCAGTAGCTG
Sequence 654
GACTCCCCGCGGTGGCGGCCGAGGTACCTGTTACCCTTTCAAAAGTAAGTTCTCCATCCC

Table 1

ATAAAGCCATTTAAATTCATTAGAAAAATGTCCTTACCTCTTAAAATGTGAATTCATCTG
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AGTATTGTTATTGGCTTTTCGTATTCCTCTTAACGTGAACCGTCTGTTCATTGTTTTTAC
CTGTTTTCGTTTTAGCAAGTAAGTACCTGCCCGGGCCGGCCGCTCTAGAACTAGTGGGAT
CCCCCGGGCTGCAGGAAATTTCGATATCAAAGCTTAATCGATACCCGTCGACCTCGAGGG
GGGGGCCCGGTA
Sequence 655
TNCCGCGGTGGCGGCCGAGGTACGCGGGGGGAAGTCGGCCATGGACTGGAAAGAAGTTCTT
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AAAGATGAAGAAATGGATTTATTTACAAAATATTACTCCGAATGGAAAGGAGGTAGAAAA
AACACAAATGAATTCTATAAGACCATTCCCCGGTTTTATTATAGGCTGCCTGCTGAAGAT
GAAGTCTTACTACAGAAATTAAGAGAGGAATCAAGAGCTGTCTTTCTACAAAGAAAAAGC
AGAGAACTGTTAGATAATGAAGAATTACAGAACTTATGGTTTTTGCTGGACAAACACCAG
ACACCACCTATGATTGGAGANGGAAGCCGATGATCAATTACCAAAA
Sequence 656
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ACAAAGTTTGGTCTGTTGCATAATTGAATTTTTAACACTCTTATCCACAACAAACACTTT
TTCGTGTCCTGCTGTGTAAAAGACATCAGATATATTACAGATTTTCAAACAGGTGAGCAT
NCTTTTACGAGCTGGGCAGGTGGGGAGTGGCGTGGTTTTG
Sequence 657
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTCCAATGAAGAATTTCTTCATTCTGA
TCTCCTAGAAGACAGCAAATACCGAAAAATCTACTCCTTTACTCTTAAGCCTCGAA
Sequence 658
CACGGGTGGCGGCCGAGTACCTTGTGGGCATTAGGTCANTNTTGTTATACACTTTCACAA
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C
GGGGGTAGCGGTCAATTCCAGCCACCANAGCATGGCTTGTAGGGGCNATCTGAGGTGCCA
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ACCACNCTTCCCAGGTTTCATGAACTTGCCCATTTCGGCAGCAACCACCCCGGGGCNCTA
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Sequence 659
CTCCCGCGGTGGCGGCCGCCCGGGCTGGTACGCCCAAGGCATTTAATGCCCACAGTAACA
GGGCTGTTTGACAGTGGCAGAAGAGGACGGGACTAAAGTTACTTTGTGCTGAGAGGGGGA
AAGAAGCACAAAGTTTGGTCTGTTGCGTAATTGAATTTTTAACACTCTTATCCACAACA
A
ACACTTTTTCGTGTCCTGCTGTGTCAAAGACATCAGATATATTACAGATTTTCAAACAG
G
TGAGCATCCTTTTACGAGCTGGGCAGGTGGGGAGTGGCGTGGTTTTGATGGAGTGAGGAG
ATTTGGTTGAATGAACGCTAAGATGGCCAGACNCACCTCTTNGATCTCAACTCTGCAGCC
TGGG
Sequence 660
CCGCGGTGGCGGCCGCCGGGCAGGTACTATGACCTGAAGAGGGCAGAGGCCATCACTGTT
GGTCCGGTCTCCACCTGGGGAAACTGAGGTTGCACAGTGTCTCTGTGGTGACGAGCAGGG
CTTCATCCAGTGCCTCTGTCCCCACCGAGGGGACTATGGGAGACATGGAGGGTGTGTGAG
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Table 1

CGGTCTCTGTCTTGGCACCTGCAGGAAACAAGCTCCTACTTCCAGAAAAAGTGCTCCTGG
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AAGCAACAGCCATGCATTCGGGGAAAGGAACTTCAGTGTTGTGTGGCTTAGTCTCCAGAC
CTAACTTTTCTTTGGTACCTCGGGCCGNTCTA
Sequence 661
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGAGACGACTTTTTTCTCACCATGAA
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TGGATGGACTCAAGGCAAAGGCCT
Sequence 662
GAGCTCCCCGCGGTGGCGGCCGCCCGGGCNGGTACTTTTTTTTTTTTTTTTTTTTTTTT
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NCTNGGGGGNGGGTTTNAGGGGCCCNNGNCCCNNGGCCNCTNTAAAACNAGGGGANCCCCC
GGGCNGGNGGAATTCGATNTCAAGCTTNTNGANCCCNCCCCCCCCGGGG
Sequence 663
TCCCCGCGGTGGCGGCCGAGGTACTTGTGGAAGGTAGTGACCAGCACAGCCNGCGCCTGC
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GGAGAGCAAGGCCCCCGCGTACCTGCCCG
Sequence 664
TNCGGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCGGTATCTGTATCGGGCCNTACTGG
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C
CACCCCAGAATCTAGATATCTTGCTCAGATTGGTGACTCCGTCTCATTGACTTGCAGCAC
CACAGGCTGGGGAGTCCCCATTTTTCTCTTTGGAGAACCCAGATAGGATAGTCCACTTGN
ATGGGGAAAGGTGACCNAATGGAGGGGGACCCACATNTTACGCTTGACAATGNATCCTTGG
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ANGGNAAATTG
Sequence 665
TCCCCGCGGTGGCGGCCGAGGCTAACAAGGAAAGCCCCTGGAGCTCCTGTAATAAGAATG
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TGATCATCATAGGCTTATGTCTTGCTGCAGTAACTTATGTTGATGAAGATGAAAATGAAA
TACTTGAATTATCATCAAACAAAACATTCTTCATCATGCTGAAGATTCCAGAGGAGTGTG
TTGCTGAAGAGGAATTGCCTCACCTGCTCACCGAAAGGCTCACAGATGTGTACCT
Sequence 666
GGGTGGCGGCCGCCCGGGCAGGTTTAATCTCAGGTCTCCCTCATACACTTCTCAGCCTCA
GCACCTAACCCTCACACAACACTCCAGTATTGATGCAGTCAATCTTGTATAACATTTTT
T
GAATGTCCAATGTGCAAAGCACGATGTTGGAAATTATACAGAGGTGAATAAGACAAAAAC
TCTTGCTCTCAAAGATGTCAGTCTTTTTCTTTGCAAGGATAACACATGTAGAGTAAAAT
G
CATAAAGGGGACTAATTTTAAATGTACCT
Sequence 667
GGCCGAGGTACTGGAGAGTCGGCTTTGACCATGGCCTCAGCTCAGCTCCAGGTTTGGAGC
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AGGCCTGGGGCTGAAGCCAGCGCTGACGGAT

Table 1

Sequence 668
GGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTCTGGTCGAAAATTT.
TT
GTTGGAATTTTAAAGAAAAGAAAGGCAAAGTAGCACTCAGATGGCCTTTTTTTGTAAAGT
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G
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GCAGATTCCCAGAAACTTTATGTATTTGGGAAAAGTAAAATATACAACAGACATATCCCT
GCCCTGATTAAGAGGGTAGATAAAAACAAAACATAAAACAATTTTACTTGAGATAGTAAT
AAGTTATTTGAAA
Sequence 669
GGATCAATAAAATCTGTGTGTTACAGCGGCAGACTGAAGGACGGGTGCCTGTTTTCAGCC
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AGCAACTGACGACAGATGCTGCCCGCATTGGTGCAGATGCAGCCCAGGTTGGACTGAGTC
ACTGCCTTGCTGCCCCATCCCCATCCCATCATGAGAAGCTAGGCATTACCATTCCTGTCT
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A
GATCCAGAGCTTGAATA
Sequence 670
TNCGGGTGGCGGCGCCCGGGCAGGTACATTCTTTTTTTTTTTTTTTAAACTTTTAGGGT
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TGCCTATTTGCATCCTAAGGGCAAAAGGCTTAGAGATATCAANGGGGCTAATNTTTTATN
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GCAATTGAACTTGGAGAACTTCAGCCACCTATGTTTTGATCTCCACCCAATGAGGGCTCT
CTTCTTAATGGCAAAAAAGTAATTTTCAGCCTCAAAACTAAAGGGCAAAACAAAATGGGC
ATCAACATTCATAATTTTTGTCAAAATAGCACTTATCNAAAAAAAAAAAAAAA
Sequence 671
GCTCCCGCGGTGGCGGCCGAGGTACGCGGGGTCTTCTCATGCTCCGTGATGCATGAGGCT
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Sequence 672
AGCTCCCGCGGTGGCGGCCGAGGTACTCTTCTGCACTGTTCTTTCTTTCTAATAAAACTT
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CAAGGGAAATCATTTAAGAAGTGTCTGGTATTTTTCAAATTTCTGTCAGTTGTTACATT
T
GTGATAAGTAAATGTTTAGGAATAAAGGATGGAGACATGCTTATTTTATTTAACTCCCC
C
CNAAAAAAA
Sequence 673
GGATTGAGCTCCCCGCGGTGGCGGCCGTGCCTCTTAATCATGGCCTCAGTTCCGAAAACC
AACAAAATACGAACCGCGGTCCTATTCCATTATTCCTAGCTGCGGTATCCAGGCGGCTCG
GGCCTGCTTTGAACACTCTAATTTTTTTCAAAGTAAACGCTTCGGGCGCCGCGGGACACTC
AGCTCCGCGTACC
T

Table 1

Sequence 674
AGCTCCCGCGGTGGCGGCCGAGGTACTGAAGCCCACCAGTGTCCGGATGGAAGTCTGCAT
CTGAGGTTGCTCAGTGTCCCGGTCATTCATTTACACATTTTTAACTTGCATTAAAGAGCT
G
TTCTTTTCTGTGGCCTAGACTCTTTTTCACTGATCTCAAAATAAACTGGTTTTTTTTCAAAA
AAAAAAAACAAAAACAAAAAAAAAACACAAAAGCTGCATGTCTAAAATTACATGGAGTTAG
TGTCTATTCTTTTTTCCCCTTTTGCAGCAACTTACACAGCATTTTTAACACCTTTTTTTTTC
TAGTTTTTTTGTTCGGTTTTGTTTTCCATCAGGAATTTGAGTTCTCTCTAACCCAGCTTA
CTGTGGGACATAGGAAAACTCAGTAGAAATACCTTTGGTGATCTTGTTGAGTTTAAGTCT
GATCTTGGATCTTAAACTCA
Sequence 675
NATTGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGCTGTAGTGGCTTCGTCTTCGGT
TTTTCTCTTCCTTCGCTAACGCCTCCCGGCTCTCGTCAGCCTCCCGC
Sequence 676
NCCGCGGTGGCGGCCGCGAGAGCACATGATGACCACGCCATCGTCCAGTATGAGTGGGCA
CTGCTGCAGGGGGACCCGTCAGTGGACATGAAGGTAACGCATGTTGTCACTGCTGGCAGC
TAGGTCTGCTGGGGCACACCGAGCTGTGAGGGAGGGAGGCCAGCATGCGGTGCTCCTGCC
CG
Sequence 677
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A
CTGTAGCAGGTAAACACTACTCTAACGTGGAGAAATGAGCTTCATGCTGAGGTAGTGGTT
GCCTTANAGCTGTTNTTNNTNCTGNANAAAANCNAAANGGGTTTGNNTCCCNGNTANNNTN
NAATTTNNTNTTTGNCCTAAAGTTTTCNTNTCCCNCNNGCCCNANNTTCCCCGGGGNAGN
TTTCCCCTTTTCCCGGGTTTTNAAAAANNGGNGGGNGGGNTTTAACCNGGNCCCCCCGGGN
CCCCCCCANNTTTTTTTGNAATTTCCCGGGNCGGGCCGTTTTTNAANNAANANGGGGGTCC
CCCCCCCNCNCGGGNNNAAATTNTNTTNAAANACATTTTTTTCCCCCCCCCCNCCCCCC
TCCNGGGGGGGGGGGNNGGCCCCCCCCCCCTN
Sequence 678
GCTCCCCGCGGTGGCGGCCGAGGTACTTGTGGCATGACGTCGATGATCGAGTTCANGGCT
NTCTCCANCTNGGNCNACATGATGCCCACGGNCTNGCCCCACCAGGTCTTNTGAAAGACA
GNTGACANGAGACATCCNCGCGTACCTGNCCG
Sequence 679
NCCGCGGTGGCGGCCGCCCGGGCAGGTACTGGTGTTGTGATCGGAACGTGTCGATCCCCT
CTTCTCATCACTGCTGCTCCAACTGGATTTATTACTCCGGGAATGGTCTGAGGGGGAAAA
CCAATGTGTTTAGCGTGCCTGCCCACCTGCGCCTGAGCACAACTATCCTGCAATCTGACC
TGCCCCTCCTGCACAGGAAACCACCTTCCCCTCCCAATTGATGGTTCAAACACTGCCACC
GCTGACTGCCCTGCATCTGTGGGTCTGTAGAACAGAAAGGCAGAACAACTTATTTTTTAG
GATTTAACGACAACCGGTTGAAAAAAACCGGTAGGGGTGTCNTGCTCACAGAGAATAAAG
ATTTGTAGAAAAGGNGCTGAACTGCCAAGGAAGGCATTTCTTGTGCCGTGTCTGGAACCG
TGTATCCTTACTACATCACTGAACGACACCAAAGCACCCCATGCACTTTTTGGGTCCAAC
CT
Sequence 680
NATTGAGCTCCCCGCGGTGGCGGCCGAGGTACAAGGGGAGGTAATGATGGGAGCTCCACT
CCTTGGACCACCAGCTGGTTCTGGACCGTATCCCCATGAATCTGTTTGAACGTAAGGAGG
AAGTCAAAAAAGTTCTTATTTAGGGTTTCTTTGAGATGTGGGGCCACTTCCATTCCCA
CC
CGGCACAGGTAGGCACGGGCATACACCGACACTAGTGGGTCTCCGATCCCTCTGATCATG
CATGTCAACCGGGGCAGGCACTCTGAAATTCCCGTTTTGGAGAGGAATTTGTTACATTTC

Table 1

AGGATGGATGCCTCCACGTAAAATCTTGGAATGAGTTCCCTGATGGAGGCAATCTTGAAA
AACCAATTTAGGCATGTTTCCTTGGCCGTGTCATTTGCATTCTCTGGAGAAAAGTGAT
CT
GGTAAGACGCTGCGGCTATCCACACACATGGAAAAGATGC
Sequence 681
GCGGCCGAGGTACCCTAATGTAGTAGTAAATTTAAGGCCTGTCGAGGAAATTTTAACACT
TCCAACAGGTGACTATATCAGGAAGGAGAAAACCAAGTGCTTCCTGCTTCACCTTCTGCT
GCTTTTGGGACTTTTTATGAAGCCTAGGTAGNCTNAGGACANGACCCTGAACCCATTTTT
TCACTGGGAGAGGAAAACCACCAGGCTTCTCAGCTATTGGCTTGGCAACTCTTGGAGTTC
CTATGGCTTCCATCAGGGGCTCCAGGCCCTGATAAGTGGCCTCAGGCCAGGNAGGGAGGA
TTCGGNGTAGCCGGGATTGGGGAGCAGCTAGGTNCAGGGAAGGNTGGGAAAATAGGGGAC
CCANTCCCCCAAAACCACCGTTTGGCCGCNATGGATGGAATTTGGAGGGGGAACTGGGACC
GNTAAGTTTCTGGCATTGCCTGGCCGGNTTGGGATGCCTTCTTCGGGACTGGCTCCCAGG
GCCGAATNTTTTTCAGGGTCTTGCAAGCCCGGCT
Sequence 682
TTGACTCNCCGCGGTGGCGGCCGAGGTACTCTCGTTTCAGCTGGGCTCTTATGGCCAACC
GCTCGGCTTGCGCCCGCCGGGTTTCCGGAGATATGTTGTATTCGGCTGGGTCGAGGGTCT
CAGGCAGAGTGCGCAGGCTCGACGGCTTATACTTTGGGAACGACATCTTGGCGAACCAGG
GCACAATTGCGCCTGCGCGATTCTGAGGCCCTTTGTCTCCCCGCGTACCTGCCCG
Sequence 683
GCGGTGGCGGCCGCCCGGGCCGGTACGCGGGATGGCACATGCAGCGCAAGTAGGGTCTAC
AAGGACGCTACTTCCCCTATCATAGAAGAGCTTATCACCTTTCATGATCACNGCCCTCAT
AATCATTTTCCTTATCTGCTTCCTAGTCCTGTATGCCCTTTTCCTAACACTCACAACAA
A
ACTAACTAATACTAACATCTCAGACGCTCAGGAAATAGAAACCCGTNTGGACTATCCTGG
CCGGCCTTATCCTAGGCCCTAATGGGCCTCCATCCTTACNNATTTTTTAAANAANANAAA
NGGGGGAANGGACCCNTCNTTTANAAAAAAAAAAAATNGGGCCCNAANGGTTTTNGCCCCC
NGNGGGCCCTNGGGGCNTTTTTAAAAAAANNGGGGGGANCCCCCGGGGNGGGGGGGGANTNTTT
TTAAAGNTTTTTTCCCCCCCCCCCCCCCGGGGGGGGGGGGGGGNCCCCCCCCCNTTTTTT
Sequence 684
CCGCGGTGGCGGCCGAGGTACCCCATGCAATATANTGGCTCTACAATCCTCAGCATGTTA
ATCGAAGCCTTGTTGAGCTTCACAAAGGTTCCATTGAAGATTTGACNGAAGGCGAAGAAG
CTGCAACACCTTTCGAACCTTTGGGCTCACTCCATTGATACCTCTGATTCTGATGACAAA
CGCCAATTTGGGTTCTGCAGGTACGAGGACATTTTGCCCCGCGGCTTGTTGGGGTCTCCT
TTACCCATGTTGACAGATCCGCGTCCACCCGAGGGTATTGGAGGGTATTCTTGCCTGGTG
CGAGCTTTTCCTCAGAGTCCCGCAGAGCGGCCGCTCTAGAACTAG
Sequence 685
CGGTGGCGGCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGGTTTCC
G
NTCTTGTTGCCCAGGCTGGAGTGCAATAGAGCGATCCCAGNTCACTACAACCTNCGCCTN
CCAGGTTCAAGCAATTNTNCTGCCTCAGCTTCCTGAGTAGCTGGGATTACAGGCATAAGC
AACCATGCCCAGCTAATTTTGTATTTTAGNANGAGATGGGGGTTTTTCNATTNTNGGNAA
GGNGGGTTTTGAACCNCCCCCCNNNGGGGGGNCNCCCCCCCTGGGCTCAAAAAAAANGGGGN
GGTTAANTANGNGGGGGGGGNGGNCNNATATTCCNCCCCTTGTATAAAAAAAAAAANANCNC
CCCCCNCCCGGNGGTGTGGATATANATATTTNTACATTNTATNTTTTNTCCNCCCCCC
NC
GGG
Sequence 686
CCGCGGTGGCGGCCGCCCGGGCAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTT
T

Table 1

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAACNGAAAT
TCTT
CANNCTTTATNAAAAAAAGGNCNTAANGGGCCTNTTATTAAAAAAANGNNTAAAANCCCCAN
AAATTCNGGGGCCCCNGGGGCNGGGCAGGGNTGANANCCCTTAAAGGG
Sequence 687
GCCGAGGTCGCGGGGGGCTTACGATGGCNACAAGTATGGCGGCTGCTAGTGGTACGATTTG
AAACGTGCTGAAGAGTATCGAAGAGCGGAAAGAACAGACCCGGAATGCCAGGGCCGAGGT
GTTGCGCCAGGCTAAAGCCAATTTTGAAAAAGAAGAAAGGCGTAAAGAACTTAAGCGACT
TCGGGGTGAGGATACATGGATGCTACCTGATGTGAAT
Sequence 688
CTCCCCGCGGTGGCGGCCGAGGTACACTCGCCAGCGGTTTTGCCACAAGAGTATACCGGA
ACAAAGGAGACANGGCTCATTTATAATCTGACGCGGCCACCCTCCTGCTGCGTTCGGTTT
CCATTGGCTGGGACGGGACCTCACCTTCTGTATTTGTCCCGACTGGCTAGCACTTAGAAC
TTTTTAAAAGAGGCAAA
Sequence 689
CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAACTGGGCACTGGATAGGTAGTTCCTTT
GGTGGTCAAGGTGGCTCTACCTGTCCTTGAGCTCTCGTGTCACTCGCTTGGTGATCCGTC
CACACATCAGGCCAATCAGGAACAATATACAGATGCTCCCACTGATCACAGAGAGAATGT
AGTTCTTAGATGGAGACGTCATTACTTGCATGGCAAGATCAGAGAAGCCATCTGCTGGGG
CCACCTAGAATGACACAAGGCAATGTGATTCTCTGAGAGAGCACTGGGCTGGTGGCAGTG
CTAGGTCTAACTTATCCCTCTCAGTTCCTAGTTTAATTTATGTCTTTTCTTTTGGAGAG
G
GAGGGGCAGGAGATAAGAAAAATCAACACAGAGCTACAACTCTTTTTCCTGGATCATAAA
ACTATACCCCACGTCTACTGCACCAAAATTAGGAA
Sequence 690
CCCGCGGTGGCGGCCGCGTTTGTTTCTTGCCGTCCTGAGCGATGGAGCCCGGGGGTGCCT
GGTTATTGTCCGCTTTCTCTCTCAGATGCTTGGCTTGTTTTTCAAGAGAACCTTTTTCG
A
TATTCATTGCTCCATCGATTGGATCCAGTCCTTGTTCAGAAAATTGTTTCAAGGCACTT
A
AGGCTGCCTGAAAGCCTTGAATCCTTGCTAAATATTCCAGTTGNTTTGAAGGTTGTACCT
Sequence 691
GCGGTGGCGGCCGAGGTACTACAGGAAGAAACTAGAGGAAACGGGAATTTCATCCATGTC
CTGTGTATCTGCTGGCAACAGGTCAGAACCGGCCAGTATGTTATTCCCTGCAGGCTGCCT
AGGGTGCTCTCCTCAAACAGATCACCTGAGCCTCCTGCATCTATGAAAGTTATGACACAG
CAACCAGTTACTCAGAGTCTGATGAGAAAAACAGATTTTAGGTTTGGGAAATGGGATTAC
TGTAATTTACACATCCAAATGCAAACTGGAGCTCTGATTTGAATTCTACCCTGGGGGAAG
AACTTTGATGCTAACCCAACAAGGTACCCTGCCCGGGCGGGCCGCTCTAGAACTAGGNGG
GATCCCCCCGGGCTGCAAGGAATTTCGATATCAAGCCTTATCGATACCCGTCCACCTCGA
GGGGGGGGGCCCCGGGTACCCCAACTTTT
Sequence 692
GAGTGACTCCCCGCGGTGGCGGCCGAGGTACACCAAATGTGACATCCTTTCCCAATATAG
ATTACTTCATACCACATTGTCAAGGAAAGGACTAGAAGAATTTTTTGATGACCCAAAAAA
CTGGGGGCAAGAAAAAGTAAAATCTGGAGCAGCATGGACCTGTCAGCAACTAAGGAACAA
AAGTAATGAAGATTTACACAAACTTTGGTATGTCTTACTGAAAGAAAGAAACATGCTTCT
AACCCTAGAGCAGGAGGCCAAGCGGCAGAGATTGCCAATGCCAAGTCCAGAGCGGTTAGA
TAAGGTAGTAGATTCCATGGATGCATTAGATAAAGTTGTCCAGGAAAGAGAAGATGCCCT
TAAGGCTTCTTCAGACTGGTCAAGGAAAGAGCTAGACCTGGTGCTTGGAGAAGAGACATT
NTTTNGGAAGAATCATTTTGGCCCAAGGTTCAAGCNNTGGGGTTATTCCTTTGGCCCCCT
TAAATTAAAAAGGATNCCCATT

Table 1

Sequence 693
TCCCGCGGTGGCGGCCGCCCGGGCNGGTACCTCAGGGACATTTAAGAGTTGGACGGTGCA
AATATATTCCAAAAGGGTGCAACATGACACAGTGTATCCCCCTGCTTCTGTTTTTGTAT
A
TTTTTGCTACT
Sequence 694
GGTCTCTGTTGGGGCTCCCCTTTCCTGAACTTTGGCCAAAGACAACAGGATATTCTTGGG
GGTTTTGTTGTTGTTTGTTGGCATNNTTTCTGTGCCTGTTGGTGATTCCAGCACAGN
CC
AGNGANCCGNGTACCTGCCC
G
Sequence 695
GTGACTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGTATAATGGAGGCTGACCAGAGC
AGTTTAGGAGATTGTAAAGGGAGGTTTTGTGAAGTTCTAAAAGGTTCTAGTTTGAAGGTC
GGCCTTGTAGATTAAAACGAAGGTTACCTAAATAGAATCTAAGTGGCATTTAAAACAGTA
AAGTTGTAGAGAATAGTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCT
Sequence 696
NCCGCGGTGGCGGGCGGCCGAGGTACAGCAGGGTGCCTCATGCAAGAGAGGACTGAGTGG
ATTTTCCTTAGGGATATTTATGAACCTTAAAGCAGGAGCTTAAAGGGAATTTGGGCCATA
TTAACCACTTAGGTCATGATAAATGATTACATTTTTGGACATTTTGGTGTCTTAATGTC
A
GCAAGGGTTGCACGATAAGTTTTGACATGCATGCATGGGAGACATGTAGAAATTCTAGTT
ACTTACAAGTTTTTGGGGAAGAAGCCTGGACCCAGATGCCAGCTTTAAATAACAGGGGAG
TCTAATTACTTCTAAATTCCTCACATAAGGAGTTTTTGCCTCTGGATGGCCTGCTTGAT
G
GNCCTAGGGNGATCTTTGCCCCTTTTATACTAANAAGCCCTTGCCCTGGAAAGGGNTNTT
TGGGCNNTNAAAAAATTGNGGGCCGGGGGGAAANGGGGGAAACCANTTTTGGGCCCCCCNT
NNNGAATTANAACCCCTTTTTTTTTNGGNGGGAAAAATTTNCCCCCCCCCCCCGGGGGGGC
CCCCTNTTTTTTGNGGGGGGGNANAAANCCCCCCCCTCGGGGGGGGGAAAAAAAAAA
Sequence 697
CGCGGTGGCGGCCGCCCGGNCAGGACGCGGNGANGACAGCGNCAGGCGCTTGATTTCCCT
GAGTCCCGGTGCCTCANCTGCCCAGNGCCCACGTTCGTAAGAAGGCAACAAGNTCTTCTC
CTCTACAGAAGGATTTTGCAAACANTTCGGCAAGNTCCAAATGATTCTGATCGCAAATAC
CTGGAAGATTGGGCAAGAGAAGAATTCAGAAGAAACAAANGTGCCACCGAAGAGGATACA
ATCCGGATGATGATTACTCAAGGCAATATGCAGCTCAAGGAGTTAGAAAAAACACTTGCT
TTAGCAAAATCTTAACTATAGCATTATTCTGAAGGGA
Sequence 698
ANCCTCACCGCGGTGGCGGCCGAGGTACGCAGNCCNCCTGTAGGGATCNGTNTTGTTCNT
GACNAGCCCTACGGTAATGCAGCCCGGAGCTTGTTTTCCGTAGCTGGGGACAATCTTCTG
TCCTTGCTGTTCATGTCGTGGAAGAGAGGGGCAGAGTCTTGCTCTGTCACCCAGGATGGA
GTGCAGCGGCGTGATCTCAGCTCATTGCAACCTCCACCTCCTGGGTGCAAGCGATTCTCC
TGCCTCAGCTTCCCAAGTAGCTGGGATTACAGGCGTGCACCACTACATCCAGAGACTGGG
ACTACAGGCATGGATTTTCAGGTTTATAACATGGCAGAGTGAATTCTGGCAACACACTGA
GTGATGCTTGNCAATGGCCACTATCAGGAATTTAAAACAAGATTT
Sequence 699
CGGNGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGTTAGTGTTTTCTGATGTCTTTT
CTAACAAATCTTTGCCTGCCCAAAAGTCTCAAAAACATTCTCACGTTTCTAGATTTTTAG
CTTTAGCTTTTGTGTTTGGGACTATGATCCATATTTAGTGAATTTATTTTTGGGGGGGCA
GAGTCCATGTTGCCCAAACTGGTCTGGAACCACCACACCCAGCTAATTTTTGTGAATTGC
GGGTACCAGCACACCGGCGCCGTCCTGGACTGCGCCTTCTACGATCCAACGCATGCCTGG
AGTGGAGGACTAGATCATCAATTGAAAATGCATGATTTGAACACTGATCAAGAAAATCTT
GTTGGGACCCATGATGCCCCTATCAGATGTGTTGAATACTGTCCAGAAGTGAATATGATG

Table 1

GTCACTGG
Sequence 700
CGGCCGACTTGATGAGCGGAGAGACCTGCACCGGTGGCACCATCTTGTCCCTGACCTCCG
CACCGGAAGCCCCCGCGTACCT
Sequence 701
ACCGCGGTGGCGGCCGAGGTACGCGGGGGAGAGAGGAAAAGAACACAGATCTCGCATGGT
TCAGATTTTTCTTTTTAGGTCCAGGAGTAAGATATATCATACGAAAATGAAAATTATAAT
NCTTCTTGGATTCCTGGGAGCCACATTGTCAGCCCCACTTATCCCACAGCGTCTCATGTC
TGCAGCAATAGCAATGAGTTACTTCTTAATCTTAATAATGGTCAACTTTTGCCACTACAA
CTTCAGGGCCCACTTAATTCATGGATTCCACCTTTCTCTGGAATTTTACAACAGCAGCAG
CAGGCTCAAATTCCAGGACTCTCCCAGTTCTCTTTATCAGCTCTAGACCAGTTTGCTGGA
CTGCTCCCAAATCAAGATACCCTTAACAGGAGAGGCCAGTTTTGCCCAAGGAGCCCAGGC
AGGCCAAGGTTGATCCCTTACAGCTTCAAACACCGGCTTNAAACACAACCAGGCCCCAGT
CACGGGGATGCCCTATGTATTCTCCTTCAAAATGCCTTAAGAGCAAGGGCCAGATGGTTT
CAATACCTATNCAGGTTTACATGGGC
CCGCGGTGGCGGCCGCCCGGGCAGGTACTGCAAGCAACAGTTACTGCGACGTGAGATCAT
CAAGAACACGTAGAGAAACCCAGCTGTAATCATGCATGGAGATACACCTACATTGCATGA
ATATATGTTAGATTTGCAACCAGAGACAACTGATCTCTACTGTTATGAGCAATTAAATGA
CAGCTCANAGGAGGAGGATGAAATAGATGGTCCAGCTGGACAAGCAGAACCGGACAGAGC
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T
Sequence 702
GCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTATGAATTATTTATTTTCTTT
CTCANAAAAGGATGCGCCTCCACTTAGCAAGGCTGGGCAGGATGTGGTTCTGCATCTGCC
CACAGACGGGGTGGTTCTAGACGGCCGCTCTAGAACTNGTGGGATC
Sequence 703
GGTGGCGGCCGCCCGGGCAGGTACAAGACCTTGACACGCCCAAAACACTTCCTGCAGATG
TTGNCGTTGGAAAACTGTCGTCTTACAGAAGCCAGTTGCAAGGACCTTGCTGCTGTCTTG
GTTGTCAGCAAGAAGCTGACACACCTGTGCTTGGCCAAAGAACCCATTTGGGGATACANG
GGGTGAAGTTTCTGTGTGAGGGCTTGAGTTACCCTGATTGTAAACTGCAGACCTTGGTGT
TACAGCAATGCAGCATAACCAAGCTTGGCTGTAGATATCTCTCAGAGGCGCTCCAAGAAG
CCTGCAGCCTCACAAACCTGGACTTGAGTATCAACCAGATAGCTCGTGGGATTGGTGGGA
TTCTCTGTCAGGCATTAAGAAGAATCCAAACTGTAACCTAAAACACCTACGGTNTGAAGA
CCTATGAAACTAATTTGGGAAATCAAGAAGCTGTTGGAGGGAAAGTGA
Sequence 704
CGCGGTGGCGGTCTGCCCAGATCCATGATGTGCAGTTCTCTGGAGCAGGCGCTGGCTGTG
CTGGTCACTACCTTCCACAAGTACACGGGTCTATTTGGCNGTGACCTTGCTCTGGAGACN
ANGATATCCCTTCAGCCTGAGGGAATTGATGTTGATGAACCCGGAGGCATCAGTTGGCTC
ATAATCACCCTGCACGTTCATGCTCACCAGCTCCTNATTGTNNAGAGACAGNCNGGGACT
CCCGGCCGAGGATGTACCT
Sequence 705
CCGCGGTGGCGGCCGAGGTCCGACGCAGCAGGCTCCGAAGATCATACAGACGCCATTACC
ACTCTTGGCTCCCAGAAACCTCTGCGCCCCGCGTACCTGCCCG
Sequence 706
CCCTTAGCGTGGTCGCGGCCGAGGTACGAGTAAATTTTCATTACCTTTAATTAGGCAATG
TTTCTTAGATAACCATAAAACTGCAAAAGCAATTTTTAAAAATGTAAATAGGACTTCATC
NAAAAGTAAACGCTTCAAAAGATACTACTGAGAAAGTCACAGAATAGGAGAAAAATCTGA
TGAGACTTTATGTCTAGAGTAATGAATTCTTGTTAACGAATAACCAACCCCCTTTTAAAA
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AAGAGATGCTCAACATCAGTAATTATTAGGGAAATGCCAATCAAAACTACAACGAGATAC
CCTATATCCACTAGTATGGCTATAATAAAAAAGAGTAACAAACCGTTGAGGAGGATATGG
AGAAACTCGAGCCCTGGTCAGGTGTGGTGGATCACACCTGTAATTTCAACACTTTGGGA
Sequence 707
CCCTTAGCGTGGTCGCGGCCGAGGTACCCATATCCAAGGCTTATTGCAACTTTTAGTCTT
GCCCCTGCTACTTACACAGTCCAGAATCACTTGGGTGAGCATTCCAGTAGGACGGTGGCA
TTTTAGGATTCAGAATATTAACCTATAAACCTGTCATTTGATTCTTGATTATTAATGTCT

Table 1

GGATCGCCTGTGGTAGGGGTGTAATCCCAGGAAGGCATTAAATATATTTGAATTAATGTA
TATTTTGAGAATAAAAGGCTATTTCTAGAAAATATTACACACTTGTCTTATGTTAAATAA
AAATTTGCTATTTATTGAATATCCCTTACCCACCCTTCTTCCCAATGAAGATCTTATGCA
TACCTTCACTGGAAGGTTTAAGATGTGACAATCTTAATAGATCTTTGTGAGACCAGCCAT
TTCTCTGTTTATATTTTGNAACCGCCANAGCAAGGGCCATGCCACCTTTCTCATTGGACC
T

Sequence 708
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATCCTTTTGCATGCTCAAGAGCCCATTCTTT
TCATCATTCGGAAGCAACAGCGGCAGTCCCCTGCCCAAGTTATCCCACTAGCTGATTGCT
ATATCATTGCTGGAGTGATCTATCAGGCACCAGACTTGGGATCAGTTATAAACTCTAGAG
TGGTAAGTGTCTTCACATTCTTTAAGCACTAAAGAAAACTTTTAATTAGCTACCTTGCTT
CCAGTAATCAAACTAGAGCTCCTCTGCCTTGTGTAAGTTGCTATAAAGTATTGACTATTA
GAATGTCTTGAACTTTGGTTACTGNGAGCCAAAGTCGGTGCTCAAAGTATATTTCATAGT
CTCAATTATATAGTAATTTANGTTCTGAAAAATAGGTTCTGGCTTTGCATATGTAATATT
TTGTGAGTATTTACTTTGGAAAGTTTGGTCGACCTAATGGATAAATTTAGAAGTTTATTT
TCCTT

Sequence 709
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGCATGGTCCATACCACTGTTTACTTTTCTAG
AAAGTTGTTAGACTAATTTTTTCAACAAAAATTCTTTATTGTCTTGGTAACAAAAGAAGCA
TACTAAAAATTCTCAATAAGGCACAGTGTCTNTAGAAGCTTGAGCATTCAACATAAACTT
CTAATTAACACGAACTTGTGCTCTTATTTCAGCCATTGCTGTGTGGGCTTGGAGCCAGGA
GAAGATGCAGAGGAATTTTTACAATGAATTACTTCCATCAGCTGCAGAAAATTTTCTAGTT
TTGGGGAGACAATTACAAACATNGTTTTA

Sequence 710
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGCTAATCCCAGTTATGAGGGCTCTGCC
CATGACCTCATCACTTCCCAGAGGCCTTACCATCTAATACCAATACATTGGGTTTAGAAT
TTCAGCATGAGAATTTGGGGGAGACAGTCAGACTGTAGCGATGATTCTGGAGTATTCATC
ATTTAAGAGACACTTAAAAATGATCAGAAAGGAGAGGATGAAGGCTAGAACTAAGACTTT
AGCGTTGAACATGGAAAGGAAGTGATGACTGCAGATATCTCCAGTACCTCGGCCGCGACC
ACGCTAAGGGCGAATTCCAGCA

Sequence 711
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGAT
AGCCATATACCAAATAAATGTTCTGTGACTAGGGGTTATGGCACAATGGGTATTGAGACA
CTAAAAACTCTGCTTCAGGCTTCCATCCTCTTAATTTTANAATATCTCTGATTTCCTAAT
TTTCTGATTGACATCTTTTGGTAGATTATCGGGTTTTTACTTTATGTTATTGACTGATCC
TTTAGAATGATTTTCTTTTTGTTCTGGGAAAAAAAATGCATTCTAAATCANATTCACTAA
TACTTTGATTCACTTCCAAGGAT

Sequence 712
CCCTTAGCGTGGTCGCGGCCGAGGTACTTACAAAAATTTTTAACATTAGGAGGTAATTAT
AAGTAGATTCTGTGATTAGGACTTCATTCATGTATCTTTTGCTACATAAACCTTTGTTAG
ATTAAATGGAAGACACCTGCTAGGTGATACTTTTTATAAAACATATGAGTAAGTCATATA
TCTTTGTTAAATTTCTGTATGTTCTTTTTTGTATAAAGATGGAGAGAAAGGATGGAGTGA
TACTAAGGACCCTAATAACATCTCTGTTCAAATTAATTACTAAGTGATAGAAGTATTCAT
ATGCCATTAAAGATTTGCCAATTCTATTT

Sequence 713
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACTGACACAAGGACTCCAGGCCACACATATCT
TCTTGAAAGCCCTTTTCCTGTTTGAAAAAAAGATCGTTTGTATTTGATAGAGCAAAAGAA
GGCCACAAAATGAATTGTCTTCTTGTGGGCTGTGTTTCAGAACGGCCGGTTTGTGGGCGA
TGCTGACCTTGAAAGACAGAAATTTTCAGATTTGAAACTCAACGGACCCCAGGTAATTCT
TTGGCTCAAGACCTGGGTTGCTTCATTCATATTTTCTTATTTCCCCAGCCTATAAGAGCA
TATTTGTGTCTTGTAAGGTGCCTGG

Sequence 714
CCGGGCAGGTACATATGCACTATTTAGAATATGACATTAATCAACCACTAGAATTAAAAT
CAGGTTATAAATCCTCAAAATCACCAGAAGTATAAATTTAAATGAAAAACCCAGACCACA
GAACAAAAACAGAAATACCAAAAAATAATCACAAAATATTAAAAACAGTATATAAACACA
GTGACAGAATTAGGACTAAACATATCTGTAAACAATAAATGTAAGGGTAATCTCACCAA

Table 1

TTATGAAAAAGACCTTCAGATCATATTTTAAAACAAATTTAAAAACTCAACTGTATGTTT
ATGCAAGAGACAGATTTAAAAATAAAGAGACTCAGAAAGCTGGAAATAAAAAGAAAGTGC
AAAGAAATAGCAAACAAATACAGGCATAAAAAAAAAACAAAGATCCCAATAGTACCTCGGC
CGCGACCACGCTAAGGG
Sequence 715
CCCTTAGCGTGGTCGCGGCCGAGGTACGTGTGCTGGATATGCAGGCTTGTTACATAGAAT
TGGTGTAAAATTTGAAAACCATGAAAAAATAAAACAATAAAGGATCTAGATGCTAATAAT
GTGGTTAGTTAACATGTTGACCATTTCAAAGCAAAATAAGTCTTTGATGTTTTATACTAT
TCATAGCAAGATATAAGTATTTAATCTGCAAAGACGTGGATTTGAAAATTCAGCTGCCAA
ATGTAAAGAACAGATTCCTAGATTATTATTAATAATATCTCTATAAATATTATATTTATC
AATAATGGGTACCTGCCCGAGCGGCCGCTCGAAAGGGCN
Sequence 716
CCCTTTCGAGCGGCCGCCCGGGCAGGACAGTGGTGTGATCTTGGCTCATTGCAACCTCCA
CCTCCTGGATTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCAC
CTGCCACCATGCCCCGTGAATTTTTGTATı TTTAGTAGAGACAGGGTTTCACCGTGTTGG
CCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCTGCCTACCTCGGCCTCCTAAAGTGT
TGGGATTATGGGCGTGAGCCACCATGCCCACCTCCTGGGTCATTCTTCTGGATATTACCA
GGCATTTTTATGCTGATCTAAGTGAAAACCTGGATATTTTTTTTCTCCAAAGTTATTTCT
TAGTTCTACCTATGACATGAGGGTGATCTTTATAATTTTTTTTTGTTTTCACTGAAGAAA
TAAAACATTGCTTAANGGGAGAGTTTGGGGGAAGTGCATANGGGATCTGCAGTTGGGACT
GGATTTTTCGGGT
Sequence 717
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TGGTGGCCAGCCTCCAAGATGGTCCTCAATGATCTTTGCATCTTCATATTTCCACCCTGT
GTAGTCCCCTCTCTCAGGGGATTAGGGTTGGTCTGTATGATCACCACATGGCTGCAGTAA
TGGTATGTCACTTCTGAACTTAGGTTATAAAGACTATGACTCTCATCTTGGGTGTCCAC
TCTCTGTCTCTCTGATCTTACACTCTAGTGGAAGCTGCCATATTGTGAACCTCATGGAAG
GCCCACAGGGTGAAAAACTGAAGCATCTAATCAACAGTTAGCAAGAAACTGAGCCTGNCA
ACAACCATGTGAGTGACCCCGGNAAGATTTTCCAGTCCCAGTCAAACACTTGANATAACC
GGCAACCCTTAAGCTGACAGCTTAACTGCNANCTGATAAAAGACACCCTTGGGNCAAAAC
CATTNGGAACCATTCATACCCCA
Sequence 718
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCNTTTCGAGGTNTTNGGGGCGGGATAAA
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GGAAGCATCAAGTTCACAGCAGTAATGCACACTGTGGCAGGAGAATCGCTTGAACACGAC
AGGCGGAGGTTGCAGTGTGACGAGATTGCACCATTGCACTCCAGTCTGGGCGACAAGAGG
GAAACTCCATCTGAAAAAAAGGAGAAATTCTTTTATTTTCTACTTCTCTTCAGATTTGTC
TTATGCATTTTCCAACTATGTATGCATCACAAGCTATTCTTTTTCTGAGTTATAGCTACA
GTTTTCCTACTGTTGTCTNCATGCCATTTTCATTTCACATGGTACCTTG
Sequence 719
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTNNNTTTTNTNNNTTTNTTNTNNNGGAGAC
AGGGTCTCGCTCTATCACCTAGACTGGAGTGCACTGGTGCAATCTCGGNTACTGCAACCT
TCACACCCCAGGCTCAAGTGTCAATCCTCCCGCCTGAGTAGCTGGACCACACGTGCGCAC
CACTAAACCCAGCTGTTTAATACACCATTTTTAACCCAAAACATTAAGAAAAATATAGGA
ACAGTAAGTAGATTACATTTTGTAAACAGACAAAGCTTACAAAGTTTTCTCAAATATGAA
AGTCATACTAAACTGGGAGACTGTTAACTTCTTGATGGGGTTAATCTCTAATATGAAGCC
NCAGTCATAGCTAACTACAAATTACATATACAATGCCAAAAATNTTCAAAAATAACATTT
TTTGCCCTTAATGGATTACAAATGCTAACCNACATAAAGACCCTGGGAAAGGGTTCANAA
TCTNCTCATTACATACTTTCAAAATATCTTNCCTTTACTTTCATGAAATGGACCCCGGAA
TCTATGTAAGTGATGACNTGNCCGGNGTTCCAGGNGTTTNTTAACTNAAACTTGAANAAA
GGCCCTAACTTAAAATGGGTTTTTGAAANCCTTTTCCAAATTNGGGTNTTTGGTTTGGAC
CCCNTTNAAAANCTTTTTTANCAATTNTTTNTTTTAAACCCCTTGGGGGGGGGGGGGCCCCC
AAAANAAAAAANGGGCCCTTGGGTAACCCCCTTTTTGGG
Sequence 720
CCCTTAGCGTGGTCGCGGCCGAGGTACTTGAAGAACATGGTAAAAATATGTTCACAATAA

Table 1

TATTTTATCTTAGAAATGTATTCAGTAAAAAATCTCTTTATTCAACTATCCTCTTGATTC
AGGGGAAAAAAGGATTAGCATGGGAGATAACAGAATAGGAAGTTTAGGAGATAATGAGAC
TTCTGTTTTAGTAAAGTAAATAAGCTTTAATAGTTTTTTTGGTCATGTATTCAGTTTACCA
GCCTTGAAGATATTTGTAGGAAATTTTAAAAGTTTCTCTATTTCATCCCCCATGATAAAA
ATTATATAGAATAAAAGCTGAATTGAACTTTCTTCACAGCACACTGAAAAATATCTTCTA
TAGCATTAATCAGATCACAGAATGCATATTTAAACCAAAATTTGACTAAATTATTTTTTA
ATTATTTAATTTTTTTTCTGANACCGGAGTCTGGCTCTTGTCNCCCAAGCTGGANTGCAAT
GGCNGGAACTNACTTATTGGAAACCTCCGCCTCCTGGGTCAAGCCAATTCTTCCCNCTTG
GNCCTCTAAAGTGCCTGGGATGGCAGGCCTGTGCCANCCTTCCTGGCCCCANAGNNCCGG
GTTTTGGATGGTTGGGTNGGTTNGGGGGGTTTTTTTTTTCCCTAAAAACCTTNAAATTTCC
CCTTTTGGTTTTTTTCCAAAAAAAAAAAAAAAATAACCCCTTTTTTTTTTACCCCCCCCTT
TTTT

Sequence 721
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CTATGTTTTCTTTAACAGAAAGTTCTGTTTTTGTGATCCTTTTAAAAATAAAGCTTCACG
GAAGGTATGAGAATAGTATTTTTCAACTTTAAATTTCTCATTACCAGAAGACCATGTGGT
AATTCTCTGTATACAGTTAGAACAGCACGGAAACTTGAAGGCCTAAAAAATTAGCTGACC
TTGTTAAAAATGTTGGCGTGAGCAGTATATTATTACCTATCTTTTTTTATTGTGTGTGTG
TGTGTGTGTGTTTTAAACTAATTGGCTGAAATATCTGCCTGTTTCCCTCTTTACATTTTT
CTTGGTTCTTTCCTTATTTATCTTTGTCCATCTTGGAGATCTACTGTAAAAGTGAATTTT
TTTAATGGAAAACCAGTTCCCAAGTTTTACTCTCAGTGGGTTTGGGGACATCAGATGTAA
TTGAGAGGCCAACCAAGGTAAGTCTTCATGTCAGTNGTTTGGTTGAAGGAAACGAGCCTA
TGAGGGTCAGTTTTTCCCCAAAANGGAA

Sequence 722
NGCCCTTAGCGTNNTCGCGGCCGAGGTACATGAACCTATTAATAAACCATTCATGCTTCC
CAGTTTGGCAGATGTGAGCAAACTATGTATAGGAATTCCAAAGGTAACTTTTTCCTTTCA
TTACTTTACAGAAATACTGTCAAGTCCAATAGAGAGCACAGACTTGGGAGGCGGATTGGG
TGGGTTTGAATCTCTGCTCTGCCACTTTTATTAATCATGTGAGTTGAGTATGTGACTTAA
TCTCTTTTAGCTCAATTTCCCCATCTGTAAAATAGGAATAATAAAAATACTGACTTCAGA
GAGGTTTGTGAGGATCAATTAGACAGTCATGTTAAGTCTGTAAATTGTTTCTGTAATGGG
CAAGATAGCAAATATTTTAGATTTTGTGGACCATGCAGTCTTTATCATAACTGCTTAACT
GCCATTATAGTGAGAAAGCAGCCACAGACAATATGTAAATGAAAAGTGTGTCTCTGTTC
CAATAAAACTTTATTTTCAAAAACCAGCTGGCTTGNCACATCTGGCCTATGGGCCCATAA
GTTGGCCCATCTCTAATGTAAAGAAAGGACTTTANCCCAAAGCCACAACTTGCATAGTAA
TGCCTTAAAAAAATGGTAACATCTTTACTGGTATTAATAATTACTACTGCATCTATTACC
AGNAGCCAATTGGAGTAATGAATCCATGAATGGTATAATGGTAAAATACTAACCCTTT

Sequence 723
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACTTACTTTGTTGCTCT
TTTTCTAAGTTTTAAAGATGGATGCCAATCTCAGGCTTCTTTTCGTGTGTGTATGTGCGT
ATGTCCATAAATTCTCTTCTAATTACAGTGTAAGCCACATCCCACAAGTTTTGATAGTCA
CAGAACTGTATCGTCACACTATTTTTTTAATTTCAGTAAGTTCTTCACTGATCCCTGTGTA
ATTTAGAAATGTTTCATAATTTCCCTACATTGGAGGGGAAGATAGTTTTGNTTTTATTAT
TAATTTCTAGCTGTANTTGAGCTCTTGTCAGAAAATATGGTTTATTTTAAGTC

Sequence 724
CCCTTTTNAGCGGCCGTTNNGGCAGGTACTCCTCAGCTTGTGCTGCCCTTCTCGAATGAC
TCGCGTTTCCTGCTTTCATCACTACACCTCCCACCGCTCTCCATCACCTGCTCTGCTCTT
ATAAGGATCCAGAGAAATGGAATAATCTTATTGCTGATCTATGTAAACAAGTTGAAGAAT
CGTCTGAAAGAAAATACAGTGTGTCTAAACTGGAAAAGTCCTGTAATAGTTTGTTCATGA
GCATTTGCACAGTGGAGTTACTGTTCATCATGGGGGTAC

Sequence 725
CCCTTAGCGTGGTCGCGGCCGAGGTACTAACTATTCCTAAATATTAAACACTGGTCAACT
AAAATGCACAAATTCATGAATTGGATTTGCACTCAAACAAAAAAAAATACCATAGGCAGT
ATCATTTCTACCTTTGTAAGAGGCAGGAATATTCATTAGACTCTATGCTTGACTTTTCAT
ATGTATTTTAACACTGTAGTAGGCTATCGGGTCTAGTTTAAGCTTCATTTCTAAACTACT
CAACAGCTCAGAACTGACAAAGATCACAAGAAATCAACTATTAACCTCTTGCCTGAAGAC
ACAAATGAAATATTCCCTATTTTACAAAGCAAATTAGATTCCAAGATTTTCCAAAGCCAT

Table 1

ACTCCTGCAGTTCACTGGGTTTCAAACTTAAAAATCAT
Sequence 726
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACTCACTTAAATAAATAATTGGTAAGATGATT
TTATCTGACAATTAAAAAAAGGTATATGTGAAAAACCTTAAAAAAAAATCTATTTCATTAC
ATGTTGAAATGTTCTGTGCTTAATCCAATACATCATTTAAATTCTTTTCACATTTGGACA
ACAGAAAAACTGAAATCTATGGATTCCAAGCTGCAAAGTATTTTATCTAAATTGCAAATC
AAAAAAC
Sequence 727
GATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACATTCTATTGTTATC
TCTATTTTTTGGATGAAAAAACAGCAGCACAAAGAAGTTCAGTAACTGGCCTAAGGCCAC
ACAGCTTGTCTTCCTGAAGACTGGACCCAAACCCAGGCAGTCATAGAACATGCTGGTCGC
TATTGGGCCGCTTGCTCTATGGGGGACGGTGCTCCAGGAACACAGCAATGCGGTTTAGGA
TTCCAGGACCTGGGGCAGCTGCTGCTTCTTTCTTAGTTCTCGACAGACCACTGAGTGCAG
TTTTTCTAAATCTTTTCCCCACTTTGATATGTGGTCCATAAAACTGCTTCCACACGTATA
ACCCACTGTGAAGTTTAAAATGATTTCATGTTTGGGCAAATTCCTACTGAATGTTAAGCT
AGATAGGAAACAAGTTCTGACTAACACAAAATGAAGGGCTGAATGAAGAAGTCNTACTTT
TATAAAGGAATTTTNCCCTTCCTCACCAAATC
Sequence 728
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGGTAGAG
ACGGGACCTCACTGTGTTGCCCAGACTGGTCACAAACTTTTGGGCTCAAGCAATACTCCT
GCCTTGGCCTCCCAAACTGCTGGGATTACAGGGATAAGCCACTGTATAGAGTATGAAAAG
TATTTAAAAGAATCTTCCAAAGGAGGACAGCAGAAATGAAAATAAAGTAAGTTCAAACTA
GAATCCTTGACACAACTGGTTTTTATTCCCAATGCCTCTTAAAAAGAATCGTTCCATGGGT
GGCAGGAGGGGTGTTTTCATGGTGTGATGCACCGTGACTTGTTATTNAAGATGTAAGTCC
AGTGGTCCATCTATCACGTTTTATACCTTTCGAAAAAAAAAAAAAA
Sequence 729
TCTNGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTT
CGANCGGCCGCCCGGGCAGGTACTTATCAGGATGAAATCAGAATCACAGTTGGCCTTTTG
CCATAAGGGAAGGGTATTTGGAGAAGAGTCAACCACCACTCATGCCTCTCCCCTGCCCAG
CAGCACCTTGGATTTTCCTGGCTTTATGCCTCCTGTTTCCCCTGGCTGAGTAACTGCAGG
CATTAGGTTCCTCTACACACGATATATTACAGGGAAATGGCAGCGATGGTCTGGAAGGGC
AACACTGGCCTTCTTTCCTCCTGAGCACTAAAATCCTAAACATGCAACTTAAAAAAAAAT
TCTAAATGTGAACACCACCTTTCAGT
Sequence 730
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AAATCTATTTCATTACATGTTGAAATGTTCTGTGCTTAATCCAATACATCATTTAAATTC
TTTTCACATTTGGACAACAGAAAAACTGAAATCTATGGATTCCAAGCTGCAAAGTATTTT
ATCTAAATTGCAAATCAAAAAACATCTATAACATCTTGTTGGGGATACAAAGTTCTCCTG
GCTG
Sequence 731
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TTGACTATTAAATTTGAAATTGTTGACATCAGCAGTTGACTCTTCTGTGTAGATCATAAT
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TAACAAATACTTTGACAAATTTATTAACCATTTATAAGACAAGACTTACCAAGGTGGTGT
TCGTTTATGAATCTTTAAATGTTTTCCAATACTTAAGATACATCAAAATTATAGGACTTC
TCAATTCCATCCTATTGTTACCAGAATATNAAA
Sequence 732
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GGCCTCCTGGGTTCATGCCATTCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGTGCC
CGCCACCAAGCCCAGCTAATTTTTTTTCTTTTTTTTTGTATTTTTAGTANATACGGGGTTTC
ACCATGTTAGCCAGGATGGTCTTGATCTCCTGACCTCGTGATCTGCCTGCCTCGGCCTNC

Table 1

CAAAGTGCTGGGATTACAGGCGTGAGCCACCACACCCAGCCTATTCCTTTACTTTCTTAA
ACTTTCTTTCACTTTACTCTATGGACTCACCCTGAATTCTTTCCTGCTCAAGATCCAAGA
ACCCTCTTTTGAGGTCTTGGATCGGGACCCCTTTNCTGTNACACNAACTGTATCCCCCTT
GGCAGACATATGAATTTGCACCCCCGCTTGGGTCTTCAATNTCCAGGGGATGAAACAAGG
GAGGNAAACCGAGGGGAAAA
Sequence 733
CCCTTAGCGTGGTCGCGGCCGAGGTACAAAACTATGTGAGAACGTATACTACTTCTCGGC
CACAACTACTATTTTTAGATATTCATAAAATAACCTCTGATTGTGTTTTCACATTGCCCA
TTCAGTTCTGTCCCAATCTTATAATTCTGATTAAATGTTCTGGCCTCAAACTAATTTTTA
AAAGGCCACTAACTCCAAATCTAGGAACAAAACACTCTGTAAAGACTCTGTAACTTGTAT
AAAATTAACTTGAAAAATTCACTCACTCCAATAAAACTATGATTTATGTAGCTCATAAGA
GGGTGAATTTTGAATATTTACTCTATGAAAAAAGCCTAAGCAATTCAATAAAAACTTGAT
AACTGCACGTTTAAGTTTGCAGCATCTTGTACCT
Sequence 734
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AAAAGAAAAGATCAAATGCAATAGATAGCACTGTAATAGATTTTGCTACATTAAAAAAAA
TCCATTTGAATACACAGTGAACTAAAACACCAGAGTGGCTAAAAAGTCCCTTCATGCATA
TTTACTTAGCAGAGAGCTCTTGAGAAAGACCCAACCAATAAACCCCAACCAAAGCAAATC
CAGCTACTTCTCTAGCTGAGAGGGTGGAATGACTCCAAAATATTGTTTCAAGCTCAAAAA
GCCTAAAACAACTCCACATAAAAAAACAAAAATCTATCTAATTGGACATTTACCTTTTTG
GAAATAAAAGGCCCAGTGGGAAAAAAAAAAAAAAAAAAAAAA
Sequence 735
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CGGAGTATCTCCGTCCTTTCACACTTTATTGTAAGCGAGGAGAGCAGCCAGGCTGCACCT
TTAACATTTCATTCACAGGATCTCAGCTCAGCCAAGTCCTCAGCCATTTTGTAATGAGGA
TCACTTTCTTCCGGTTCCCCGTGACCTGTCCCTCGCCTCCTCTAAGCCTCAGCAGAAAGG
CCTTCAACATCCACTTTTCCACAACATTCTGTCTATGATACCTGCATTCTCTGAGATGCT
AGAAGCTTTCTCTCCAAGCTCTTCCCTTTCCTNTCTGAGCCTTCACCCGAGTC
Sequence 736
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CAGTTTCCGCTTTTATTTCCTCTGAGGGGAAAAAAAAGAAGCATACATTANAAAACTGGA
CAGCAGAAAGACTGAGTAATTTCTTAAGTTCTATAAACTCATTTGGAACTTCTACAAAAA
GTTGGAAAGAATGCAAATTTAATAAAAATTAGATGCTAAAATTGTTTCATCTAAATTTTT
TAATTTACACAAATAACATAAAACTATATGAATAGGTACCTCGGCCCGCGACCACGCTAA
GGG
Sequence 737
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GATGCATTATAGAAATTCTTGTCTGCTAAACTTCATAGCAAACCGATCCCAGTCCTCACC
TNATTGTGTGGTAGCCCAGCAGCAGAGAAGATAGGAATTTTCTGCCCCCTAGCAATACTG
TTCATCCCATCAGATGGCCGAAATGCCAGTCTGAATCATTTCCTCTGGGTAGATTCNACA
TTGAGGGTTGATTGGCTGACCTAATGTNTTTTCCAAAAAGGAAAATTTCAACAAGTTGCC
CGCATTATTCATGAATGANAATTAGATNTCATATCAAATTAAAAGAAANGAAAAAGCACC
AGANGACCAGAACTACATAAAGCATCTCTTTACTACAAAAAA
Sequence 738
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CAGTTACTTTTCCAATTATTTTTACATATACAAATATTTTCTTGGTAGAAGAACAAAAGT
GGCACTATTCATTGTGTAGTTTTTTTTGTAACTTATATTTTACCCTAAGCATTTTCTCGTT
GTCTTAAATTATTAATNGAAAATTATTCATGGCTAAATAATGCCTAGGCTGCCATGAGTC
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AAACAAATTCTTTTTTATGGNGCATTTAAAAATCTACCTCCTTGTAGCCATATGCNNGGGA
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Table 1

TTCTTTATGACCTATTCTGNGTTCCTGGGACTNTACATTAATCTTTNCCCATGGATATTT
ACCATTGGAAAGGG

Sequence 739
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CTAGCAATGGTCACCCCTACATACTTCCGCACACATCTTTCAAGAACAGGACACCATTAC
CACACCCAAGAAAACCAGCATTTAATGAATTTATTCAGGAGTNTCATCCAACATACTCAA
ATTTCCACAGCTGTTCCGAAAGTATCCTTCAATTCTGGATCCATTGATGGNTCACAGGTT
GTATTTGGCTGTTACATCTTTTTAGTTGTTATCCTTCAGAGTAAAACTGGCCTGCCCCTC
TTTCTTTCTTTACAATATTGACTCCTTTGAGGAACCGGGGCTGGATGTGGAGCATTCTCC
ATTCATCTGATTGTTTCCATGTGACCAGATTCGGGGTCACAAAATTTNTGGCAAGAACCC
TTCACAGATGACCATGTNTTGGTTATTAGGTAACAATAGATTCTCAAAGTAGAGAACTGG
GAAATTGACCTTTGTCCATTCACAAATAGAATTTTTTTTTTGAAAATCTAGAATTCCTCAN
GAATNAATTGATTTCTTTTCTNTTTTCTTTTTT

Sequence 740
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACATTGTCTGCATTTTGAGATTTTCCTATTAT
CTTTCTGGTGTTGATTTCTGTTTAATTATACTGTGATCTACAAGCAGCACTGTATTATTT
CCATTCTTTTAAATTTGTTAAGGTGTGTTTTATGCTCAGAATGTGGAGTGGACTATTTTG
GTGAGTGTTCCATATGGACTTAGAAGAATGTGTTTTCTGCTGTTGTTAAATGAAGTAGTC
TATGTATGTCAATTATTGTTTGATGATTGATGGTGTTGAAATCAGTTATGTCCTCACTGA
TTTTCTGCCTGCTGGATATGTCCATTTCCAATAAAGGTGTGTTAATCTCTATCTATAATA
GTGGATTTATCTATTTCTCCCTGCAGTTCTATCAGGTTTTGCCTCATGTAAGTTTTGGAT
GTTCTGTTAAATGCATACACCATTAAGGACTGTTAGGTATTCTTGGGGAATTGACCCCTT
TGGTTTCTATGTAATGCTCTTCTTTATCATTGGATAACTTTCCCTTGCTATAAANGCCTG
GTCTGNCTGGGAAAAAAANACACAGGTNGNTACNTCTTCCCTT

Sequence 741
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTCAGGTTAGAGATGACTTCAATATATGTCG
CAGACCTCCCAAGGTGAGCATCACACAGCACTTATCATAATCCGAAGCAGCTCCACAGAG
GCTAAGATGAAAACAAAAATCTCAGGAAATTTATGTTTATAAAAATGATACTTGCAAAAA
AATGAATGGAACCATCTCCATTGCTTATTTAGAGTGTTGACTCACTGAATAAGATTTTAA
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GCTCAAAGAACTGCCCATCAACCACTTGGTTTCATCTTTGGACACCACACTGGTTATCTT
NCTTTGGCCTCTGCCATAACGGGTCCAGGCTACGTGCACCAAAGGGAAAGAATTGGGGT
NCTTCTTCCCTNCCCTGGTTTGGTTAGGA

Sequence 742
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTTTCCCTTGCCTCAACTTCTCATCCTGGGT
GATGAGACTGTTACTTTCCTTCTTGTATAAAGAGGGCAACTTTCATGTAGAAATTTTACC
TCCTACTTTTAAGAAAAAGGAAAATCAGAGTGCTTTAAAGGAAAATCAGAGTGCTTTTCT
TGCATCTGCTATTTTTCAAGTGTCTTTAACTCAAAAAAATCAATATGCCAAAGTGGCATG
TTTGGGGGTATCTGGTTCTGAATTCCTTCAGGAAAGATAGAAAGCAAAGCAAAATAATA
GGTTTAAAACTAAAAATATCCAGGTGCGGTGGCTCACGCCTATAATCCCAG

Sequence 743
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCCTCCTTGGCAGCATCAATCAGGCAGGGCT
CAGCCCACACCCGGCTCCTAAAGACAAGAGAGCAGAGAAAGCAGAATGGTGTTTAGAGAC
CATCGCAGTGACCTGATCCTGAAAGCACCTGTAGGAAATTGGCCTCCGCCAAGTGAATGT
GACAATGCAGTCAGCCACAGTGACGGAGTGCAAGATCGGATCACCACACAGATCCAAGAG
ACCGCTCACCACACCTGAGAAACAAGAACCCAAGACAGCCTCATGGAGGTGGAACCGTGC
TACGCAGTTATGGCTTCACTACTGAATGCGATCTTGCAAAAG

Sequence 744
CCCTTAGCGTGGTCGCGGCCGAGGTACGCGGGTGTTTTTTTTTTGGGTAATTTTCTTGAGT
TAGAAATGTAGTTAGAACTGTGACTAACGGCATTGCCTGGAATGTGCTACAAACACGATT
AGATATTCATTTATCTTCCTCGTATTAGACTGCTTGTAAGAGACTCAGTGTTTAGACATT
CATTTCTCTTCCTTGTATAAGACTCCTTGTATAAGACTCGGTGTTCATTTATCTTTTTAA
ATTAAACCACAACAAATATATGAGTTTTTAACCATTGCAATGTGCAATAAATAAATATAT
CTGAAGTAGCATTAGCCTTCTAGTTTTAAATAATAA

Sequence 745
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTTTTTTTTTTTTTTTTTTTTTTTCGTCAAAGTCA

Table 1

CTATTTGGGCCCTAACATAATCCTGCTCAGAGCGACGGAAAAAAGGCAAGCCTTTTCAAA
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TATCTATCAAAATTAACTTTAAGAGAAATACTCTCTTTCCTTAAAAGCCCTTATTTTTTA
AGACACTAGAAAATAAGTTACTATAAAAAGTGGTGGTCTGGGGGGCTAAAAACAAAACAAA
AAAAATCCTCTTTTCTACATTTTTTTAGTTTTCT
Sequence 746
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTAGTTAAAATGCT
TTACCTCAATGGTTGAGATATTTTGAATGGATTTTTCAAGGGGGGGGAAATGCTTATTATA
ATAATAAACCAAAATACTTAACAGAAAATTGTCAGCTATTCTGACAAAAATAAACATTTT
GAGAGACTTTATTTCTTTTGTCCGTTTCTGTGGTATCACTCATTGTCGTTAAGTAAGTAA
AGCTTTTTATATTTAGGTAAGAACTGATTTTATTTTTTAAATTATATTTTATATTTATTA
GCACAGAAGAATAATGAGAGCCACATTTTAGTTCAACT
Sequence 747
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCTTTTGTTTAGGTATTTCCCTCCTGCTGTG
TCCAGGATTGCTGTGTGGTGGTGATGAGTGCTGGGAGGTGAAAAATTAAAATAAGCCATT
TACCAGTCAGCATCCCAATTAAATATTTGATGTAACTGTGATCTTTGAGCCAGGCTTATA
TATTCATTTTCAAGCAGAGGAGTTCCCCATTTTAAATAGAGGCATTGTCTGATGTGTTTA
TGGTTAACTGCATCTGGCTTGGGTCTTTCTGTTTTCCTTTCTTTGCTGAATTAGAAGGGG
TTACTCTGAAGAGTCCAGGTCTTACAGTGTGGTT
Sequence 748
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TCTTCTAATTNAATNCCANAATACNTTCTNTNANCCCTATGCCCTNATACTANTANCTTG
ATGGTTAGCGGGTAAGTAGGTAGTAGTANAANANCANAANGGGAAATTNGGGGAGCAAAA
ANGGGANAAAAANAAAAAA
Sequence 749
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACTCACTACATTACAAAATAGTCTCTAACA
TAAAATTGCCTTAATAACTATACTATTATAGAATCTGATAAACCTTACATTATTAAATTG
ATTATAAAATCTTCTTGGAAAAACTTTGGTATGTATCTTCAGAAGGTTTTTTAAAAATAA
TATTTTAAGGGCCTGTAAACATTCCATTCTATTAAAGCACAGNAGAATAAGTAATGGATA
TTCAACTGCATACAGAATATATAATCAAAAAAACAATTTATTATTGTATTTGTAGAAAAT
CATTACCAGAGTAAGCAAAAA
Sequence 750
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTGATTGTGGCATATTCAACTATGATTTTAG
ACAAGATGTGTGTGTGTGTGTGTGTGTGTAGACAAAATAAAATTCAGAAAGAGAAAAT
CTATTCTACAATGAAATTCAATCTCTTACTTAGCTATTTTGAAATTGTGTCCCAATACCA
CATTAACAGAGCCAAAATGAAATTTAAAATTATGGTTATACTATTATTCACACTAGGTAG
GGTCAGGTTTTTTTGNCTGAATTAAATGGCTCCTTTACNCTAGCTACTTANGAACCACTT
NCCATACCCTNAAGCTAGAGTAATA
Sequence 751
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTGATTGTGGCATATTCAACTATGATTTTAG
ACAAGATGTGTGTGTGTGTGTGTGTGTGTGTAGACAAAATAAAATTCAGAAAGAGAAAAT
CTATTCTACAATGAAATTCAATCTCTTACTTAGCTATTTTGAAATTGTGTCCCAATACCA
CATTAACAGAGCCAAAATGAAATTTAAAATTATGGTTATACTATTATTCACACTAGGTAG
GGTCAGGTTTTTTTTGTCTGAATTAAATGGCTCCTTTACGCTAGCTACTTAGGAACCACTT
CCCATACCCTCAAGCTAGAGTAATAGATACCTGACC
Sequence 752
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGGGAGCCAT
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TCTTTTTATGCAATGTTATCANGTAAAAAAATGGCTAAAGTATATTAGCATTTACCCGAG
TGGTATTCTTTTATAGAACTCAGCTACTAAAACCAGGGAGAGTACTTGGTGTATTTCTGA
AACACTCTGCGAAGTTGTGGATAGCTTCTGGTGGTAAGGATGGTATTGAACACGTTTACG
TCTGTCCCCTTTCTCCTTTCTCCTGCTTCATACAAG
Sequence 753
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTATTAT
ATAAAATAATAATGCATCTTACAGGGGAAGTCATAAATCCAATGAAATAAAGTATTTACC

Table 1

TGACATATTTTTCCCATCTTCTTATTTCAACCATTTGACTGGTTGTCCAGCCCCAAATTG
TTGGACTTTTTTAAACAATTCACACTGACTGGCAGTCTTCACCTTTAAATNGTTGAGTTC
CATCCCTTTAAAATCATTTAAAAACATGATTTTTAAATTTATCTCCATTACCTTATTTTG
NGTTTACTTTTTTACTTTTATTTATTTCCT
Sequence 754
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGGTGGGGAGCTGTAT
TTATTTCCCAGGGCTGTCAAAACAAATATCCATAAATTGGGTGGATTAGAACAACAAAAA
TTTATTNTCTCTANAGAANAACGTTTTCTTGCCACTCCCTGGCTGCTGGTCATTGCTGGC
AGTCCTTGTCCTTCCCTGACTAGTANCTACATCATTCTCATTTCTGCCTCTGTCTTCATA
TGGCTGTCATTTCACTGNGTGCTTGTCTCTGGGTCTTCAAGTGGCCTTTTTATAAGGACA
CTGGTCATTGGATGTAGGGCCTACCCCAATC
Sequence 755
CCCTTAGCGTGGTCGCGGCCGAGGTACATGTTGGAAGGGTTTTTAAAATGTTTTGAAACT
GTGCACAGGCCAAACCCAACTTTCAGGACATGGGTTTTCAACTTCTGGATGGTATGATGG
GGTGATAGTAGGGTATAAAAGTATCCTGAGAAGTTGAAAGCAGTGTGTGAATGGGGTGTT
CTTTTCTCCCCACAATCCTTTCCCATCTGCTGACAGTAGACTTAGCACCTCACAGATGCT
TGGGCCTGGAAATGAAGCCATGAAAATGAAGCCCTCAGCCTTCTTGGAGATCAGAGCCAT
GGTCCTCACCCACAGCACATGGG
Sequence 756
CCCTTAGCGTGGTCGCGGCCGAGGTACACAAAATATTAAATAGGATATTTATTTCTAAGC·
CAAATTTCAGAAAACAATTTACAAACTTTTTTTAAAGTATAAACATAGTGTATGCTTACT
ATAAAAGGAAAAGTATAAAACATTACTCAAGTATATATAGAAAATGAGTGGGCTGCTGAT
CCCCCTCTATATTATCTATTGCTGTGTGACAGTATTACCACAAATACAGTAGCTGAAACA
ACACATTTGTTTTCTCACAGTTTCTGTGGGTGAGGAGTTCAAGCATAGCTTGGTCCTCTG
CAAGCTTACAATCCAAGGGTTG
Sequence 757
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TATTCTCCAATGGAAGTGGGAACAAAGAGAAAACCCCTGTGTGTCCTAGCACAATATGGG
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GTACCTGCCCGGGC
Sequence 758
CCCTTAGCGTGGTCGCGGCCGAGGTACTTGTTTTAAAACAATGTTGGAAATGAGGAAAAT
GAGCAATATCAACATTTTATCCTGAGGGACAGGGAGTAGAAAACAAGCCAGAGGCTGCTA
GTTACATAGTTCAGTCTTAGGGATGAAGGGATTTATGTCTCTCCTCCCTCAGGTACGCGG
GGACTACACTGGTGTCTGACTTTTTTTCCTAGAGATTTCTCCCTGAAAAATACAAGGGCTG
TTGGTGAGAGCAGACTTGAGGTGATAATAGTTGGCCTCTGGTCTACAAAGATTTCATAAC
TCCTTGGAAAGCTTC
Sequence 759
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CCATTGTGAGTTGTTCAGTCTGAGGAGTTAGGTATAAACCCAGAGTGGTATTCTCTTTTC
TGTTGTGTTTGGTTTTGCTTACATATTCAGGAGCTGCTCTTTACCCCCAGAACATCCGTA
TATATGTTTTTTTTCTGTTTCTAGATTTAAAAATATTCCAGAAGCCTGGCCTCAAGATAGA
TAATATTTTACTTTT
Sequence 760
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAT
ATCCTTNATNAGGNAAAAATTTTNNTTTNAATTAACNGGAAAGTTTTNATAAAAAAAGGA
TGTTAAATNGATTTNAATGCTNTTTTTTGNATTNGTNNATANATTTTTTTTAAATTTTTTAAA
NCGNGNAATTGGGTNNTTTAATNGGGNGTTTTTTTTTAAA
Sequence 761

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTACAGATATAAAAAGGCTACTATTCCAAGAACAAAA
TCCTGGAAACAAATGTCTATCAAGAAAGCAAAGATAATCTAAACAGCAGCATATTCATAG
GATGACAAACTATTCAACCATTATAAAGAAAACCGAATCAAAAGCACTGGCTTATTAGAC
AAGAGTTTCCCAAACTATCATGCTAAAACAGTAACAGCGAGCTTCCAAATTAATGTTGCC
TTTTTTTTTTTTTTTTTCCAAACTGAAAGGAGGGTGGGGAAAACAAACGCATCATATGTAAA
GCACTGAGTCCAGCCT
Sequence 762
CCCTTCGGCCGCCCGGGCAGGTACGCGGGTATGGTTTTACGAACAAATTTTTAAGGAAAA
AAATTATCATGGTTCTAATCTTACATGTTAACATTTCCTTGTTATGTAGGGATCAGACTT
GTTATAACATAATTCCACTTTATAATTCAATGAAGAAGAAAGTTTTGTCTGATTCTGAGG
TATGTAATATTTCATTATTATTACCATATTGATATTCTCTATATAAAAAAATTTACATAT
TGTAGTTTTCAGGTAAAAGCTGTTGTGAACATTATTTTTTTGTCTAGTGTAGTTAATTTAA
AAAAAAAAAACAACTG
Sequence 763
CCCTTAGCGTGGTCGCGGCCGAGGTACGCCTAAGGGANGNNNGGAACTCATNAAAGAGAC
AAAANGTGCNTTTTTTGNTTNNAAGGCATGCTGTGGTGGTTGGGCGCAATAAAATAGTTGG
GGCCCCCGANTGCCANTGACTTGCTTTNTNGTNGGNAACNAAATGGCCCATCANGTTGGA
CNCACCTGNCCANTTCACAAAGACCTTGNCCCCATTCNTGGGAATGNAAGGGAGNGTTAA
AAATAAAAAAGTGTTGACCACTCCCTTGGATGGGTTTAGCCAAACCTTGGGNTCCANGCC
CCTGGAAAATTGGTTTTAAAAGGGGGGGNAGNTNGGGATCCAAAACCCTGGGGGGGCCAAA
ATAAGATACAATCCGTANCTTGTTNGGGAAANTTCAAATTTTAATTGTTCCCCCCAAGNA
TTNGAATTANNAAAAAAAACCCCAAAATTTGGGGGAAGGNAAAAAAAANGT
Sequence 764
CGCCAGTGTGATGGGATATCTGCAGAAATTCGCCCTTAGCGGGCCCGCCCGGGCAGGTAC
CGCGGGATTCATTTGAGTGGGAATCTCAAAGCAGTTGAGTAGGCAAAAAAAANGAACCTN
TTCATTAAGGGATTAAAAATGTATAAGGCCAGCACCGTGTAAACCTTCGACTTTCAAAGA
ATTTTCCTGGAAANCCCATAATTGGTAGGTNATGGGTTTTCAATTTGGTCCGTTNCGCCA
AGGGGGGGTAAAGTTNGAATTCCCCTTGGGGCNAAGTTCCAACCCCANTAAGGCCTTCCT
NAACNTTTTNGTTTTNNAACCTTTTTTTTTTTAANGNCCTTTTTTTTGAAATCCCAAAAAA
AAAAATTCNTTTTAACCTTTTTTTTTAAATAAAGGGGGAAGGCCAAGTTTTTTTTTCAAAA
ACTTCCCCTTAAAAAAAAATGGNTTNGGAAAATTAANTAAAATTTAAGGTTCCANGGNTTT
AAAAAAATTTTCCACCCCAAGGCCCTTACCCNCCAANGGGGNAAAATTAACCAAGGGGGA
ACCTTTTTTNGAA
Sequence 765
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAAGCAATGTTTTTTGAAAGTTTTCTATCTGT
GGNTTGTTGAATCCACAGATGCAGAACTCATGGAAACAGTGCCCACTGTATGTCACAATT
TCAGAAAATCAGTATTTCATACAATCANGCTAATAGCCTAATTTGTTGAGCACAAGAAAA
ATACACTGAACCAATTCTGATTATTGCANGAGAAATGATTGGCAGGATATTGGGAAATAA
GAATGAAGGGCGGANAGAATTTCACATGGATTCAATATACTCTCCGTCAGNGAATTTTTG
TT
Sequence 766
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAAGCAATGTTTTTTGAAAGTTTTCTATCTGT
GGTTTGTTGAATCCACAGATGCAGAACTCATGGAAACAGTGCCCACTGTATGTCACAATT
TCAGAAAATCAGTATTTCATACAATCAGCTAATAGCCTAATTTGTTGAGCACAGAAAAAT
ACACTGAACCAATTCTGATTATTGCAGAGAAATGATTGGGCAGGATATTGGGAAATAGAA
TGAAGGGCGGAAANAATTTCACATGGATTCAGTATACTCTCCGTCAGGAATTTTGTTCCC
TTGATCTTTTTGTGGTTTAATGCCTTAATTTATTGGGGCCCCTCTCATANGTTTGGGGGG
Sequence 767
CCCTTAGCGTGGTCGCGGCCGAGGTACAATCAAAGGAGTCTAATGGAACCAAGTAGCAAT
GTTCCCGAAAACAAACAAACAAAAAACCCCAAACATTTTGCTGTTTCTTTCCCCTCTGTA
TTTGCTAACTTTATCATGACTTTATTCTTAAAGCCTATCACTGGTCTGCTTTTATTAATA
GATTAGTGGAAATTTTCACCTGGCCTATTAGCACCTTATAAAGAAATAGATTAAGAGTAG
GAAATATATAGATGAAGATGTACTGTATAGAAGTTGTGTAAAATCAGTATGAAAGTTCAA
TGTTGCTGTTCTTGCTCAGTGGATTTTTAAAGAAATTGAGTAGTTCCTATGTGGATTTTTT
TTTTTTCTTTTCTAAACTG
Sequence 768

132

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACATATACATTATGTAATNNANAAGCGTGCATG
GGGATGAAAAAAAAATTTTTTNNTNTATAATCNNGNTACAATATATACAATAAAACACCTA
AAACGCAGAGGCTTGCCTTGTTTNTCCACAAATANGTTAAATACCCAAATTAGTAATTAA
ATGGATTGGTGGTTATGGTAGGAACACCAAGACNAAAAAGCCAGGCCGGGACCGTNATTT
TAATTNNGGGCCAGTACCACCACNATATAAAGGCCACCAACCAAAAAAAGTCCANANANG
CCAANAAANAAGNCAACCGCCCCAAGTTNAAATNGTTTTGTTGGGGAATTGNCCCAGTTA
NTTCCAAAANGGAATTTTTGGTNCCCANTTANTTAAGGAACCAATTTAAATAATTCCCCC
AGGTTTANGGAACNACCTTNGTTNAAATTAAGGTTTTTTTTTTTTGGGGTTNACCCCTTTC
GGGGGCNCCGCCNGNAACCCCANNCCGTCCNTTAAAAGGGGNGGCCCGAAAAAT
Sequence 769
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTATTTTTTTTACTAAGGTTTTGTTTTGGAGA
CTTGTTTGAAATAAAGTGATCCTCATTCAGGATTTAGAAACAAAAGTTATACTCCACATG
CTAGGGATTAGGAAGGCTAATGTGAACTGATCAAAAGTATGAATTATGGAATGCCTTTAG
AATAATCAACTTTTAGGTAATTTGATACTGCTATAATTTCAAGCTTAGAGAAAAGTTGTA
AGAATGGCATAAGGAACTCCTATATATCC. TTATCTAGATTCACTAAATGTTCATTTTGT
GCCATTTGTGTTATTCTTTGTCTCATCCTAGCCCAGTCAGCCTAACACCACCCAGGGGAT
AAACCAGTAGTCTGATA
Sequence 770
GATATCTGCAGAATTCGCCCTTTCGAGCGGCCCGCCCGGGCAGGTACCTCTCATTTGTCA
CTTTTCAACACTTCCTGGCAGGCAGGCAGCATAACTGGTCCTGCTGGGTGATCCAGACCA
CACTCTGCAACTCTTTCTTCTGAGCCAGGCTCCCCTACTGTCTTTTCATTTATGTCAAGG
CAGGGGAAGACCTCAAAGGGCTCTTGCATCCCAGTCTCACTTCCCAAGAGAGGCACGAGG
CCCTCCAGGATGTGGGGACAGGAACTTTGGGGCAAGCCCGGGGCTGTCCAGAAGATCACC
AGGAGGGCTAAATAGTAGAAAGGAAAAGTCTTATTGGTGATATGTTTGCAAACTGGGAAA
AAGATAGCCTCCAGTGTGGAGCAAAGATGCTCCTTCTTCAAAGAGGGCAAGGGCAGCTTG
GATTTTGTGCCTTACANGGTCNGTATTATATAATAGAGTCATGCATATTCANTAGGTTTG
GGGGAAAAGCTATATATATTTATGAAGGGGAGCCAACTACATGGGCAATGGATAAACATA
CATGTAACACATCCATGTTCACTTTAGGGGCA
Sequence 771
GGATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACAAATAAAGTATTCCA
AGGGNGGNAGAATNGAAAANGANGNCTNNCANCTTGNTNNCNTTTGGGAAATTGGGATAT
CCTTTGGGGAAATGTAGTAATCAGTATATTCTGGGNAAAACATTAGTTAGAAGAATTGAA
NTAAATAAAATTTCCATTGAATTTGGAATATGTTGTCCATTCTCCCTGTAAACTAATGCT
ATCAANGATAAAGTANGAAATACCACATTTCAGNAAACAAGCTTGGAAGTAGNACAAGGT
CCTTCATTAGNGCCNTAGCCTTGGNAAACCCTTAATAANCCTATNTAAATAAAATTGAAA
ANTTTTTAAATTTATNACTCCTGG
Sequence 772
TGCAGAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACCACCAATAATGAGGCCCACATT
GTGTATGCTAAAAAAAAAGTGNTTTTNNTTNTTCCTTGGGCCTACAAGAACATGTTTCTG
TCCGCTAAGGAGAAANTNAAGAAAAACAATGGCCCCCCTTNCCTTCCCNATNAANCCCAAA
ANCCTTAAAACNTCACAGGGGGANGTTGNAATTTTAAGGAANTCCACCCCTTTNTGGGGGN
NNCANTTTTTTTTCCCCCCCCAAAANAACCCAACNCCCCATTTACCCTCCTTNGTTAAGAAA
TTTTCCNTTGGAATTNAATNGCCNACCTTCCTTTTAAANAAGGNANAAGCCCTNNACCNA
AGGCTTTCTTTTTCCCCCCCAATTTNCCCCCCTTNATTCNTTGGAAAAAANGGCCCNAAC
GGGGGAAACCCCCCACCCTTTGGGCCNTTTTTTGGNGGGTTCCCAAGGGGGAAAAAAACC
AAGGGGCCNATTTANCCNAAAACCCAATTCCCANGGANATTGGTTTGGNAATTTTAATTA
AAAAAATTNGGGGGCCCCNACCCATAATTTTTCTTTAAAAAAAAANGGTAAAA
Sequence 773
CCCTTAGCGTGGTCGCGGCCGAGGTACTATCATCCCCCAAGGCCTTTTACAGTCTGAAAT
ATCAAAATTGAAAGCAAAAATAGGATGACCAAAGGACTACTATTTNACTCTCTTTTCAGN
AACNTCNTACAATATGTATGAAAACCTAAAATATCCACTNTATGGGATCATCANNGGGGG
GAANNTAAANTGTTGCCCNTGTTTTNGNAAANGGGGCATTCANGATGTATTTGGGATGTN
CNCANGGNCCTGGGGCANTTTTATNTCAAGGATGNAAGGGGGNTNNCATTAACCTGAACCA
AGTGGANTGACANGNGTCTTCNCNTTATAAATACCAANGGGGGCCGNGTTNTGGCNAACCC
CANGCCACCCCAATTGGAACCTTATGGGGGGGGCCTTNGGCCNTTTTTTTANAAAANAACCA
AAAAATTTTTTTCTTAAAGGGGGGAACCTTTTACCCGGNCCTTCCTTNTTTTGGGGGGG

Table 1

Sequence 774
CCCTTTCGAGCGGCCGNCCGGGCAGGTACATATACATTATGTAATTAAAAAGCGTGCATG
TGTATGTATTAAAAATAATGGTATATAAAACAAAATTACAATTATATACCAAATAAAAAC
CACNCTAAACGCCANNAGGGCATGCTTGTTTATTCCCACCATATTAGNTAATAACCCAAA
TAGATAATTAAANTGGAATTGGGTG
Sequence 775
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGAGAGGGGTCATC
CTCCAATCATTAACTACTTCTAATCTTCACTGCTACACAGAAGTTTCCAATATTTAGCAA
CAGATGGCTTTGCTTTTACCTTATAGATGAGGCCAAAGCACCAGGTAGGTGGAAGGTTCT
TGTATCGGTTCGAACCCCNACAGCGCGCCAAC
Sequence 776
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGNCTGCC
GTGGAGAGGATGGATGGGAGGGGGAAGAACGAGAGCTTTGTTTAGAGGCTGCTGTANTAA
TCCAGGTAAAGGCTTTTAATCATGTCCTGAACAATGATCAGCAATGGCAATGGANATGAC
AGAACANAATTTAANAAGGAATAAAAAAGGCTTGCTGACTACTTGGATGTGGGTGANG
Sequence 777
CCCTTAGCGTGGTCGCGGCCGAGGTACTGCAAGCCAAATGCAATGAACAAACCAAGGTTA
TTGATAATTTTACATCACAGCTCAAGGCTACTGAAGAAAAGCTCTTTGGATCTTGNATGC
ACTTCGGGAAAGCCAAGTTTTTCCGTAAGGGTAAAATCGGNAAANTGAAAGNAAAACCTTT
AAGACCAGNCAGCTTTGAAGGTCAGCCTTGAGTAANACAGNAATTTAATACCAATTTTAA
GAAGGAATTTGGAANAAANGAAAATGGCCTTGAAANAGGTTAGGCCAAAGGGGCCTTAGG
GTTAAGTTCNCTTTAACCCCAAGGAAAGGAAGGCCTTNCCCATGGGGGGGGGGAAGNAAAG
NANGNCCTTNAAAAAGGCCCTTTTAACCCTTAAAACCCCTTTTTTCAAGGGGGAAAAAAA
AATTNTTTGGAAAGGTTNGNAAAGGGTCCCANGGTTTCCANAAGGTTNGGAAAAAAGTAA
AGGAACCTTTTTTGGGGGATAAAAAAAAAGGGAAACCCTTTCCCAAGTANTTTTTTTTTGGG
AAAAAAGG
Sequence 778
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGTTATCAGGATAATACTAGCTTCACAGAAGA
AGCTGGGAAGTATTCCCTCCTCTTCTATTTTTTTTGGGAGGACTATGTGAAGAACTGGTNT
TAATAAAAACTCCTTATTAAGGAAATTTTTTAACATACCAAAAAATAGTAAGAATAGTAT
CATGAGTTCCTGTGTTGTATTCCCGCCTAACTTCAATAATTATCAATAGTCCACCATTCT
TATTTTACTTATACTTCCCCTCCCCAACACCTTACTCTTTTGGCGGGGGCTGAAATTATT
TTAAAGTAAATCCCAAGACATATCATTCACCTTTAAATACTTCAAATGTATATCTTCTAA
CAGGATAAAGGACTTTTTTTT
Sequence 779
CCCTTAGCGTGGTCGCGGCCGAGGTACTACGAAGCTGCAGATCATTACGCTGATATGAAT
GACTGCTTGAAAGAACAATGACTCTGGCACAGCCACTGCTTTTCACCCAGGAAAGCAGTT
TTTCACAGAATGGCTTTGATTTATACTTTGCACACCATTGAGAGAATAAAAAGAAAATCT
AAAAGTTAGTCTTAGAGCATACAAACATTCTATATACTATTTCATCAACTTTATGTGATA
ATGATATATAATTTATATATACTGAAATTATTTTCAGGATCCACTTACTGTGCTTAAACC
CGAAAGTGAATGATTAAAGAGGCAATGGAATTATCTAATGTATCTTTTATAAATTAAGAA
ATCAA
Sequence 780
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGACAGTGTGATGGATGATGCTGCTGGTTGT
AAATTTCATCGTGTGTGTCTAATTTTTTTTTCCTGTATGAATGGGGTAAAAACAAAACANN
AACTTTTTTTTAGGAAGATTGTAATTTTGCNTGTCATGTTTTTNGTAGGNAATGAGGGGN
ACTCGTTTGNAGTCTTCACCTAACNCATCCCTGNGNAGTTTNTGAAGTTTTGGAAAGNCC
ATTGAAANNATTGTGTTGCCCCCCAATGNCCCTTGGACCNGCCTTNACAGTCCGNCNCTT
NNGGATTCTTGCAACCGTTGTC
Sequence 781
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGCGGATGAG
TCTTTTAATAGAAAAACACACGTGCAACAGTATCAANACACATTTTTTNGCAATCCTGAC
AGCAGCTGAACTTCAGTTCTTCACCTTGGGGGGTGGCCTGTACATATCAAAATCTATCAA
ATTGGACCCTCAACTATGCATTTTTCTGNGTGCAAGTTATATCTCAATTACAAACAAACA
AAAACACAAAACCCTATGGTTAACCCAAAACCTAAACTATNACCAAGAAATATCAATTGG
GGTTATGGCATGACCATCCTCCCCAAGAAAATAAAATGCTTGACAGATTCTGAGCGGGA

Table 1

Sequence 782
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAATAAATGAGTTTGCAGTGAATTGGGCCTT
CAAATTACCTCAAGTGACAGATAGTAAGAAAAGCTTNTTTGAGCAGGTGGAGGTCACTGA
ATCCCCTACTATGCACTTATCAAGATTTTACTTACTTTAATTTACTGGAAATTGATTTTT
TAAAAAATGACTACACTGTAACAAGGGAAGGGATCTGGGTTTTTTTTGTTGTTTATTCTT
GTTTTTTTTTAAGTAGTTCAAATTCTGAAACTGTGATTTAAAAATTTTTTTACAGTCAAGCA
TTCTGATTTTGAACATAACTCCCTTCCCTTTCTGTGTAACAAAGGTCTCTCTGTTATCTC
TTAAATTT
Sequence 783
CCCTTAGCGTGGTCGCGGCCGAGGTACTCTTCACTGTCTTTGCCATGAAACTTTATAACA
TGGCTCTCCAGGTGTTGAATCTGGTGCCCTGTCACCCTGTGCTCAGGGAACACATGGCGG
CAATCAGCATGTGAGGCGCAGAGGGAGGGCAAGCTCCCCTTGTGATATTTGAGGTATCAG
CTGACTCAAGTCTCTCTCCCTTCTCTCCTTATTCTCATGCTACCTNTCCCAACCATTGTC
TTAACTTCCCTGGCCAGGATGCCTGCCATATTAAATGGAGAGGAGGCAGTTTCTAAATGG
CTTGACTTTGGTTGAAGTCTCAACTCAGGAAGCTCTGAAATTAATCCACCC
Sequence 784
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACTCGATTGTCAACGTCAAGGAGTCGCAGG
TCGCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAAGTTGAAGATTAGTCCGCCGTA
TTTCGGTGTACCCCTGGGAGGTGCCAGTCATTGAATAGATAAGGCTGTGCCTACAGGACT
TCTCTTTAGTCANGGCATGCTTTATTAGTGAGGAGAAAACAATTCCTTAGAAGTCTTAAA
TAT
Sequence 785
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGAGGATATGTGTGCATTACATGCAACCACTA
CACCATTTAATATCTGGGGTGTGAGTATCCGTGGGTTTTTGGNATCCGTGGGGGGTCCTGG
AACCAATTTCTCCTGGATACTGAGGGATGACTGGATTACTGTGTGTTTGTGTGCTTGTTT
TTAAGCTTCAAAAGATTATGTGATCTAGGAGTTGTTAGATTTTATTATTGGTCTTAAAAG
ATAAGCTTANATGTTGTTACTTTTTTTGGAGTTTTTAGTTTACAGTGATTTCATGAATCGG
GCAGCTTCANACCACAGGAGACATNAAGCAGGTTTNAATTTTCAANGAAAGGCNTTTACA
AGGCAAAAATATTTTGATTTGGTTTAGA
Sequence 786
TGAATTCGCCCCTTAGCGTGGTCGCGGCCGAGGTACTAAAACTAAAACTGAGCAGTTTAAA
ACATTCATTTAAAGGGGATATCTAATGTGTTTATTATTAACATAAATAATGTTTTTTATGAA
AAATGTAACCTTNGTTTTCCAAAACAAAAATGTTTAGGGCAAGAGTAACATTATTTTACA
TTATTGCATCTCAGTTGAAAAATAAATGGCAACAAAAATTCTTATATCTGCTTCTGCAGT
TAATCTGNTCATTTTGTTTTGGTTGAANTATATTGAAGGAAATCTGTTCCTCCACACAGT
TTGTGTAGTGGGAAAAAGGGGGGAC
Sequence 787
CCCTTTGAGCGGCCGCCCGGGCAGGTACGCGGGATTCCTGGTTAAGCAGGCATTGCTTTG
CCCTGGAGCAGCTATTTTAAGCCATCTCANATTCTGTCTAAAGGGGTTTTTTTGGGAAGA
CGTTTTTCTTTATCGCCCTGAGAAAGGATCTACCCCCAGAGGGAGNAATCTGTAGNACAT
TCTTTGCCTACTTNTTACTTTTATTTAGGCTNTTCTTCCCTNCAATTTCAATTTTCCTGT
ATTACCACCCTTTTTTCCCCTTTTTTTTGGGGGGGGGAAGA
Sequence 788
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGCAGGCCTCCTACACCTACCTCTCTCTGGGC
TTNTATTTCGACCGCGATGATGTTGGCATCTGGAAGGCGGGAGCCACTTCCTTCCGTGAA
ACTTGGCCGTAGGGAGTAAGTCGCCGAGGGTCTNCNAGNCGTTCTTTNCTTGAAGGATGC
ANAANACCCATGGCGTTGNGCGGACCGCGCNTCTTCTTTCCATNGGAACATTCAAAGGNN
AGNCNCAAGTTTTGNATAGTANTGTAANTTTGGGNGGGTTAAAAAAACCTNCCCAANGNAC
CGGCCCTATTGNAAAAAAGNCCTTGNCTCCAANTGNGGCCCCCCTTGGGGTAAGTNAAAA
AAAAAAGTCCCTTGTAANCCCCAAGGGGCCCCCCCCTTTTTTTGGGGGAATTTCC
Sequence 789
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTAATTTCTTTATAATTTGTTCAGCTATTT
AAAAAGATAATCCACAATCTCCTACCGCCATTAGAGCACAGGAAAAAAAAATTCAAAAAT
AAAGGAAAAACATGGCTCATATATCTACAGAAGTCACAAAAATACTATAGGGCACATATA
CCCAGGCCTCAGCGGTGGGAAGAAAACATACAACCACCGGGCAAAATGTTTGAACACTGA
AGACGGGAATTTTTTAGGGCC

Table 1

Sequence 790
CCCTTAGCGTGGTCCGNNGCCCGAGGTACTCAAGTCGCCCTTATGGAGCCCTTGATTCAG
GCTTCAATAGTGTGGACAGTGGTGATAAGAGATGGTCAGGGAATGAAGTAAGTGTTTTTT
ATGTTCCGTGTGTTATAACACCTGATTAAGAGAAAACAGAATGATGAAAATGAAAAGCCG
TCTTAACTGGATTCAAGTTTCTCACTACATAAAATACAGAAAAGTCAAGGTGGAGGCAAG
ATTCCCACCCTCTCCAGCAGAATTGGCATTCTGCGTCCTTACCGGCTTTCTGTCACGTGG
ATTTCCGCCTGTTTCCTCATTGCCTCATGGAAATAGTTTCATATCATAGAAAGGCAAACA
GGAGCTGAGCCAGTTTGAAACTGAACCTACAATCTGAGGTGGGGGGTAATCTCGAGCAGA
AGTGCTAGATGGTGAAAAAACAAGTAGGACTTTCGGCTGATGGGTAGAAACAAGGACCTT
NGTAAAGAATATTCATGTGCTCAAAAAGGAATAACTTCCTGGCTAATTCTTGCGTTTTTC
TCGTTTTTAAAATTAATTGGATATTATGTTTTCTGCTCTTAAAAATTACTNNGTNCACAG
AAGTCTACCAAAAAAAAAAAAAAAAAAAAA
Sequence 791
GATATCTGCAGAAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTAATTCTTTTCCTCT
TTCCTAGACCGATTCTAGTTTGTTGCCTTCCCTTTCCTCGGAAACCCCAAGTTTGTGGAT
GCTGCAGACACTCTGTGCCCCCCTGCATGCTGGGTGCCTGGCCAGCTGCCAGGGCATAAA
GACAGAGACGATGTGGCCTTTGTCCTTAAGAATGAGGTTTGAAAGCCTCAGTTCTTCCAT
GTTAGGTGATTNCTTGCAGCTCTTGGTATCTGCAGAATTAGTGTGAATGCTTAAAAAATA
TTAACAGCTTTATATCATCAAAGTTTTAACAGTACCTGCCCGGGGCGGNCCGCTCGAAAG
GG
Sequence 792
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAA
GCTGAAGGCCACAGTAGCTAGCTAAAGGCCACACCACTGAACACTAAAACTTAACCTTTA
CTGGCTACTTTGTANATAACATTCACAGCTCACCATGAATGCAGCTGCAGTCAACTAACA
NATATGAAGTTACCACTGTATTACATGGTTATATTAGGGACTGCTTNTACCTACTGGAGG
CTGGGGAGGAATGTAACAGCACAAGCCATAATGAAGTTTATATACAGGCTTAATATAAAA
NAAAACCCTAGAATGAACTCAACACAATTAT
Sequence 793
TTTTTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACCATGCAGGGATAGCTG
AGTCTTCATCCTCCTCAGCCCCTATCTGTTCAGTGCACTGAACACCAGCTGCTCTCTTCC
TCTCTGGCTCCCATGGCAGCCATGGTCTGTTGCAGAGAGAAGAGGATTGCCTGTTCCCTC
TTTAAGGGAACCTCCGTTTTGCTTTCTGGAACCAC
Sequence 794
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACGAACTTAAATTTATGATGAATATCTTTGAT
AATGAGAAATCCTGAGAGATTTTACTTTCAATTTTATTTTAATTTGAAAGAGCATATGAC
ATCTGGAATATTTTTAACATATAGCCATACTGTTTATTTAAAATTTGTAATAATAGAAATA
GAGTAATTCTACTGTTGGATTTTAATTTTTTAATCATATTAAAGTTTAACTGGATTTTATT
TTAGGACTAAAATATTTAGGACTAAAATAAAATTTTATTAATTAATTTAGGACTTTTGGGA
AAAGATATTTCAGAAGTTCAGTGCATATCAAAAAAGCGAACAACAGAGGCTTCATCTTTT
GAAAACTTCATTGGCTAAAAGTGTCTTCTGTAATACTGATAGTGAAGAAACTGTTTTTAC
ATCCCGAGATGTGTTTGATG
Sequence 795
CCCTTCGAGCGGCCGCCCGGGCAGGTACCCTAGGTGATCTTTGGCTTCCTCAAGTTTTTG
CACCACTCAGAATCATTTCATATACCACCTTTGGCAAACATGCCAGACCTGCAGTAGACT
GAAGGAAGCTCTCCCAAGCTCTAAATTGATTAATTTATTAGTTCCTAGAAGAAAGAGATT
ACATGTTTATCTTTTTGTTACAGAAGAAACTTTGAATAGCAGTTGAAAATTTGGCAGGGT
GGACCACCTAACTTGACAGTGTATTATTGTGTCTGTTTTGAAGGAATAAAATGGAATTAT
TTATAAAGTTTTCATTTGTATTAGAGA
Sequence 796
CCCTTAGCGTGGTCGCGGCCGAGGTACACTATCTGACCTAATCCTCAACACAAACTAAGG
CAGGAGACACAGGGCTGCAAGGACATTTGCTGCCATCCAATTTGTGCCAGCCTGTTTTAT
CAATCTGAACCTATATTATTTTTTAAGACCTCACGGCATCACTGAAAGATGAGTATTATTA
GTTGGAATTTTTAGGGATGAGAAAACTGACCCTCAGGGAGAATAACTGACTTGCCCCGGCT
CCAACAGTAAGTGGCCCTGCTGGGATTTGAACCCAGGTGTGTCTGACCCCGAAGCCTGAT
CTGACCTCTGACAGTCGTGATAAAAATAAT
Sequence 797

Table 1

CCCTTGGCCGCCCGGGCAGGTACCGAAAAATGATTTTGTTATATATATTTACCACAATAA
AAAAGTTTTAAATTTATTATAGGTGACACTGTTTGCTCACTGTAGGTCAGGTATTTTTTG
GTTTTTTTTTCTCTTTATTTTATTTTTGACCAATGGATTCACGTCACCAGGTGATTTTTT
AAACAGCTTTATTGAGATATATATCACGTGCCATAAAATTCACCCATTTAAAGCACACAG
TTAAATGTTTTTTAGTATAGAGTTCTGCACCTCTTATGACAATAAATGTTAGAATATTTT
CATCACTCAAAAAGAAACCAGTATCCATTAGCA
Sequence 798
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATTTTTATGTTTACAGCTGTAACCCCTGAG
TTATCAAGAGATGGAACATTAGATATGATTTATTCCTATTTAAGATAATAGGACATTGCT
TGATTACATTTTCAGAAGATATTTATCCAAAGAAATTTTTTTTTTTTAATCTAAAGGAAAG
GTTTTGATTCTTATGAGAAAAGAATGAGATTTCTTTAACTGGAAAATTGATTTATGTCCT
ACAGTCCATTGTGTAGTGATGTTGGATCAATCAGGTATCNCTAGGGTGTCTGNAGAAGTA
TCTATATATTGCTTTTTAAGTTCTTAT
Sequence 799
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCATGTAGCTCTACTTTTCCATATACAGAGTT
GTTTCCTAGCTTTCTGCTAATCTAACTGGATTCCTCTTCCCCATTTCCTCATTTACTAGA
TTATAATGCACATCACATAATAAAAGCTTAAAAATGGGCTTTCACAGTTACTGTTTTCTT
TTTAAATAATTGTGAGAGAGCTTTTGCATCATTTATTATCTAATCATGATTCAAGTGACT
AGGCTGTAGCACCCAAGAACCTTGCCTTAAAACAGTTTATTTTACCCAATAATACTACTT
TGCCTTCTTACTTAAAAATGTCCCGTGCTTAACCCTTTTGCTCTTTATTTTGATTTAAGC
ACTTGACC
Sequence 800
CCCTTAGCGTGGTCGCGGCCGAGGTACTNTCTATTTTTAACAAGGCTCCCTCAAGATATT
AATGTGACAAACTTACATAGCCAGCTGTAAGATAATTCTTTCAAATGCGCAAGTAACCTA
ACAGATTTGTGCATGTCAGCCAGTAATTTCAACATACATTATAAATATGGCCAATTTTCC
CAAATTCTAAATGAATGGAGATAAAATGCTATATAATAAATATGTTAGAGCACCTTTCTT
GAGAAACTTNTAAAAGGAAAAAATAAAAGACATAATTATACTCACACCACCAGTAAAACC
TCTGGTCACCTGTTTTGGGTTGTGGGAATGCCCCCAGCAGCCGAGAGACCTATATT
Sequence 801
GATGGATATCTGCANAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTGATTATTCTCC
TGCTTAGGGAGAAGCGGAAGAAGGCCCTTGGAACTGTGAGTTTTGCATTCCAACTTGCTA
ATTCAACATAGATCCTAATTCCTTAAATGCTTGTAATTAGAAATTCTCGTGAACTGTATT
GGTTTTTGTCAAGCAATCTGTTTGGGGAACTTGAGCAACTGGGGCACTGCTGGCTAGGGT
GAAGTTTATTTAATTTGGTTTTATGACATTCTTCATCTTGGAAATGGGGTTTTCAAATAT
TGCTTTCCCAAGCATCATTACTTATTTGCTGGTTTTTA
Sequence 802
CCCTTTGAGCGGCGCCCGGGCAGGTACGATAGGCATGCAATTAAAGAAGACCTGCCTCAA
ACATTTTCTGTGTGACCTGAGGCANGTCCTTTTATAGCTATAAACTAGGGACAATATTTG
CTGTCATTTTTTCTACAAATGTCACAAAGAACAAATTTGAGCCTGTCGCTGTGAAAGAAC
TTAGCAAATGAAAGCATCCTAGGGAGTGTTTTAGATATCGATATTTTTATCCAATTAACT
TTTCAAAATGAGTTTATTTGCTCACTGAAACTGAAGTACCTCNGGCGGGACCACNCTAAG
GG
Sequence 803
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGGTTCAGCTGTCTCTTACTTTTAAC
CAGTGAAATTGACCTGCCCGTGAAGAGGCGGGCATGACACAGCAAGACNAGAAGACCCTA
TGGAGCTTTAATTTATTAATGCAAACAGTACGCTTGGGAGTCCTCAGCAGGGGGATCATT
CACAGTGAGGACAGACACAGGTGAACCTATGGGTCGTGGAACAAAAGTTATCCTACACCT
GAAAGAAGACCANACTGAGTNCCTNGGCCGNGACCACGCTAAGGGCGAATTCCATCACAC
TTGGCGGC
Sequence 804
CCCTTAGCGTGGTCGCGGCCCGAGGTACCTTGCACAGTGCCTTTTAAATTCATTTTGCTG
GACAGTTGGCAGGCTCTTTCACTTGAGAGGCTTATATCTTAACGATTTAGAATGGAGAGT
TTGGCTCAAGCTCCCTGTGTGTGGTCTGTGCTTTCTATACTTTTATTCTTGGTATTCCAG
AGTCTGGAGGCTTCTCTTTTTAAAAAATTGCTAGGCTCCTGCCAAATGTTATAATTTGGGG
ATGTGAGTTCACTAAGAAATCAACTGACAAGAGGCAGATTAATAGGAGAAATGACATCGA
AATTTATTAGCATGCAGGGGGAAAAAAATTGATTACCAAATATCCCAGTAGGGTAGAGATG

Table 1

CTTATATACCCCACCTCTTAAGAGAGAGGGAAAGTGGATGATTTTAGGGGAATAGTAAAT
ACTTTTTATGGGAACTCACTGGGCTTGAAGAATATAACAAAGGCCTGGGACAAAGTCTGT
TGGGCCCACCAGAACAAGACAGTGGTTTATGACAAAAGTCTGTTGAGAATGTATTGAACA
GACTTCAATCTTTCTTCTTGGAATATGATTCAAGTTNAAGGAAAACTAGGGAAGGGACTA
GAGGGAAATNGT
Sequence 805
CCCTTCGAGCGGCCGCCCGGGCAGGTCCGGGCAGGTACTATTACTAGGTTCATTGTTTCC
AGAGGGGTGAAACGGGGCTTTGGAGAGGTTAAATAACTTGCCCAGGGTCACACAGCTATT
AAGTGGTAAAGCTGGGATTTACATGAGCCCAGACAAAGAACCCAAGAAGCTAAGCTATTC
TCTTGTAATACCTCCAACATAGGAGGCAAGAAGTGAGGTATTATACAGGTTGAGGAGATA
AAGGGGAGAGAGGCCTGCAGTGCTAACAGGAGGAGCTGGGATTCATCCTGGCTTGTTCTG
ATAGGTCAGTTAGTCTTAGAGATACCCATGAGGTCACCTACTCAAAATGGGGCTCAGAGT
AGCCTTGTCCCATTCTTGTCCAGTGGGCGCAGCTACAGTCTTCCTGGCCTGGAGTGACTG
GAGGCTGTCCCCACGTCCCACTTCAGTGAGGCATTCATGTGCACCCAACACACTTTCTAG
CTTTATTTGCCTGGAGGGGAAGATTCTCCAGAACCTTGTTAAGATGCACAGTGTGGTCCT
CGGACTGGCAGTGTGGCCTCGGCAGTCCCTGGG
Sequence 806
CCCTTAGCGTGGTCGCGGCCGAGGTACACATATATACACACATATATAGATATATACACC
CACATATATATTTGCTGACATTTTAATGTGAAGTTTTAGTCTGGGATATAAAATGGAATG
TATGACATCCTCAAATGTCTGAATACTGTTCACTCCTATGTTTTACATTTAATTTTCCAA
AGCAAAACATTTCAGTTGAGGATTTTATTAGAAAATAAATAATCATTTAGCCATATCTAG
AAACCAGAATAAACAATGCCATAAAGCCTATAGGAAAATGCAGGTCAGATTCATAAATAT
TCATGTGTTTACTTTCAGTACAGGGAGGAATTTGAAGTAGATAGAAACCGACCTGGATTA
CTCCGGTCTGAACTCAGATCACGTAGGGACTTTAATCGTTGAACAAACGAACCTTTAATA
GCGGCTGCACCATCGGGATGTCCTGATCCAACATCGAGGGTCGTAAACCCTATTGGT
Sequence 807
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GCAACACCCCATAACCGTCCCGCTGCAGAAGAGCATCANANGTTCAGAAGAATGCAAAGG
ATCTCAGTGGGAACGCGGACAGGAGAGCCCCAAACCAACACATGCTAGGGCTCTCTAGGC
CCTTTCAGGCTAGATCTTGACGAGAGAAGAGTAAAGATCTTTCTGAGGTTGGTGCAACTG
AGGAAACGAAAGTTTCGGCCTCTGCTGTCAGATCTATGAAAGGAAAGAACTGTGAACTTG
TCCCCTTTTGTTTTCTTTGACTTAAAACAAAAGAAAATCACTGGAACAAAGTCTTAAAGT
AATAACAGAAATGTCAGAAAAGTTGAACATCTTATGGGCACATGCGGTGAGTTACGCTAA
CTTATAGCATCCACTGAGATTAGCCCGCATAGGATTCTTCCATGTTAGAGCTAAAAGGA
Sequence 808
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GGGCATTGTGACACTTTTCATATATTATCTCATGAAATCCTCACAATAATTCTGAAGGTA
GCTGGTATTTTTATCTCCACTTTACAATTCTGAGGCTTACAGAAGTTAATTCAGTGGCCC
AGGGTCACACAGTTTACAAGTGCCACATTGGTGAATATAAAGTAGCAACTTCTAAGTTTC
ACTCTCCCACTTCCCTAGTTATTTTCCTAAGGCATGAATGTCTGGGAAATAGCATGCATC
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GCACGCTTNCTCTGTAAATTAAAAATGCCAACCCGAGCTTTGGGAAAAGCCCATCTTTTG
ATATGAACAATTAGGGCAGTTTAAGTTTTAGAAATNAAGAAAGTCCACTGGTCCTGCTTT
T
Sequence 809
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GAATATTGCATACCTATTAGAAAAGTCTTTTAACAATTAAAATTGGAAAATGACTGACAA
ACTTACACTATTTGATTTAAATAAATAAATAAATGGTCACATGATAACAATCTCCTGATT
GATATGCTTTATTTAACCAGGTTCTCAAACCATTGGATGTGAAACCAAATTTTACAATG
CANAGGTAAGTGTTGAGTGTTTAATGGGATTTCATATTAAACATTAAGATCGTATTTGAC
TAAAAATCTCTTATATACATTTCTAATACTGAAGCAAATCGCCAACGTGACTGTAAATTA
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TTTTCAGCTTACATGGAATCAATGTGTCTTGATTTTTATTCTCGGTAATTTTATAAGGCC
TTCATCTCCTTTCGGTTAAATGATTGCCCTCTCATTCCATTTAATGGNGGTTGTTACACT
AGCAATCTGTTGGAATATTTACATGTGGGTTCGGGATTTTCCAAAAAATTGGAATTANTAG

Table 1

AACCTACCGCTGCAAAATAGATTAATATTCACATGGGAAAAATCCTGGNCAAGGGGAANT
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TNGGGGGAATGGCTTAAAAGCCCTTGGGAAAAACAAATTGGCCAAAAANGGGAGTTACCT
TTTAATTGAANAANTTTTTTTTTTACCCTNAAAAAANGGGATAAAATGNACTTGNCCNAAAA
AAAAAAA

Sequence 810

CCCTTAGCGGCCGCCCGGGCAGGTACTCCATTTCTTTTTATTCATATTATTTCACCAAAT
AATATTCCACTGTGTAGATCTATCACATTTCGTTTAGCAGTTTATCAGCTGGTGGACAAT
TTGGCTGTTTCCATTTTTTGGCTGTTATGAATAATGCTGCTATGAGTCATAGAAACCATT
CCTCTTACTCAAGAAACAGGTTCTCCAGAAACTAAGCTAAACTTGTTTGAAATGTAAATT
CTCAGGTATTCTCAGTATAGACCTATAGATTCACTTAGCTGGTGGGGTCCACCCAACTTC
TTTTAACAAGTCCTCCAGTGGATTCTGATGCAATGCTAACATTTGTGAACACTGTCAAAA
TCAAAATGGAGTCACTTGTGTTTAAAAATCCTGACAAATAAAGCCAGGGACAGCTATGAA
GAGAGGGTTCTCATGCATCAATGCCTGATTAACAAAAACTATCCCAAATGACTCTGCAAA
AACCC

Sequence 811

CCCTTAGCGTGGTCGCGGCCGAGGTACAATCATTAAAACTATGTTGTAATACTGTTTGTC
TTTGTATCCATTCTGGCGTGTCTCCATACACTTCACTAATATTTGATATACCTGTTTTAT
ACCAATATAATGCTGCTGCTGTACGTAGAAGCTGTAGTCACCATATCCTCTATTTGTTCA
ATTATTTTTTCATCTTCTGGCACACTAGGATCTATAACAATGACAATATCTTCAAAGCCA
TTATTATTCAGCTTAATGAAGGAAGTATTTGACTGGTGCAGCAGGCACAGAACTAAGAGG
AAAACAAAACCTCTGAATAACCCCATTGTTCCTCTCTAGTTATTCCTGGCTCAAATGTTG
GTTTGTTCCCCGCGTCCTGCCCGGGCGGCCGCTCGAAGGGCGAATTCCAGCACACTGGCG
GGCCGTTACTAGGTGGATCCGAGCTCGGAACCAA

Sequence 812

CCCTTAGCGTGGTCGCCGGCCGAGGTACCTAAGAGTTATTAATACTATTTCAGTAAAAAA
AAAAATTTAATAAACCCTGTGTGATCCCATTGTAACAGAAAGGCTGATGTTTTCTGTTGT
GAAATACAAATGCAAGGAAAAAATCATTTCTTTGTTTCAAAGGATGCATTTCTTCCATAA
AGAATAATTTGTATTTATTTTTAAGGGTTTATTTTAACTTATACATCANCCTATNTAAAA
TACATTTCAAAATGATCTGTGCTCTTTAAATTACCAAAAGCAA

Sequence 813

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TCCAGAATACAAAGCTTCTTTCTGCCTTTCTCATCCACATAATGGAAGACACTTCTTGGG
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GCAGGGACCTTGTCAGTCTTATTCACAATATCCCCAGCCTCTAGAACAAGGCTGGCACAT
AGTAGATGCACAAAAGGTGTTTGCTGAATGAATGGATGACTGAGTCTGTGTGGGGTAATG
ATAGGGCTAAGGATGGGACTCTAAACTCAGGTTTCCTCTGTGGGTTTCACAGTTTACTGG
TCTTAAGAGGAGAGTTTCCTAAACTTGCCTTATGATAAAAACCACCTTCAGCATTTGNTA
AAAATTACCCATTCCTGTAGATTCTGAGTCAGTGAGCTGAAGTGGAGCTGATGAATCCT

Sequence 814

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TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTTTTNNCA
ANNATTAAAATAAAAAATTATTTTTACTACAAACAGANAAACGAATTAAACTANNANCCT
AANATACTTTNTGGAATTGAAATGATACATTATATATACCTATNANGATAATNGNNTATA
NCGNNNCTAAACTACAAATTAGTCATAAAAANGACTTNTGTNCTATATCAATTAAAAACT
GGTATTAAAATTGANTATNATAAGACAATA

Sequence 815

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAGTATTATGTATCCATAAAAATTAAAAAAT
CTTTAAAAATGCATATGGGGGTCAGTAGGTAAAAGAAAAGAGAACCAAGAGAGCTGCAGC
CGGGGAGCACAGCTTGCTTTAAACATGAGATCCAGCTCAGTGATCATGCGGGGGAAAAGG
CCCGGCATTGCTGGAACTCCTAATATTTAAAAAGATGATGGAAACTTGAAATTTTATATT
TAATCTTCTCATTTTTAAGTGTTGGCAATGTATTGAAGACTTTGAAGCCTCTCTGCTGGT
CAAACAAGATGTATCTGTAGGCTGGATTTAGTCCACAG

Sequence 816

CCCTTAGCGTGGTCGCGGCCGAGGTACAACTGTAATAGCTATTGGTCTTCAAGTGGGTTT
AGATTTGGTGACATCAGTTTGATATTCTCTTAAAGGAAATAAATATTCAAGAACTGATTA

Table 1

TGTTCTAACATGATTATATTCATGGTGTTACATAGGCCTCAATTTTTTCACAGAAAGATT
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GCCTGATAACTTAGTCAAGGATATACTGTCTGTCTCACTACTTTGGACTTATATGGCTTC
AGATTAAGTCATCCAAGAAACATACAT
Sequence 817
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACATGTAATAGACACTA
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GGGTAACTCTTTCCCAATTTTTAACTTTTACATTACAAGTCATTTTCAGAGTAAAAAGTC
ATTTAACAAAGGCAGATAGAAAGGCCTCAAATCCNTGAGGACCAAAAATCCCAACACATT
TTCAAAAGGGAGAAAATTTCTTTAAACTTCATGGGAAAGTATTTTTAACATAATAGAGA
GGCTTTATGCAGTCTTTGACAAGATGATACTTTTGGAATAGAACAAGGAAGAGGAAAATA
TTTCATATTATAAA
Sequence 818
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ANTTAANTTTTTNAANNNTNNTTTTTTTTTTTTTTTTNAATNTTTNTTNNTTTTATTAAAA
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GCNNGGATGGANTCAAANTAAAAAATTTTTTTTCCTACGGAAAAAANAACTTTTTTTGGT
TTNTTTTTAACAAAAANNTAGNAAAATTTCNNTTNTTTTAAAAAGNTAAAATNGGNTTTT
TTTTTTAAA
Sequence 819
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ATGTTCTAACATGATTATATTCATGGTGTTACATAGGCCTCAATTTTTTCACAGAAAGAT
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TAGGAGAATGTGTGGGTCATCCTAGTTACTAATTACTCTCACTCAAGATGGAGATGTTGT
CCAGTTTAACATAGTCTTAAAGTTTTCTTAAACCCAAATAATTTATGA
Sequence 820
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AATGATTGCACAATTATAGGATAGAAATTACTATCTTGTGCTCTAATTCAAATTGCTCTT
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ATCTTTGTTTCTTTCCTTAAAAACTTAACA
Sequence 821
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CAATGGGGTAAACCAGAGAGCAGAAAGCCCTTCTTTAAAATGAGCCTACCACTGCTTGGC
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TTATCTAAAATCTTTTTAATTTTTTAAACAGTCACCTGATTT
Sequence 822
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ATTGTGCCTGTCCTCCCTTGACTGTCATGCATATAATCAGCATCTTTCCCACTAAGTGAA
GGGCCCAGACTCGAGCACAGGAGCACAGCACCCCTTAAACTCACGAGGGGCTGCATTCAC
ACCATCAGCAGGGAGATTACACTTGTGTCATTT
Sequence 823
CCCTTAGCGGCCGCCCGGGCAGGTACCAAGACTTTAGAGGGCAAAGAACAGAGGATTCTT
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TACGTTTGTGTTCCTGGGAAGAATCTTGGACTCAGGCGTGGGCAGCTGGATGCCTGGGTT
CCTTAGGCTTCCTCCAGGCAATGTAGTTGCCTCTTTCTCTCCCCGCGTACATAGTAAGTG

Table 1

TATGATAGATGTTTGATTTGTAAATTACAAATATAAATTATCACCCCCATTTCCATTTAT
TTTCTTGATATATCAAAATGTGTTG
Sequence 824
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TTACAGGGTGAATCAATGATAATGATCTTTGCAGCTTTCTGGAGTTAAAAAGCATCAAAA
TTGGGAGATATTAGATGATGACATCTAAGTATTAAAATAAGGAGATATTAAATGATGACT
CCTAGAAATGAACCTGAATAAGGACTACCGCAATGTGTGTGGTGTGGGAAAGGACAGTTC
TTTTAATGGCTGGCTGACCCAGCCTCAATTTTCTTGCAGCTTCGCCGACACGAGGTGACC
ATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATA
Sequence 825
CCCTTAGCGTGGTCGCGGCCGAGGTACCTCTCATGGCTTTTTGGTTCCAGCANTGAGGGC
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GTNANGACAAATTTTGAGTTTTAACAAGGACAAAAAGTTGAAAGAAAAGGCACAGTTAAC
AAAAAAGGGTGGCTAGATTTATCTTGGGTGATGGAGGAAATGAGAGAGGAATGCTCTTGA
AAGGTGGTCTGTGGATCTGTCTGAATAG.·AAGAGCACAGTNAGTATGCATTGCCGGAGAA
AACGTCCTTGAAGCTGCTTGTCTCATGTGTATGATGTG
Sequence 826
CCCTTAGCGTGGTCGCGGCCGAGGTACTCAACAAGCAGCTGACTTATGTTTTATTGGACA
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CCTCTGTTTGGTGTGTGTATCACTTGCAGATGCTGTCTACCACCTTTTCAGTGACATCCT
AGAAGCTTCTCTATTACCACAGNAACTGGCTAACTANANATGATCTTTCCCTAATTTTCA
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AGGGAATATTC
Sequence 827
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TATTAGGGGATGTAAGGATTACAGAAACATCGTATTTTTTAACATATAGTATTTTTTGAA
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TGAAAAATTGTTGATGTAAGATGGAGGCACATTTT
Sequence 828
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TACATTTTTTTTT
Sequence 829
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ACAAAAAAAACCTTTAATT
Sequence 830
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TATTTGTTGTAGCTTGTATATGAACATAATTTTCTTTAGAGGTAGTCACTGTTCTCTCCA
GTATGACCCAGGTTTCTTGACTCTGAGTAATGCACCTTCTATAACTATCTAAATTTCTAT

Table 1

TGAAGCTTTTTGGATTATGAGTATGCTGACTTTTCACGATTGGCTGGTGCATGTTTAGAC
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GCTGTGACCACATGCCAATATATGTGTCACAAAGTCTACATATGTTACATTCCTTGGAAG
TCTCCTTAAATGTTTCACA
Sequence 831
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AGGCAAGCTGCCTGTAATTGAGCTTGCTTGTATATGACCAATCAACCTTTGCTTGTTGAA
GGGTTAGTTATCTAGTTTCCTTCTTTTCTTTTTTGGAATTTGGTCTTTTAAGGTCTTGAT
AATCTTTCTAGTCTAGAGCATGTGAACAGAACAGAAGGAAAATCAGGACTCAGTTTACTT
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AATTGCCATGGNTTTAAAAAAAAAAAAAAAAA
Sequence 832
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AGAACACACATGGAGAAGAGAAAAAGCAAGTCCACAGAGCTTTTAACATACACTCCCTCA
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CCAGCTTGAGAAACTATCCACT
Sequence 833
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TATAACTTGNGAGGAAAAAGTAAAAAGGNCAAGAGTCTAATTCATTTTCAGTTTTTAA
Sequence 834
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Sequence 835
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GGAGACACTCANAGCCAGGTGTTTCCCTTGATGGGAATGTGATCAGGNGCGACATGGGCT
CACAGCCTCNCTGAGGCTGGATCTTTT
Sequence 836
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TAAAATCAGCCTTACGTGGGATCTGCCCAAAGTATTATTTGCAAAAGTATCATTTTTCAGT
TTTAACTTTTAGGGGGAGCAGGGTAGGCTGGGGTGACACACACAAATCTAGGCAGGCAGA
GAGCTTGCTTTCCTCAGCTTCTTACCCTTAGTAAGACCACTTTAGTAGGACACTTAAGTA
TTTCAGTCAGCGGATTTGAATCTGACTTCTTGGATGCATCTGTATCAAAACATACCATTA
GATGTGTTACAGAACTGAGCAGCATATCATTAGATGTGTTACAGAACTGAGTCCTACTTA

Table 1

CAATAATTAATTTAATTTCAATAGCGATCCCCACCATTTATGTCCTAGGCATCTACACAA
TTGGTCTCTGAGCGAAAACACAGCCTTATCTGCAATAAAAGCCTCTGCTTTGCTTTGGCA
TGTTTTTACAATCCCGCGCA
Sequence 837
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGCAAACT
TTAATAGGTTTTCTTAGCTTGACAACTCATTCTCTATATTCACNAACATCTCCTGACTTG
TTCCTTCAGTGGANATACCCTTTTCTAGCCAGAGTTGGCAAAAGTAGCAATAGCATGCAT
TGGCTTGTTTGANAGGCCCTGGGTGAGCCTTTGTTGCATAAAGTAGGAGGTCTGTTATTG
TCTTGGTAGCATATGCCTTCATTATAAGTTTGCCTCTTTGAAAGAATATTCAAAGACCAA
CACAAAAGAGAACATTTCCAGATCCAAGAGAGTGTATGTAGAAACAGTGACAAGTTAGAA
AATCAACTTAGGTATCAGATAGCAGCCACAAAATATGTTCTGAGGAAAAATTCATAGCAA
TTTATAACAGCTGAAAAAAAGAGGGAGGATGCGGGAAGGTAGATTTTGTCAGAACTTACT
AGACTAAGGATTTATTGCATATTTTTTACTAATTAAATG
Sequence 838
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACAAAAATAATGAAGCCAGCTAATTACCAT
CAGGTTACAACTTTACAAAGAAGTGAAGCAGCAAAGAGCTGAAGCAGAAATGACATAGGA
AAACAGCAGCAAAGTCCTTGAGTCCCAACAGTCCACCTCAAAGACAAACATACTAAAGAA
CAAAGGCCCCTAATCCACCTCCTCACCCGCGTACTTTTTTTTTTTTTTTTTTTTTTTTNC
CAGTTTCTGTTTCAAATTCTTTATTATACATCATGGTTGCACAATTTGAGGCTGGTTAAA
TACAATTGGTTTTCAAAATCTCTTTGAATATTTTCTGGCTTATTACATGCAAATGACCAT
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AT
Sequence 839
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TGGTCTTGTAGTCGGTTTGGAATTTTCTAAGTCAGGGTGGGGTGGGGGGACTGTGCACGA
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GAGGCTGGGAGGGAAATCCAGACAGTTCTCCGCCTCTGACATCAGGTCCAGCTGTTAGCA
TCGTGCTGTGGGTCCCTGAACAAGAAGCAAAGTCAGGACTGGTTTGGCCAGGTAGGTGAG
GATCCAGTGTTGGGTGATTCTGATCCATGCAGCCCTTAGAGGCGACACAGACGTGAACTG
GACATTCTAGGAAGAAAGAGCCGACTGCCGGGTGACCTGTCTAGTTCACATCCACTCACC
ATTTCCCTCCTCGTTCCTATTCTTAGAAATAAGACTCTGACGCTCTCTTTTATACAGGCT
AGTCCCCTATAGGCATGTCATGGTGATTATTTGCAATCCTNCTGACTTTCCTAAGAAGAG
ATCANACTTAGCAGGGTTAGTC
Sequence 840
GTGGTCGCGGCCGAGGTACAAATAAATGTATCTTGGGTTAAGTGCTATAAAGGAAAAGAA
CAGGTTCAATGGAAGGAAAAATTAGAATTGTTGATACATGAATGGAAGTAAATGACCCGG
ACTTCCAACTCTAAATCTCTGTCTCATTTCACCTCTTTGTAAATAATCATTGCTATTATG
TTAAATATCACAACTACTGTCATTTCTTGTTTACCCACTACATTCTAAGCTTGGTGCTGA
CATCTTTGTATTTATTATATAAAATTCTCAAAATTACTCTGCCCGTTAGGCTTTCTTATC
ACTTATTTCAAATGCAAAAATAAGGTCCAGGGAAGATAATTATGTNACTTGTTCATGATT
GGAGAGCTAATAAGTGTCAGAGATGAATTNAACCAAAGTTTGGTGTGACAAAAGCCTCTG
GTTTTAAGCAAAAGGGGAAAAAAAATTCTCATTAACTCCAAGGATTATCATCAGGGAGTC
CAACAGGGTTCCCAATTTGGGAACTACCTATATTCAATTATCATATGGCAAATGGGTCCC
CTTTTGTTAGATGGAGAAGGGCCAAAAAAAAAAAAAAAAAAAA
Sequence 841
CCCTTAGCGTGGTCGCGGCCGAGGTACACTTAAAAATGTATGTGCTGTTCTAATGCTACT
TATTATTATTCCCTTCCTTTGTAGAATGTATCAACACTAAAAGTGTTTAATCCTGACTAT
AACAATTATTTGTTAACTATTAAAGGGGTAATTATACTCTAAGCTTCCAGTTTTCAGTTA
AAACAAAAATGATTAATATGCCTATACAGAACTTTCTCCAGCACTTGGTAAGTATTTTTT
AAAGTGAAGTCTATTCAGACTGCAACCAGTAAACTATTTATGCTTATAATTTTTCTCACG
ATGGATTTCTGTTCCTTTGGTGCATTGGTTGTGTTTATTTTATGTGATCTTTTTTAGCTA
CAAGGTGGGAAAAATGACAGTGGTTTAGAAGATAAGAAGCACATGAATGTAAAGTAAAAT
ATGTGGAGATTTTTGGCCACTCTGTAAACTACTATCTGAAGTAGTTTTAAATATTTTAAG

Sequence 842

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTACAGTGGCGTGATCATAGCTCACTGCAACCTCCAC
CTCACAGGCTCAAGTGATCCTCCCACCACAGCTTCCAAATAGCTGGGACCACAGGTGCAA
GCCACCACACTTATTAATGTAGATTTCCTTTGTAGATGTAGATTTCTTTTACAAAGTGAC
AGCTTTTCAGAGCTAGTCCTATGTCTGCAGTTTCTCAGAATAACCAGCTCAAAATATGCC
AGAGAAGTATATTTTGGGGTGGCATATTCTAGTCTCCTCCAAGTCATATTTTGGGGTGGT
GTGTCCTGAGCCCCAACAAGATAGGTTTCATTTTTGAAAATTGCTCTTTCAGTCCCACTG
TTCATTCTCATAAGCCCAGGAATCACCACCTGTTGATTTCCTAGGCATCTTCTTGCTCAN
GGTAGTTAGATGTTTGGTGGGACTAGAAAATGCAANGGAGGGAGAAAAAGGAAAGGCTTG
GTGNATGTCAAAGATTTTTAA
Sequence 843
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGCCTATTAATTGAT
TAGGAAAAATAGGTAGACCCTGAGTGAAAGTAGAAAAGAACCATTCTGGTAAAAATTCTG
AAAGTAGAAAAGAACCTTTAGCTTTAAAGGTATGTCTTAATAGAGCAGTGCTAAGACAGG
TGGTTAGGTATGTGAATGCATGCCACTTAGAAAAGAATATGAAGGAGAAGGGACCAAGAA
GGCAGATACATTGCCCCTGATAAAGAAGTCATTTTTCTCTCACCTTTACATAAATATCAN
GCCACTAAAAATCTAGGAGCACAAATAATGAAAG
Sequence 844
GAGCGGCCGCCCGGGCAGGTACAAGAGAACGGACGGCACTTACTGAGCCCATCGCAAATG
TCAGGCTCTGTGCTATACTTACATTATCCCATAATCTTCAAGACCCCTCAAGACCCCACA
AAGTAACACAAAGCAGGAAACTAACTCANATTTACTTGCCAAAGGTCACACAGTTAATAC
ATGGTGGAATCAGGACTCAAAATCANGCCTGTGTGACTCCAAAGTCCAGTGCTCTCTCCA
CTTTACCAGGTAACCTTCATAATACCGGATTGGAAATCAAACCTGTCACTTTACTTTTCT
ATGTCCCTGAGTGANTCACAACTTTTTTCTTCANCCAGCTTTTTTCATT
Sequence 845
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGGAAATTGGTTTGATTGCCATAGGCTAACCT
TGGACCAATCACTGTGGCCAAATACATGAGGTATCCTTATTGGCTCCTTCTACTAGCAAC
AGATGGTTTAGAGAACAGTGTATCACAGAGAAATGGGGATCACTATTATAGGCAGATTGA
ATAATAAATGTTCACTCTACTACTCAATAAATATTTGTTGAACAAATCAAAGCTGATCCC
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GAGAAGAGAGAAATAGAGGAAAAGTTGCACAAACTCTTCAGCCAAGACCACCTAGTGATA
TATAAGGGATATGTT
Sequence 846
CCCTTCGAGCGGCACGCCCGGGCAGGTACTTTATTTATTTATTTATTTATTTATTGTTTT
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TTTCCCAATAAAATGTAAAGTTTAATATGTGATGGCTAAACTCCTAGGGGGATAAGGAGG
CGCTAGGAGAATAGGCAGGTTGGAAAAGGGTAGTCGGGACTTGTCCAGATTCTTGTGTGG
TAGTCTGGGTAGTCTGTATATTTACCATATGGGCTACAAGACACACACACACACACACAC
ACACACTCACACACACACACACACACACACACACCCTTGTGAGCATTTATTAATTCGCAG
TTGATGGTGCATAGTTTGGGGAGTGGGTAAAGGATATGTTACTTTTGTA
Sequence 847
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GTGTTTTAAGTTTANCCTTTTGTTTTTGTTTTTTGGTTGGCAGTAACCCNATTTTAATGA
CTAAGCTTTTAAAAATACAGTACTGATCATTCTATTTCCCCCTNTATTGATCCCCACCTC
CAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGACTAATCAAACTA
Sequence 848
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AGTGCTGAAAATCTCATGCACTCTAGCTATGAATGCAGGTCTACTTGAAGCAAAACTCTT
CAATCTAATTGTTTTCTCAATCTTTGTAAACCAGTTTTAAGAGTCACCAGAAATCTGTAG
TTTAAGGCACCAGATACATTTCTTGGCTGAGCCTTGTAGGACCAATATGCTGGACCAATT
CGGTAAAATACACCATAAATTATGACTGCTTTATCTGAATGCATGGGACACTTGCTACGA
TGGCGGGAATTATTACCAGGAGTTTAGGAGCCAGACATGGGTTCTGTATTTTTTCATACAT
TGGTGATCAATTCAAATCTCTTTCCTTTGCANCCCAGGTTTGGTCAGTCTGGCCAGGAGT
GCAGATTATGACAAAAAACAAAGCTAAAAGACCTGAGCCATTAAGGTTACAGTCTCAATA
CCACCGAGTTAAACAACCTATTTAAATGCAAGACTATTGATTGGAAT
Sequence 849

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTCGGCCGAGGTACAAAAGTTCTGAAATAACACTATA
GGCTTAAGGAATAAGGGACCAGAAGTAGCCTGGTAGCCAGTGTATTTCTGGCTTTATACA
TTCCTTAGGAAAAAAAAACTTTATAGATGTATTTAAGTAGAATTAAGGTTTACACAAATG
ATTTTTTTGAGAGAGAGAGTCCCTAGGACCTAAACATTCGTTCTACGGAGATAGGGTCAAC
ACGCAGATATTTATTTAGCAGCATGGTCTGCAGAAGTAGGAGGAGGTGACCAGATGTGAT
GGATTATGCCTGTAATTCCAC
Sequence 850
CCCTTAGCGTGGTCGCGGCCGAGGTNCCACCTAACAAATTGGAGGAAATGAAAAGACGAA
TCAACAACATTTTGGAGAAAAAATTTATTCTACTTCTAGAATTTCATTACTACAAGTGCT
TAGTTCTTGGTTTGGTANATGAAGTGAAATCAAAATTGGATATTTGGAACATTAAATATG
GGAGCAGAGAATCTGTGGAATTATTGCTGGANGACTGGCATAAATTTATTGAAGAAAAAG
AATTCCTAGCTCGACTTGATACTTCTTTTCAAAAATGTGGAGAAATTTATAANAATTTGG
CTGGAGAATGTCAGAATATTAATAAACAGTATATGATGGTGAAATCTGATGTTTGTATGT
ATAGAAAAAATATATATAATGTGAAGTCCACTCTACAAAAAGTGCTGGCATGTTGGGCTA
CTTATGTGGAAAACCTTCGCTTACTAAGGGCTTGCTTTGAGGAGACNANGGAAGGGAGAA
ATTAAA
Sequence 851
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CTTGAACATGAAAACTCATCTTAAAATTACACGAATTAAGTAAGCATGCAATACAGACAC
TTGCAGGATGCCTGGCCTCTGGGAACTGCTCCTGTCTCTGTGTGAATGTAGAAGTGAGGC
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TGGCTCGTTAAAATGATTAGCTGGCAATACAGGTATGTTTGGACTGCTATTGGTGGTGAA
GTTTAATCTTCTAACTGTGTTTTGTGAAAGGAAATATTCCCTAAAAGCTTTGGTGTCACT
TAAAAAAAAACAACTATATATGATTGAAAGAAATTTGAGATATTTTTTGTTTC
Sequence 852
CCCTTAGCGTGGTCGCGGCCGAGGTACTAGCAGATGATGGCACAGTGACAGCTGGGAGGG
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CTGGTGACCGTGCCAAAGTCCTTCCTGCCTTGCAGAGAGGCCTNTCTTCGTCGAACATGG
GCCTCAGGAAAGACAGCCTGAATGCCACTACCCCAGGCTTGTGGAAGGTTCTGCATCAGT
GTGGCATTGTTGCGATAGCCCTCAGTTGATGCTTGTTTGTGGTGTTGGGAGGCAGGAACT
ACTTTAGGAGGGTGGAGGGGTGAGAATGAAAAGAGGACTTGCCCTGAGCCACCCAGCTGT
GGTCACCTGATGGC
Sequence 853
GGNCGGGCCGAGGTACGCACATACATACACACTAACGCTCAGCATAAACTTTCCATTACA
CTTAGACAATGACTTGTGGAGGAAAAACAAGGATAAACAAGAGTCTCAAGAACTTAAGAA
AAACATCAGAGTTGATTATTTAGCACTTTCTCAGGATTCTAAGGCAATANGCCTAANTTC
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TGCTGCTTCTCCATTCTGTTTTCAAAGAACATTACAAAAATAAACCAGTGNGTTCTCTAA
CAGTTCTAAAAACAGNTTG
Sequence 854
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AGCTTAGAGTCAGATTTCCTAGGTTCAGATCCAAGCATNACTACTTATTTTCTTTAAGAA
CTTGGGCATCTGTAAACCAGGGATAATATCTTCTTCAAAGGGCTGNTGNGAAGATTCAAC
AAGGTAATACATAT
Sequence 855
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CCTCAAGTGATCCACCTGCCTTGGCCTTCCAAAGTGCTGGGATTATAGGTATGAGCCACC
GCACCCAGCCTTCAATTTTTTTTTTAATTCTGATAGAGCACCATCTACTACATGCTTAATA
TTATCCATAAACAGACATGTCTGAGCACAGAAGATCATGTTAATGAAAGATTATTGAAAG
GTACCTGCCCCGGGCGGCCGCTCGAAAG
Sequence 856
CCCTTCGAGCGGCCGCCCGGGCAGGTACAGAAAAAAGCATAATGAATACAACAACTAGCA
TCAAACTCAGTGTATATAAGAATGGCTAAGTGACCATTAGTCATGTGAAAAGCTTAACAA

Table 1

CTATTAAGCTCTTATTTTCTTACTAAAAAACAATTTTAAGTTCTTTCAAGGCTATAGTTA
CGCTTTACATAAGAGGCCCTATTACCCACTAATTCTTAAAATTTCTACCTACTTAAAATT
TCTTTAGACATTTCCAAAGGTTAGTAAAGGAAGACATAAGATATGCTTACTTAAATCCTT
GCTGGTTCCATGCCTGGCCATACAT

Sequence 857
CCCTTGAGCGGCCGCCCGGGCAGGTACCATGAAATAGGACCTTCTACGGTTTAAAATAAA
TGTTTGTTTTTTTCTAGCCCTGTAGGTCAATGAATGCCTGACTCCAGTGACAGACCATAA
TTATCCAAATCTCTCATTTATGAATATGGAATATAAATATGCTAAATTGATTATGTCATG
AATAGACTTCTTTTTTTGCATAACAATGTTTGGAGTTTCTCACCTTTCTCCTNNCCTTNTT
TTTCT

Sequence 858
CCCTTAGCGTGGTCGCGGCCGAGGTACAAATGTGAGTTCTTCTCCAGACCATCAATATAG
ATTGGATTTATACACTGATCGCTGTGTCTCTCCTTCGTAATAACCTTACCCCATGTTGCA
ACAAACATGGACTTGTTACAACATCCCAGAGTGAAATCTGAATGTGGTCAAGAAAGTTCA
GAAACAATAAGAGTGATGCAATGCATACCACAACTCAGGCCCAGTGCAAAAGTCAGGCCC
CAGCCCTTCCCATATAAGGGACTTGGTCATTTGAAAAATCAAAACCCAAAAGGAACAACT
ATAGGGACCTGTAATCAATTAGAATATTC

Sequence 859
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGGCTGGACTTGAGGTGGTTTAAGTTGGCAG
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CAGCTGGCCTTTTCCCTCAAAACATGGATAATCTTCAAACCTCCCTGAACAGGTGGAAAT
GCGTCTTTCCTCTAAGCCAAGTTCTCAGTCCACATTAGTCCATACTTGGCTACAGAATTG
ACGTTTGTGGCCACAATCCTACTAGAAATGACCTTTGGGTAATATCCTTATCTTGTTGAT
CTAGTTAGGGTCAAGTAAA

Sequence 860
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AAATATAGATGAACAATGAAGCATAAACAAAATTTTAATATCTTACAGGCTAAAATATTT
AGAAATGAAAGACAACAATAGCATATAAGTTAAGAAAGGGGGTAAAAAGAATCAAGAGCA
TTCTAAGGTCCTTATATTACCTGGAAGGAGAGTAAAGATAATGACTATCTTCAGGCTGAT
AAATTAACAATGTATGCTGCCATTTC

Sequence 861
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ATCGGTTTTCACTTGGAGGGGCCAGTTCTCTATATTTCAATCTATTTTCTATATCAGAAA
TGAGCAGGCATTTTAAAAAATGGCTTTCATTGATGGAGAGGTAAAAGTGAAATGGCTTTG
TTGTATTTATATTATAAAAGGCCATTTCCCAAATCTAGAATTTATTACTAAAAATCAAGT
TTGCATTGAGGGGAGGAGTATGATTTGCTCAAGCTTACTTTTTTTTATAGGTGGGGTTTTT
ATATTTTCAATGTGATTACTCAC

Sequence 862
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GGAATATAATTTGGAAGGAATAACGTTGTTGAAAAACATCCTCTACAGACAATATGAACA
ATGCCTTAGTCATCTATTGATTATGACAATATACTCTTGAACAAATTGTTTTCGGTTCTG
GTTTCTGTGGTACCTGCCCGGGCGGCCGCTCGAAAGGG

Sequence 863
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TGCTTTGTCCAAACCCAGTTGCAGGAATTTATGTCTTAAAGTAAACCATCGTATGATAAT
TTCCCCTGAAAATGTGCCTATTAAAAAAAAAATAGGATATGATGGGAGGCAGACATAAACA
TTCTGGTCAATTTATTGGTGTTATTATTTATTTCAGTTAATAAACTGCCCTTTCGCTATG
CTTCACTTTCCACGTGTTTAGGCAG

Sequence 864
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATGCTCTAAAATGTAAGGATTCATTTATGAG
AGAGTGAACATACTGCTTGTAGCTAAAACATTACAGGAGACCTTAAAAAGGGGTATAATT
GGTCCCTATGTGAAATGAACCTGACATATTTTTATAAATTATTTGTGCATGACTATCTTT
TGNTGATAGCACTAGGAAGACTTNTAACGTTTAAATACTTTATTTGCCCTCAATTACTAT
TTAAAAGTCCTATAATTTTAAGTAATTTTACAGCTGACAAAGATAAATATTTTTTTCTTT

Table 1

TAGTTTTTCTAATGTCTTGGAGGTAAAGTGGAAATGGCCTGTTTTGACACATAATTTCTA
GAACTTGGAGTTAATTTTGATCAGTTCCATTTTGGGT
Sequence 865
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GGTATTAAATCAGCAAGGTCCCCATCCCAGAAAAATGTGCAGTTTGTCCAATGGGAAAGA
TGCANAGACAGTTTCAGTTAATATACTAAGTGCTAAAGATTGGGATGTGCACAAGAAGCT
GGAGGTAAAAATTCTGGAAAACTGAACGTGAAGTCACCACTAGGCAAGCTGCCTGTAATT
GAGCTTGCTTGTATATGACCAATCAACCTTTGCTTGTTGAAGGATTAGTTATCTAGTTTC
CTCCTTTTCTTTTTTGGAATTTGGTCTTTTAAGGTCTTGATAATCTTTCTAGTCTAGAGC
ATGTGAACAGAACANAAGGAAAATCAGGACTCAGTTTACTTAATTTAAAGCAAGCCATTG
GTTGCTGCAGTTCAGGGGGAGGTTAAAGTTGCTGGGCTCCACTCTCTTATTAGCATGGATG
CTTAAAGAACTTCAGGG
Sequence 866
TAGATATAGGATAGTGATACNTTGAANAGGACTATGAAAAGGGACAGTAGGGCTTAGTGG
AAAAAGTTTTAACGANNTCTACNGTTATTGAATNAAANTACATATAGCGNGATTCTTATT
ACTTGAAATTAGGAGGAGAAAGAATTTTTTTGAGGTAAATTNGAAAAGACATAAAATAGAC
TA
Sequence 867
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCCGGGCATGCAGCCAGGCTAGACCGGCTC
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CTTATTATGCTTGATCAGTTAACTCTTGCTTAGAAATTTAAAAAAATATTTTTAAGTGACA
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CAATTCTGCTTTTGTTAACATTTGAATATGTTGTCTTCCATGATATATAACAAAATTTGT
CTGGGTATTGCATATGTCGCCTTTCCTTCTTAATATTGCATTTTGAGCATTTAACCNGAA
CACTAAATATTCTCCCTAGAACATATGGATTTTGAATAATTTAGCTAATTATAAAAATAA
CTTCCCTAATGGTCCTTTGGGCTCTTTTAAGGTTTTGCTGGTATATGTTCAGGGGATGAA
CCACTTAAGGCTCTTTGACCACCATACTGNCCATACTGCCATACTGGCATACCTGNTTTT
AAAAAAAAA
Sequence 868
CCAGTGTGATGGATATCTGCANTTTTCGCCCTTTCGAGCGGTTNTTNGGGCAGNTTNTTT
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ACAAGAATTATGATAGTTCATTGAAAAAGGTTGAGAATTCAGAACTTGTCAGTTTCCACC
AATAATGGCAAAGATACAATATGACAAAGTTCAGTTGCTTAAATGAATCTAGGAATGAAG
AATCTAGAAATTATAATGGAGAGGTGATTAGGAGTTTAAAATGGTTTAT
Sequence 869
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GCCTTGTATTTTAGATGAAAGGATTTATGGCTGGAATTAAAAGAAATTAAAAGGCAGAAA
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TATATATATGGGTTTTTTTTCNNGAGCNTTATATCATGGTGAAATGAGTTCAAATGGACCC
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CTGGGNGGAAAATTGGTNTNCGGTTAAAAATTCNCCCCAACATTCCCANNCCGGGGAAGCC
CTTAAAAGGGGGTAAAAGCCCCTNGGGGGGGGGCCCCTTANTTGGGNGNGGGGGNGCCCTTT
AACCTNCNCCNNNTTTTAAAAAATTTTTGGCCNNNTTTTTGCCCCGCCCTTTTTNANAAAATT
TTGGGGCCCCCCCNCCNTTTTTT
Sequence 870
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ACATAAATCCAAACTTGGTTCAAAGGTAGCTATGTTTTTTTTAAAAAAGGTTATTATAACA
GACAAAGCAAATGCAAACTTATCCTTCCAAACCCTGATAATTGGTAATACCAAATAACTG
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Table 1

AAAAACT
Sequence 871
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TAAATACTGTTCTGTTATTTTTGAAATCTGATCAAGAATTGACACAATAAATCTCTTTGA
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AAATCCTGAAATAATTTGGAATATTCTAAAATTCTGAAGAGAATATGAACGGATTGTTGG
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TATTTGTCTCTCCTAAATAACCAGTATGGAATTATAGAAAGAAAGGTGGGGAGAATAGTC
CGTGTGATCTNCTGGGCAGCATTAAAGCCTGTTCCATCCAGCCCCTGACTATTTTGGTCT
TTCTTTGCCTTTGAAGGCCCAGAAGACATTTNCATTCCTTCGAAGNTTTTATGGTCTATA
CCCCTCTCTTGCCTNCATATTNTTTTGCAAGNGGGGGCCAGAATTTTTTTGGATTCCCNT
TAAAAATGGACCTTGGGGTNTTTTANCCATAANCCTGTGAAAATTCCAANGGGGGGGGGG
CCCCTTNTNCCCCCCCGGGGGGGCCCCGGGGGGGNCCCCNCNTTTTTTTTTGNAAAAAAAANN
GGGGGGGGNCCCCCAAAAAAAA
Sequence 872
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AAAAAAAAACCATTTTGAAGCCAAGCTTTTGATTTAACCATGAATGAAAACAAATGGGAAA
ACAACAACNACNAAAAACAAAACAAAACAAAAAACAAGAATGACCAAATACAGAAATTAT
TA
Sequence 873
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ACATAGATTATTTTGTCAGTGGCCATGTCTTGCTTTGCTTCTGTGGAAACTACTCTCCAT
CTTCTGGAGTGGAATGTCCCCCATTGCTATCCACATGGTCCTCGCCTCCCTGATACTGTA
GTCTCAGATGGCACCTNCTGAACTGGGCCCGAGCTCAATCACTTTCCCAGACCCTGCCCA
CCTCGCTNGGAGCNTCAGTGGTCCCATGGTGGGCAAAGGAACCCAGGTTTNG
Sequence 874
GATATCTGCAGAATTCGCCCTTTNCGTGGTCGCNTTTCGAGGTACTGAGGATGACTAGAT
GACAAATAATAAGAAAAAATGGCATTGACTTTGTATAGAACTTAATAATCAGATTTTTAA
AGAGGTTAGTCTATTCTCTTATTTGAGAGATATGGAAACTATCTAGGCCTAAAGACTGTA
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ACCAACAGTTTAATTTAAGAAACATTTGACAAGCATCTCCTGTGGATAAGACCCTATGCA
AGATGTCATGAATATAAATATGCACAGTAGTACCTGCCCGGGCGGNCCGCTCGAAAGGG
Sequence 875
CCCTTANCGTGGTCGNNTTTNGAGGTACTTTAAAAATAACAGAGTGTGATTTAAGAATAC
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AAAGATTACAAAGAAAGTCAAAGTAAGCAGAGGAAAAAGATACCAAAATGACAGCTTCAG
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CACATCTGCTACTTCCATAATGCCTATGCAACTGTCATAAATTAAGAGTAGAGAAGGGCA
CAGGGCC
Sequence 876
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TGNTAAAATTCAGATTCCTGGACCCACCCTAGACCTACTGGATCCAAATCTCTGCAGACA
TGGCCTGGACATCTTCATTATAACAAGCTTCCACATAGATTATTTTGTCAGTGGCCATGT
CTTGCTTTGCTTCTGTGGAAACTACTCTCCATCTTCTGGAGTGGAATGTCCCCCATTGCT
ATCCACATGGTCCTCGCCTCCCTGATACTGTAGTCTCAGATGGCACCTCCTGAACTGGGC
CGAGCTCAATCACTTTCCCAGACCCTGCCCACCTCGCTGGAGCTCAANGGGTCCCATGGT
GGGCAAAGGAGCCAAGTTTGGGCAACAAATCCCTATGCATTTAGAAGTAGATGGGGCTGC
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Table 1

ACAGCAAGAGGGCAGATGAAGCNGACTCAAGAGAAACAGATNAGACCAGAGAGACCCTGG
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AAATTCTTACCANAAAAAAATTTCCTTTTGGNTTNGACGCTTAATTGAGGNTAATTTCTAT
TNTGGGCAATNTCAAAGNNATTCAANGAAAAAAAAAAGGG
Sequence 877
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTAATTTTTTTTTTTTTTTTAATA
GAGATGGGGTCTTACTATGTTTCCCAGGCTGGCTCGAACTCCTGAGCTCAAGTGATCCTC
TCACCTTAACCTCCTGAGTAGCTGGGACTACAGGTGCANACCACTGTGCCCTTACTTCTA
TTCTTACTTGACAAAGGAGAGGAAAAAAAAAGGAAGTTTAGAGAAATTAAGTAGTAACTT
GTCCAAGTTTACCCACAACCACTAAGTGGTAAAGCTGGGGTTTGAACTTCAGCAATGTGC
TTAAATCTCAGTAACTGAAAATCACTATGGAGGACCTTTAGGT
Sequence 878
CCCTTTGAGCGGCCCGCCCGGGCAGGTACATGTTTGTAAAATTCCTTAAAATATTTATGC
TCAAACCAACATTTCCATTTTATCTATCTTAAATATATCTTCCTCTTCTTTACGCCTAAT
TTCTTAAACTCCCAGAGTTTTTTTTCTGTA ·.GATCTAGTCATCTGTAGCACTTCTCACAAA
TTAAGCTCTCTTATGCCCCAAACAGTAACGAAAGAGGTCTCTTAGTTGGACAATAAGCAG
TGAAAGATATTTCTTATGGGACAAGAAATTAACATTATTAGTCAAATGTTGATGCCGGTA
GGCTGAGAAATGATTCTCACTTAAAAGCCCCTGGGTTTTAAACCTCTCTTAGAAAAACAT
TAGT
Sequence 879
CCCTTAGCGTGGTCGCGGCCCGAGGTACAAGGAGCTAGATCATCAAGGAAGGTCAGGGCA
GGGTTCACAGGATGAGGGCACTTTGCCATTCTTTTGTGATTTGGTCAACAAATGACACAG
GTTATTTACAATCTTGACCTTTTGGAAAAGATACAGCAGGTAATAGCCTACAGGAAAGAG
GAGGTAGAAAACAAGTGCCACAGTAGA
Sequence 880
CCCTTAGCGTGGTCGCGGCCGAGGTACATACAATAGAGTATTATTCAGCCTTAAAAAGGA
TGAAAAAATCCTGACATGCTAAAATATAAATGAATGTTGAGAACATTATGCTAAGTGAAA
TGAGCCCATCTAAAAAGGCAAATACTGTATGATTTCACTTAACTGTGATATCCAGAGTAA
ACAAATTCATAAAAACAGAAAGTANAATAGAGGTTTCCAGGGACTGGGAGTTACTTGATA
TAGAGTTTCAATTTTGTAAGATAAAAAAGTTCTGGATATTGGTTGCACAGCAATATGAAT
ATACTTAACACTACTGAACTGCACACTTAAAGATGGTTAAGATGGTAAATTTTGTTAGGT
GTTTCTTACCACAATTTAAAAAAGAAATTTTAATTAAAGGAATTAAAAAATTTACAAAAT
ACTATTCATCATTGNGTTTCCAGTTTATATTCAACCACAGCAGTATTTCAGGTATAGTAA
TTAACTTACTTTCA
Sequence 881
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACTGCACTCCCACCTGGGTGACAGATCAAG
ACCCTGCCTAAAGAAAAAATTTAAAAAAAATAAAAAATTTAAGAATTTTCTATGCCCTTTA
CCAGGCCAGCTTAATCAGACTTCTCTAGGCCTAGGACAGGCTTAAGATCAGTTAATTTAA
AACACTTCTGATGTTTCTTGAGCATTGAAAAGTTTTATTCTTTCTGCTTGTGTTTTCAAT
CTTTTTGTGTTTGTCTTTTACTAAGGCTAGAAACACGTATTTGGTTTGGTTATCTGAAGT
TTAATTGCATTCATTGTGTTTATAGTATTTATCCCTGTAGTGTTGGAATTACCAGTCACT
TACATTCATATTTNAGTTTTTTTGCCT
Sequence 882
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTCTTGAATATTTCCAGGGCACAAGATA
TTCTTATACAGAAACCTCAGAATGGAAAATAGCTAAGACATAAGCAGTGTTTCACAGAAC
CATCCATCAGTCTTTTTTAGGATGTAGCAGTCTTCCATGTATCACTTAACCAATCATTAT
TCTTACCCCATCTTTTTGGGCAGGGGGTGGTAGAATTTAAAATTTACCATTACTAAGACA
GGGTGATAGTAAGCATAGAATTTTGGGATGTCTTTTTTTTTCCTTGCCCTAAACCTTCAGA
GTTCTGCCAGGTGATTCAAATGTTTAAGATCCCATAATCTCGCCTGTGTGCTCAAGCGAA
CACTAACACTTTAAAAAGTGGGAATGAAAAAATCTGAACTGGTTGAATTAGACACAGTAT
TTGGCCCCATCTTTCAATTTCAG
Sequence 883
CCCTTAGCGGCCGCCCGGGCAGGTACTCAAAAATTTAAATAGCCATCTAAAAACATCTCA
GGTAAAAAATCTGTCCCCTGCATTTGAAACCAAAATTATTTTTTCTCACTAAAACACATT
TTATTTAATAGTGAGGTGAAATTACATTAGCCCTCTTCACATTTATTTGATTCAAACCTT
TTTTAAAAAACTTAGATTCTTTTAAAAAAAATAAATTAAAGAAAAATGACATCATTCATCA

Table 1

GATAGCCAGCTACATGTGTAGTTTGATCATTCAGTTTAACCGTTTTATCACTGTTGATAT
GAACATTGAGTACCTCGGCCCGCGACCACGCTAAGGG
Sequence 884
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTGATACATGTAAAGTGCAAGGCACCTTGCTA
GAGAGCATANGAGCTATACTAAGATATAGAGTCCTGCACAAATCCACAAAATAACATGAA
TACAAAGTGTCCTAAAAGTCATGCCAAATAAAACAGANCATATAACTGGGCAGAGGGATG
GAGAGTCACATGCTGGAGGAGGTGAGCGTTGACATGGTCTTATGGGATATGAACTTGAGA
TGTTGAAGTAGAACTGAGACATTTCTGGAAAACTANATGTATNAACAGAAGCANGAGGAA
TAGGAGATGGTTTGGAAAACATCAAGCAGCTCAGTTTCTTGGGGTGGTCCAGGAGAAAGA
AGCTCAAACAACATTCAGTGATAACACTTAAAANNATCAAAAATTT
Sequence 885
CCCTTAGCGTGGTCGCGGCCGAGGTACAATAAACAAGACAGTGCCTGCTTGTGACCAGGG
GCTGGGCCTCTTCATAGCTCTTTTCCCTGCCTTTTGTCTTCAGAGTTGATCTGCTTCTTA
CACATTCACTTTTTCAGAGTTTGCTATCTTAGAAGCAAGGATCATTTTTAATTGGTTTGT
TTACTTCAAAGTCCCACTCATCAGAGGCAGNTGTTTCGCTTATATTTGGCTCAACTACTT
TNTCTGCTTGGTTTAGTAACACTAATGTTTACTAACATTAAAATGAAACCAGTTTTGCAG
CTAGCATCTATTGACCAAATATAATTATTTATTTCAAACTGTATATTCCAAAATTTAAAC
ATATTCAATGCTTATTGAACATCTAAACATATANCCTTAATGAATAANGGGAAAATATAA
CCATCTGGTTTTTGGATCTGAAAGCCACAACCCACCTGCTAGANTANTTTGGGGAAAGGC
TTTTTANTTCCAAGTTCAAAGGNTGAATTCTCCCGAGGGNNGNNGGGGGNCTTCCCTTCT
NAACCAGCAANAAAACCTNGCNCCAGTTTGGGATTTTGGGNGGAAAATAAACCCNAATGA
NGCATTTTACTTTCCTTTTTT
Sequence 886
CCCTTAGCGTGGTCGCGGCCGAGGTACATATGGCTCGGCAAAGGGGGACTGGATTAATAA
ATTCTGGTAATATAGTAAGGACAAAATAAATGTAAAAAAGATAGAAGTAAATGGAGAACA
TCAACATGAACGCGTGCTCCTTTGAGTAGAAAGTAATTTTTCTGCTTTGTCACTCAAATA
GCTGGCAGACCTGACATCACCCTGCCTCTGCTTCCATGCTCTAAAACTTTCCTGGGCCTC
AGATTTGGATGCTAATATGATTTTCCACTTAGTGGATAAGAGCTCCCTGGAGAAGGGCTC
ATTCTTGGATGGACAACAGAATTAGAGCCTGAGTTCTAAGAGCTTAATAAAACAAAAG
Sequence 887
CCCTTCGAGCGGCCGCCCGGGCAGGTACCCGATGAAAGTTTAAATCTAATCAACAGTATT
ATGCACTGGTTGAAGAAAACCAGGATTAAGACGGAGGATAGTCAGCATGGAATCTAANAA
GGGAAAAGTCCGNTAACTATATGTGTTCATNAGATTCTAAAGCTGTTAAGGGAGAAAGAC
CCTGAGTCTAATGAATATAAACTTTAAATTTAAAGAAAAACATGNTCTGTTATAGAAAAG
TGGGCTTTTAANTTTTGTAAAG
Sequence 888
CCCTTAGCGTGGTCGCGGCCCGAGGTACCATTAACCGTCTTTTAAAAAATTATTATTAGT
TTCAGTGCTGTTTCTTGAGGGAGCACCGGTGGTGCAGGTCAGGTTTGTCTTCTNAAT
Sequence 889
CCCTTAGCGTGGTCGCGGCCGAGGTACTAAACAGGCCAGATATATTCTCTCATTAACTTA
TTGCCTAGCAGAGAAGACCAACATTTTTAAAAGTTTATACATATAGTTAATTTCTATTAT
GATTATATGATACAAATGGAAAGTGCTATGAAAATGTGGAACAAAAGAGAATAATCTGTC
TGAACAGTCAAAGAAGACTTCTGGGAGATGACATCTGAGCTAAAGGTTGAACAAGGAATT
GGAAAACAGCTGGCATGTGCAAAAGACTTGAANACTGAAGGAGTTAGCCTTTAAAAAAAT
GAAGAAAGTTCTATTTGGCCAGAGCAGAGTTTCAAATAGTGCCTCACAGGCCACGTTAAA
GACCTGAGGCCTTTATTCTAGGAGAATAGGGAGCTGCTCAAGGAATTTAACTTGANAAGT
GACAAAGATCAGATTTGCAATTGCCTTTCAAGGTGGTAGGTTACAAGGGAGTTGGGTCTC
TTGACCCTTTGCAAATTATACCCCATTTCTTAACCTAAGAAATGGG
Sequence 890
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTGCCTTGCAAAATTATATTACAAGAAGAAG
CACACTTGTTATAGAAGTGCTGAATTGTATGGAACCTAAATCTGTCAAGTTACCTGTCTT
TCAGGTCCGTCTCCCCACCTCCCAGACCTCATTATATTATCCCGAAAAGAACACGATCTC
TTTAAGGCTAGGCAAGTATTGCGCTGATGAGCCAGGGACTGCCCACCAATTGGCAGGCCC
ATTGGGTGATAAATGTCCAAGGACCTCTAGGCTGACGACACATTTTTCATCATTAATCCA
GTCTATTGTAACCAGGGCCACTCACATTGATTCGGACTAGGGGGCATCATCTGCTGTTAA
AGAGGGTGATGACTCGCTAAAAATGAGGG

Table 1

Sequence 891
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACTTCATGGCTAAGCATGTGCGGGATGGAA
CCGGTCTTCCTGGGCTTACATCTTTGCTTTGCCTCTTCTTTCCTGTGATGAGTCTTGGGG
TAGGCCTCAAAGGCTGAATCTTCAATATAAATACAACAGTGAATGAACAACAAATGGTTA
TTTTAAAGATCTATCTTGGATGGCTATTTAATTTCACTAAACCCCAGGTTGCTCACCTGT
TGACTGGAACAAACAATAGTCCCTTCTTCATGCGGGCATGGTGAGGGTTTTAACCCCGCA
TTGTCCACAAAGACCGCTTAAATTATAGTAGATGCTCAGCAAATCTGAGCTATTATTTTT
ATCACGACTGTCAGAGGTCAGATCAGGCTTCGGGGTCAGACACACCTGGGTTCAAATCCC
AGCAGGGCCACTTACTGTTGGAGCCGGGGCAAAGTCAGTTATTCTCCCTGAGGGTCAGTT
TTCTCATCCCTAAAAATTCC
Sequence 892
CCCTTCGAGCGGCCGCCCGGGCAGGTACTACAGAACAGGAACAATCTGCCATGTGTGTTT
ACAACTTCAGAAAGCCCTGGAATGACAGTTGCCAGGGCAGTTCTTTGAATTTGCAGGTCA
GAATTAGTGGATGATGAATTTTTTTTCACACATGGTCAACTCTGTGCCACCTGCTACAAGA
TGTTGGAACAGGTATATTTATTTATTTAATGATGATCAATGATTCTTCCAACATCAGGGA
ACATCAGGGAAATCAGCTAGTATATGCTCTTTTTGAGGATTTTCAGCTCCAAATCCTGAA
AGCATTCATGAAACTACATAAATTACTTTTGTTAAGCAAATCATCATAAGTAAATCCAGT
CATATGAATCTGGAAGGATTTGCTGGTGGGCACTAACACTGACCACATGTTTCAAGTGTG
GGCAAGTTTACCATCCATCACGGATTTTGTGCTTGGTGAATTGTAGGGAGTGAAAGAGAG
AAGGATGTTTGGCCCAGTTGTCTTTTTTACCTATATCTGAAATTCTTACTTAGTCAAAGA
ACAAAACATTTAGACATTTCATTTCCTTTTGGGGGTTTTAAGTGATACATGTTTAAAAAT
TGTATATTTTAGAAGAAAATTGTTTTTATTATATATAATTTATTAAAATTCNGGNGGAGA
AGACCAAATTTTATCCTGAGNAAAAANATTTAAATTTGAAGNTTAGGTTGGCTTTTTTAAN
ACCCNCCGGCCNAACCCCAAC
Sequence 893
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAGCATTAAAAAAGTCCTACAAATTATTAGA
GAGAAAATACAGGTTGCACGCAAAGCATAAAGAATGAGAATGGCATAAGACATCTTAACA
GTGCCACAGAAACTAAAAAGTAGTTCTGAGTAAAAATGAACTATTTACCCAGCCAAACCG
TTAATTAGGTATAAAGGTAGAGTTAAGACATTTATAGACATACAAGATATTAAGATTACT
GAGTCAATTGATATTCAACAGGGGTGCAAATGGAGAAAAGTCTTTTCAACAAATAGTGG
TGGGACAAATGGATAGCCACATGCAAAAGAACATATATATAAGAGCTAAAACCATAATGC
TTTTAGAAGAAAATATAGGGTTTATCTTCATGACCTTGAATTTGACAAAGGATTCTTGGA
CATGACACCAAAAGCACATGCAACAAAAGAAAAATTGGAGTGATATG
Sequence 894
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTCACACAGCACATCAGTGGCTACATGTGAG
CTCAGACCTGGGTCTGCTGCTGTCTGTCTTCCCAATATCCATGACCTTGACTGATGCAGG
TGTCCAGGGATACGTCCATCCCCGTCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTC
CGAGGAGACAGAAGGGAGTGTCGGACACCATGACGAGAGCTTGGCAGAATAAATAACTTC
TTTAAACAATTTTACGGCATGAAGAAATCTGGACCAGTTTATTAAATGGGATTTCTGCCA
CAAACCTTGGAAGAATCACATCATC
Sequence 895
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTCACACAGCACATCAGTGGCTACATGTGAG
CTCAGACCTGGGTCTGCTGCTGTCTGTCTTCCCAATATCCATGACCTTGACTGATGCAGG
TGTCCAGGGATACGTCCATCCCCGTCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTC
CGAGGAGACAGAAGGGAGTGTCGGACACCATGACGAGAGCTTGGCAGAATAAATAACTTC
TTTAAACAATTTTACGGCATGAAGAAATCTGGACCAGTTTATTAAATGGGATTTCTGCCA
CAAACCTTGGAAGAATCACATCATC
Sequence 896
CCCTTAGCGTGGTCGCGGCGAGGTACCTTGAGCTGCCTCAGCACTCTTTTGCCATTCGTG
CTAGAAACAGCCAAAGCCAGACAACCAAATTACAGATGCTTAAATGTTAATGCCAGACAC
CAAGGCTCCGTGAACTTCCCTGTTGAACATCTGACCCCGACTACTTGAGGACATGAAACC
TAACTGTGCAGCTAATTACACCTTCCAAGGGCAATGACATCGGGTCCTATGATTTTATTC
AGGAAAGCAATAAGGCAATCGGGGTCACTGTGAACATCATTTGAAGGGAAGTAACTTCTT
AGCTTTATTCCACAAATGGTCTAT
Sequence 897
CCCTTAGCGTGGTCGCGGCCGAGGTACCGGTGTAGTGTATAGAATGGTTTGTATCAAACT

Table 1

AGATCTACATTACTTTACTAGAAATATAGGGCAATAATAAAATTTCCAAAGCCAAACTGA
ACGATAATATATATTTCTTTAGAAAGTCTCAGAAAACCCATTCCTGAATGACAAAACGGA
GAGATAACTTACAACTAGGTGATATCTGAAGTTAAATTTTCTTGGTTATCTATTTCAAAA
ATTCACAACTATTCTGCACTAAAATGTTTCACTGGGTCAGGCACAGTGGCTCATGCCTGT
AATCCCAACACGTTGGCAACCTGAGGCAAGAGG
Sequence 898
CCCCTTCGAGCGGCCGGCCCGGGCAGGGTACCNCGGGGTNGGACTCTNTGGTTTTTNAAA
ACCTTATGAACCATTAACTTGGGAACCCCGGCAAAANTAAGCCTNGGGGGGGCTTGAGGGG
ACTTTTANGANNNAACCNTTTAAACATTTGGTNTNNTTNAAAAAAAAAATTNCAGGGTTTN
CCGTNCCTTTTCCAAAGGGGGGGAAAAANGCNCNAACNTTTTTTTTTTTTTTTTTTC
Sequence 899
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGACAGATGCCTGGGTAACCATGTCCAATGT
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TCCGCTGGTAAGAAATCCGCCACACAAGAAAGCACTGACATTTGGAGCCTCATCAGGTTC
AGAGTTGAAAGTGAAATAAAGGATAATAATCTTTGTCTTATTTTCTTTGTTTTAATGTTT
CCCAACTTACGTTAGGACAATGTCAACAAAGACAGATGTCCCTAATAGTAATTGCAGGAC
ATGTGTTTTCTCATTCCTATC
Sequence 900
CCCTTTGAGCGGCCGCCCGGGCAGGTACATTGGAGGGGGCCATATCCAGGACCTGTGATG
TGTATAGGCAGACCAGACTGGTAGGGAAGAAAAGCAGAGATATCAAGTGGGGGACATGTG
TTTGCCCTGGGGCTCTATTGGCCTGGAATTTTGTGGTAGGAGGAAGGCACAAAAAGTAGA.
CTGGGATTACAGGCGTGTGCCACCGCGCCCGGCCTAAAGTGTGTTTTATAATAAAACCTC
AATCTGAAACATTTTAATAAAACCTTTAGATGACTAGATTTATGTTTATTTTGGATTTAT
GTTTATATGAATAAAAAAAGAAAAAAGACGAG
Sequence 901
CCCTTAGCGTGGTCGCGGCCGAGGTACCTATGAGATGCATTTGAAAACTTACCTTGTTTA
TATGTTTCTTCTGTTGCAATTTCTTCCATTACCTGGGAATAGCTGCTTTGGACGGCAAAC
CAAGCAATGCCCTTTCACAGCTGTGGGATGAATGGGGAAAGAAGTCTTGGTAAGGAAGCA
ATTCAGAGAACATGGGAGCATCTCATGGCAGCAGTCACAATTTTGTGTTGCGTAATATTT
CAGGAACTTGCAACCCTGATAACTTGTGCCTGCCTGTCTGTAGGCCTTTAATGATGTTTT
ATTGAATTTTGG
Sequence 902
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCTATACAAGGCAAAATGAACTCTAAGTAAAA
AAGAAAATCACACTTCTAAACACAAATTAACCATTTCAGTATTTAATTGCTCCTAAAAGG
TGTATTCTACTTCATTAAATGTAAGAGAAAAGGTTACCTACATTACGCAGTTTAAGAAAC
AGGATAAACTTTAGCATATAAACCAGTCTTGATTACAATTTCACACTTTCAACCATCTTA
TTTATACCTCTACATTAGATAATCTTTAAATTTCCATCATAAGGTTTTCCCATGGTTAAC
CTNCCATATAAAATTTTGGTAATCCTGCCC
Sequence 903
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGGTGACAGGAGAGAGCTCATGTGACCCGAGT
CTGGGTGGTCTCAGGCATGGTATAAAGAACTAGGCCAACCAACTGCACTAGACATAGAAA
CTAGCTGAATAAACTCATCCACTCCGATTTCATTTCAGGTATCTCATGAGAAACTAGAGG
ACAAAAACAATTCCAAAATTAACAAAACAAAGTTTACTCTAGCCATCAGTGCCAATGAAC
ATAAATGACTGCCTGAGAGTTATATTAACAAAATAATTAATTCAGACGAATTAAGGAATT
AAACCAGCTATGGGAAATATACACTCTATACTTAGATGCACATT
Sequence 904
CCCTTTCGAGCGGCCGCCCGGGCAGGNACTTAAATAAAATAAAATTAAAACAAATCATTT
TAGAGATAAAGAGTGAAGTTACTAGAAAAAGGTGACTAGGACTCTGTTTATGAAGAAAGG
TTAGTATTTAAATCATGAAAAAAAGTAAGAATACTTAATTATTCAAGTAACTTAAAATTG
TAATTCAGAATGGCTTTTATGTATCTAAAACAATCTGGGCTGCTATAAAAATTCAGTCAA
CTTCTAAACTTCCAAACACAAAATAGTTATACTCAGTCTAAGAATATCCGACCTACCGTG
CAGGACCAGAGGGCTCATCTC
Sequence 905
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAAATAAAATAAAATTAAAACAAATCATTT
TTAGAGATAAAGAGTGAAGTTACTGGAAAAAGGTGACTAGGGACTCTGTTTATGAAGAAA
GGTTAGTATTTAAATCATGAAAAAAAGTAAGAATACTTAATTATTCAAGTAACTTAAAAT

Table 1

TGTAATTCAGAATGGCTTTTTATGTATCTAAAACAATCTGGGGCTGCTATAAAAATTCAG
TCAACTTCTAAACTTCCAAACACAAAATAGTTATACTCAGTCTAAGAATATCCGACCTAC
CGTGCAGGACCAGAGGGCTCATCTCTTGCCGAGCTTAATACAGTTT

Sequence 906

CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTGCTTTAAATGCATACTAAGCTGTGAATGA
CTGATATCAGAGACTTTCTTGGAAGTAGGTTTCATAGGATGGAGGACAAATGAAACTTTA
TGGGCGAAGAAAGAAGGGTCAGTTGGGTGGTGCATTGAAATAAGTGGTTCCAAAAGCAAA
CTAGGTCAACTTTTTAACTGGCTAGTGAAAATGAGATTCCTCAGGATACAAAAGCAAGGA
GAAGACAGGAATAAATCAGGACTCCAACAGGCAGAACAGGATTTATTTAGGGCATGCAAT
GTGGAGGGCCCTAATGGGAACATGACAGTGT

Sequence 907

CCCTTAGCGTGGTCGCGGCCGAGGTACAAATTGCATTGTCAATTTATATTTGTTTCCCCA
CTAAAGCCTCCAAACCTTGCTTGTTTTGTTTAAGTATCCCTGGGGCTCATCACAGGGCCT
GTTGAAGTTCTTTTGAAATGAATTGAAGAATGTGAATAATAGTTCTAGTTCTTCGGGATA
ATGGAAAGCTAATAAGGTTTATGCTAGAGGCTCTTACTGCTGGGACTCTCTTCTTGTTTT
TGGTTTTTAGGAAAAAAGCTAGAAAATCCAACTTCAGCTAGAGTAACAGTAGTAACTGAC
TTGAAAGTATGTCAAAACAAAAACTGTTAA

Sequence 908

CCCTTAGCGTGGTCGCGGCCGAGGTACCTATGAGATGCATTTGAAAACTTACCTTGTTTA
TATGTTTCTTCTGTTGCAATTTCTTCCATTACCTGGAATAGCTGCTTTGGACGGCAAACC
AAGCAATGCCCTTTCACAGCTGTGGGATGAATGGGGAAAGAAGTCTTGGTAAGGAAGCAA
TTCAGAGAACATGGAAGCATCTCATGGCAGCAGTCACAATTTTGTGTTGCGTAATATTTC
AGGAACTTGCAACCCTGATAACTTGTGCCTGCCTGTCTGTAGGCCTTTAATGATGTTTTA
TTGAATTTTGGT

Sequence 909

CCCTTCGAGCGGCCGCCCGGGCAGGTACCCTCTTCTCAATTTTGCTATGAACTTAAAACT
GCTCTTAAAAAAATATTTTTTTTAAAAAAGGAGGGGNGTTATTATCAGAGATCCCATAGAC
CTTAAAGGATAATGAAAGAATGCTATGGGATAACCTTCATGCTAAAAACTTCAACAACTT
AGAAGTATGAAATGAATGAACTNTCTCCAAAAAAAAATACAAGTTACCAAAATTGACATGA
ATAATAACAGAAAATNTNGANTAACGCTCTAACTATTAAAGGAACGTGAAGTTTGTCAAA
AGCTTCCCCAAAATAAAATTCCAGGACCAGATGG

Sequence 910

CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCAATGGGGTAGGGTGTCTTGGGATCTGACT
GTTTCTTAGACCTTCAATGCTTCTTGGCTTTCCTCACTGCTAGTTATAATTCAGTTTTCT
CAGGTCTAAGTCATTCATCACTCTTTTGTCTGCTTTTCAGCTTCCAAAAATTCATTGCTA
TTATCTCCTCTCCTGTTTTCCCTATTGGTGTGTTTGTNTCTTTTTTCTTTAAAAAAAATTCC
TTTGTGG

Sequence 911

CCCTTAGCGTGGTCGCGGCCGAGGTACAACCTAGCCAGCTGCACAGCAGCTCTCCAAGAA
AAAGGTGTATATTAGACAGATTCAATTATTCATCTTGTGATTATGAGTAGTAACCAAATT
GTCTATGTAATTTTCTTATGGTGAACTACCCAAAGCAAGGCCTCACCTTAGGCTACCAGC
TTGACTCTTAAGTGGACAGAAAGAGCCAAAGGCTAAAAGGTTTGTGAGAAACCTCATGAG
CACTGAGTGTTCTAGTTCCAGATGAAAACCGGTTTCAGGTATGAAGCAAGAGGGAGTGCT
AATTGGTAGAAGTAATTACATCTT

Sequence 912

CCCTTAGCGGCCGCCCGGGCAGGTACAACAGAGCACAATGCTTAGATTTGGGTGGATTTG
AATAAGATGAAAGATAAATTATGATTTTGTTCAAGTGTTAAAATAAAACTAAGACACTTA
AGGACCACAAAAATTTAGACCAAAGTATCTTGTAAATTCTACCTGGTGAAAGTTTGATAT
AGCACACATATGACTTTTCTATATTATTTTCTGTTTTGAGTTTAGTAGTAAGCAGATGGT
TTGTATTTTCTTTAGTTGCAACTAAGTGATCAGTTTCATGATTTCTCTTACTATGAAACA
TTTTTTTTTTTTTCTTAACAGTTATCTT

Sequence 913

CCCTTTCGAGCGGCCGCCTGGGCAGGTACCACAAAGTTATTGCCTACATCCAGGTCAAGA
AGATCTTCTACTGTATTTTCTTCTAAGAGCTTTTACATATAGGTCAATGATCAATCTAAA
ATTAAGAGTTGTGCAATCATTAACTCTAGCTTTAGACTGGTATACTAATTGGTTTGTATA
CGAACTGGGTTAAAGGCATAGGACACATGCAGGCTGTGTTCATTTCACAGCAGGGCTCTG

Table 1

TAATTAGGCAATAATTACTTACCATCATACCTAGTGAGGCAATATGGGAGAAACAAAACA
GGCCATACAGCTTCACTATTATTCCTACT
Sequence 914
NNCACCCCTAGCGTGGNCGCGGCCGAGGTACTTGAGGACCAAGCCACAGAGCAAGCGCTA
AAAAAAAAGTTAACTAGAACCTTACCACTNTTNCACGCACCCCAATTNCATAAAATGTAT
CAGNAAAAAAAAACAATNATCTAAAGANAAAAAAGNAAAGAAAAANNATNNANCACATAG
GNAACNGGGTGTCAACTAGGNAACNGACCTATANNAANNNAGGAAGANAGNGNCTNCCTT
CCTCAATNNNCAGANNNACGGAGGGGAGGCTCAAAAGGCCCGAGAGGCTCNCTACAAGGA
GAAAG
Sequence 915
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGAAATGGTAAATATATGAGTAAATATAACAC
ACTTTTTTCTTTTAAAATTTTATTTAAAAGGTAACACTTTGCAGCAAAATAATTAACAAT
GTATTGTGGGTTATATAGTAGTAAGATGTTTGACATAAATTACATAAATAATTGGAGCAG
GGAAATAGAAGTGTGTTGTTGAAATGGTTTGATATTATATATGAAGTGGTATATTATTAT
TTCAAGGTAGCCTTGATAAGTTAAAGGTTACATATTGNAAACCCTACAATAATCATTACA
AAATAAAGAGATATAACAGNAAG
Sequence 916
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCATAGAGGTCCAGACCCCTTGCGTCTGGCAT
TCCTTTGGTCTATAATTCAGTAAACTCTGCTAAAAAGGAAACGAGACTAGCTTGCTGTGG
CCCCTTAAGCGACCCAGGGTAGCTTGTGATGGTTCAGATTATGATTTGTTCTAGAGCTTT
TCCAGAGGCAGATGTTGAGGAGTTTATCCTATTTGNCCCCTNCCCTTTAAACAAACAAAA
GTGCCGGCTGGACGCANTGGCTCATGCTGGTAATCCCANCNTTNTGAGAGGCTNAGGCAG
GCGG
Sequence 917
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGCCTGGCATGCATCTTCTCGATGGTCTGTT
ATCTTGTGGGAATGACATTCGTTAAGTTGTTTTCTGTGTGCATCCCACCCAAATAAAGAA
TGTTTCATCAGCAAAGTGAATTGCCGTATAGTCATCAGACTCTAGAAATAAATTATCAAC
GATGACTGCAGTGGGTGAGGCTGTTTGTTTATCACATCACTTGAGAACAGAGTAAAGTGA
GTTTCATATTTTCCTGAGTCTTGAATTCTCATTTTAGACATCTGTTCAGAAGCTTTCTAA
GCCATGGAGTATTCTAAATGAGC
Sequence 918
CCCTTAGCGTGGTCGCGGCCGAGGTACTACAATTATAAAGTTACCAATAACTTTACATTA
AGAAAATCATTTTCTTCCCCTTGAAAACAAAGTATGTCCTCACTTTCCCTGCTCTTTTAT
TCATGGCAGTATGAAATGTGTCCCTGATTCCCTCCGACCTGCCACAGAATACTGAAACAG
TGGCCGTGGGAAGAAATACCAGATGGTATGCATATGGCTTTGGGAACAGCTTTCAGCAGT
GGTCACTTGTCTTTTTTTAATGCATTTCAAAATGTGTTTGGTTAGCAAAAAATAATGAGA
TAATTCCCTCAAATAAATG
Sequence 919
CCCTTAGCGTGGTCGCGGCCGAGGTACAACAATTTATCCATTCCTTTAGCAATAGTTGGA
CACTTAGAATGTAAAACTGTTCAAACAAATTGGTATATTGGAGTTTGGGTAGAAAGAAGG
GCCGTTGGAAGAGGAGGAAAAGAGGGTGAGATGATGATACATTAATATAAAATTACTGAAAGGT
GGTGTTCACATTTAGAATTTTTTTTTTTTAAGTTGCATGTTTAGGATTTTAGTGCTCAGGAG
GAAAGAAGGCCAGTGTTGCCCTTCCAGACCATCGCTGCCATTTCCCTGTAATATATCGTG
TGTAGAGGAACCTAATGCCTGCA
Sequence 920
CCCTTAGCGTGGTCGCGGCCGAGGTACTCGCTATTTCTAGTTCAAAATCACAGATTTTCA
GATTGAAAAAATTTCAATCCACTTATTTTTCAAATGAGATAACTGGGACAAAGAGAAATT
CCATGACTTGCCCAAGATTACCTACAGTTTAACTGTCAGCGGGGCTTAAAACCACAATCC
ACATCTCCTGACTCCCAATCCTTTCACTTAAAACAAACAAGCAAACAAACAAAAAAGATT
TCTAATAAAGTGGAATAATTNTAAGAAAGGCAAGTATCACTATTTTAC
Sequence 921
CCCTTAGCGTGGTCGCGGCCGAGGTACTCACATGTAAACTTCTACTTTCCCCTTCAGATT
ACAGCAACCATCATGCCAAAGCTATACACTCTCAGGGAATCCCTGTGGATTTCACTGATG
ACCACTTGACCAACTATCATAAAGATCAAGGCCAGGGGTTCTCAAACTCTCAACATTTGT
GTGCTCATCTCCCCTTCACCCAGAGACTCCCCAGGGCTGCTGGGCCACACTTTGGTTTGT
TTGACTGGAACATAGTTTGAAAGGGATGGAAATTTCCAAAAGGTGTTAATAGACACATAA

Table 1

AGATTTTTAAATATTAAAAAAAAGAAAAAGAAAGA
Sequence 922
CCCTTAGCGTGGTCGCGGCCGAGGTACATACAGTATGCACTCCCTTCTCTGTGTTTTTTG
TCTGAGTTGATGATTTGGAGCTCAAAGAGCTAGCGGAGGGAAAAGCTGAAGCCATTCAAA
CACATAATGAGAATTGGAGATGTAAAAGAAGGCTGAGTTCTAGGAGTTGCAACAACTTAG
GAGATAACAGAACCAATTCGGAATGAGCAGGAATTGTAGGAATGCAGGCGAGGACTAGAA
GAATCAGCTACATGCTGTTTACTGGCAAAGCAGGAGAAATGTGACTGAGGACAGTATGCC
ACTGAAAACTGATGAAAGAGGAGGGAGACAGGAGG
Sequence 923
CCCTTAGCGTGGTCGCGGCCGAGGTACTGTTGTCTCATGCTCTCTTTCTGTTAATAGCAC
CTCAATTCTACTCTGGGGGACATTCCTCCTCTCTTTTTGGTCTGGAATGTCCCCTGGCTT
CAGGGACAGCTCAACATGGGCCTGGACAGTCAAATTCCATCCCCAAGCTTGGGACTCAGG
GAGACCATCCAGTGACTTGTTCCTGAAGTGCTGGGAAGGCAGAGCNTCCTTTCTGCGGGG
TGCTGAGTGATGGGACGACAGNGTGGAGCTACTGNGCTCTCCAAGCCGGNGCCCAGGACC
AGCCTGCCTGAGAACGAAGCCAGC
Sequence 924
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTGCCTTGCAAAATTATATTACAAGAAGAAG
CACACTTGTTATAGAAGTGCTGAATTGTATGGAACCTAAATCTGTCAAGTTACCTGTCTT
TCAGGTCCGTCTCCCCACCTCCCAGACCTCATTATATTATCCCGAAAAGAACACGATCTC
TTTAAGGCTAGGCAAGTATTGCGCTGATGAGCCAGGGACTGCCCACCAATTGGCAGGCCC
ATTGGGTGATAAATGTCCAAGGACCTCTAGGCTGACGACACATTTTTTCATCATTAATCCA
GCCTATTGTAACCAGGGCCACTCACATTGAT
Sequence 925
CCCTTAGCGTGGTCGCGGCCCGAGGTACCTACTGTGTTGAGCCCTCTTCCATCTCCTGTA
GTTTCGTCAGATCCTAGGAAGTGTCCCTGACGGAGAAGTTTTACAAAATGAACTTCGAAC
TGAAGTATCCCGATTGAAACGGAGATCTAAAGATCTGAATTGCCTTTATCCCAGAAAAAG
ACTTGTGAAATCTGAAAGTTCAGAGTCTCTTCTTTCTCAGACAANTGGTAATAGTAATCA
CTATCATCATCATGTGACATCCANAAAGCCACAAACAGAGCGGTCCTTACCAGTGACTTG
TCCATTGGTTCCAATTCCTAGC
Sequence 926
CCCTTAGCGTGGTCGCGGCCGAGGTACCCAAACACAAGATTGCTAATAGACTGCTAATAA
TAGAACTTAATAAATGAAATAATTTATTTCATTTATTGTTGCTTGGAATACAGAAAGTGC
TTAGTAAATATTGAATGAATCAACAAAGTACCTCCCAATATAGAGAAATCACTTCTGAAA
AGGATAAAACCAAGTTGATCCTATTCAATCGAAGGCATCTTTTGGGGCTGTTACAGTTAT
TTCCTTTATTTGAAGAAGGAATATGATATACCTACTTTGTTCCAAGTCACTGCTTATAAT
GTGCTAATGGTACCT
Sequence 927
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGTGAAGACAGCTACACCTGGTTTCCTCCCTC
ATGCCTTGATCCCCAGAACTGCTACCTTCACACGGCTGGAGCACTCCCAAGCTGTGAATG
TCATCTCAACAACCTCAGCCAGAGTGTCAATTTCTGTGAGAGAACAAAGATTTGGGGCAC
TTTCAAAATTAATGAAAGGTTTACAAATGACCTTTTGAATTCATCTTCTGCTATATACTC
CAAATATGCAAATGGAATTGAAATTCAACTTAAAAAAGCATATGAAAGAATTCAAGGTTT
TGAGTCGGTTCAGGTCACCCAATTTCGAA
Sequence 928
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGAAAGAAAACAAATACCAAGTATTTACAGAT
CCAGAGAAAGTTCACAAGAATGGGAGGATGCCAGTTCCAATGCTTTGTAAAGTCAAAAAT
AGCCACATTGCAAAACAAACAAAAAAAAAACGAGAACGTTCCCGAGTGTGCCTCCAAAACA
TAAAGGAGAAAATCATACAGAAAAACCTCATGTAAGGGTTGGAACTTGAGCAACCAGCTA
TCCAAATACAGAGGGGAATCCTCGCTTAGCTAGGGCATGGCCTGAGAGAAGCCCCTTCCT
GCTTTCAGAGCCTACAAGTAGTCCCCA
Sequence 929
CCCTTAGCGTGGTCGCGGCCGAGGTACTTAAGCAATAAATCTGAGCAATTATCAGGTTAT
TTTATTGCATTTCTAATGAGTTCTTCTAAAAAAAGTCAATCAATTATCACTGCTATATAT
GTTCTGTGTGTAAGGAGTGCTTGAGAGTCTTTAATTGTAACATTTATTAAATAAGAATAA
GAGGACATTTTTTAAAGGAATTAAAGGAACATTAATTCCTTCATAAATGTATAGTGCTTAA
GCTCTGCTTTAAAAGGTCTTTCCATGTGCTCTTGGGTAACCACTTAGGGCTGAATTCATA

Table 1

GTATAAATATCAATAAATGTTGCAATCACAA
Sequence 930
CCCTTAGCGTGGTCNCGGCCGAGGTACGCGGGTGGGAAAGGGAGGATGACTCACTTACTC
TGAAATCTGGGCCCAGGAAGGACCTCTCCCATCCTTGGAGCCTCCTCATTCTCCTGTCTC
TCACNNGTCCCCCCACCTCTACCATGATGTCCTCATTCTGGGAACCCCGAGCAGGGATAG
TGGCTTGGGCCCTTCNTCTGGCTTTTCTCCCCACNCTTTGCTCCACTTCTAACATTTTTC
TNCCTTCATCTNACATGAAAGGGACAANGGGTTAACCCCAAGNAGGGAGGGCAGAAAACA
ANGNNCCCCACATCCTGGCTNTGCCTTCTGAC
Sequence 931
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCAGGGATTTANAGACAGGGTCTGGCTCTTT
TGCCCAGGCTGGAGTGCAGTGGAACAATCATGGCTCACTGCAGCCTCACCCTCCTGGGCT
CAAGAGATCCTNCCACCTCAGTCTCCCTAATAGGTAGAACTACAGGTGCACACCACCACG
CCTGGCTAATTTAAAAATTTTTTTTTATAGANACAAGGTCTCACTATGTTGCCCACACTGG
TAAAGTATTTTTAAATTTGAGACATGAATAATGATGCAAATCATCCTTTNTATGGGTCTG
ATTCTGTTCTGTTACCTTATTCAAGGACTAA
Sequence 932
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGNAT
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GATCATCCGCCTTGGCCTCCCAAGTGCTGGAATTACAGGCATGAGCCACCGTATNTGGCC
ANANAAATTTTTTAATATAAATTTTTTTCAGTTACCACTTAAAGGGAAATATGATTAAAAA
AACTAAATAAAGAAGAGCTTTAGTAAAACCATGCCCTCTTGCTAATCTATTAANAGTCAA
ATCTGAA
Sequence 933
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGTATGTTTCCACTTATGGACAGATAATTAC
GTAGTAAACATAGAAACACACGAACTGAAAGGACACACACCAGTATCAGAACTAAGTCAC
CCATGGGGAGGGACAGAAGGAAATAGGATGGAAAGGGGGTTGAGGGACTTCAACTGTATTT
GTGATGTTTTAGTTCTTTAAAACAAAAATCTAAATGACATTTGAAATATGAAACAAACGC
AGAAAACATCAAAATGTCAACAATACTTAAACCTGAGTGTTGGGTGCCTGAATGTTATAT
TGGTCTCTGCA
Sequence 934
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCCAGTATATGAGCAATTGCTCAGCAGTGTTT
GGATATAGGGAGTGGATAGCTATTATTAATTGCAGATTATTTTGGAAGGAAAAACACACA
GAGAATTATGTATCTTTCAGTGTAAATGTTAGTTCTAAAAACAATCATATTATTTACAAA
GCTGCAGTTATAGAACACAATTCTGATTTCTGCCTCACCCCCACGGTTAATACTGTAAAA
CATTTCCTACGTTTCATCTGATAGTGTTATTAAAAATAGCTGTTATTTTTAATAGCTATA
CTAAAACATAAAAATGTTTAGGCCAGGCGT
Sequence 935
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AAATGTTGTTGTTACTGTTATGGAATTTATCACAAATATGTAATTATATGTTTCGTAGTG
ATTATTCATCACCCCTACTGGACTCTAAGGTCTGTGAGGATATGTCTATTTGGTTTACCA
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AGTGAATACATAAAGGTT
Sequence 936
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CAGGAGGTTGTGGGAACATATAGACAGTGACCAAACTTTTAATGAATACAGGAAGATTTT
CTGGAAAAGATGACATGTAGCAGACAGCTGACAGACGAGTTTACCAGGTTCAGAACTTAA
GTGATAATAATCTTTTTATCATAAAATTTTAAGTGTGGTAGAGAATAAAAGTTTTGAATT
AAATGTTGAATGAAATGTGTTAT
Sequence 937
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CTCAGGGGACAGATGGTCCCTAAGGTGCAAAAGAATGAACTGGTGCTGATATATGACTGA
TAAGTTTCTGTAACGGGCCACTGACCATTTCAATTCCCAAGGAACATAAATTACCTTTTA
GCCTGTGTATTTACACACAAATATGCAACCTGCAAACTTCTTCTGAGGACAGATGTCAAC

Table 1

TACTTTTTCATTTTTTTTTTTTACAGTCAAA
Sequence 938
CCCTTAGCGTGGTCGCGGCCGAGGTACCAAGTATACTTCACCAGATATCTATAGAACATT
CCACTCAGCAACAGCAGAATCCAGCAGAATATATATTCTTCTGAAGTGTATGTGGAACAT
TCTCCGGGATAGACCATATGTTAAGTCATAAAACGAGTTTCAATAAATTTAAAAGGACTG
ATATCATACCAAGTATGCTCTCTGACCAGAATGGAATGAAATTAGAAATCAATAACAGAA
GAAAATTTGGGAAATTCACAAATATGTAGAAATTAAAAAACACACTCCTTAAACAACCAG
TGGGTCAGAAAAGAAATCACAAGG
Sequence 939
CTTCCATACTCTTTTAATTGGATATGCCAGTGTGTNTCANTAATTTCCAGTGGCTGTAAA
ACTTTGAGAAATTTTGTAGCTTTTAGAAACCACATACCTGTATTGCCTGATTGCTTATTA
AGTGATCTCTTAGAGGTTTCCAAAGTTATGAGTTTGAGTTTACAAGTGCAGTTTTTTTCC
ATGAAAATTTCAGTGGTGACAAATTATAGAATTTATCATTCAATTCAGTCTTAACTAGAA
ATAATTGCATATAATAAAACAGGTTCTTGACTGTTCTTTT
Sequence 940
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GTTGGTCGAATGCCTCCAAAGCCCTCGACCTTCCCACTATACTTCACGCATCTCTAGAGA
AGAGACAGAAGTAGCCAGGATGAAGGTCTTCAGGTTTAAGAAGAACTATGAAAAAGCAAA
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CTATAGGTAAGATATCAGA
Sequence 941
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GACGGAAAAATTTGATATCAAAGGAAGTATCAAAACCCTTGATGTGGTTAAGAGCATGGA
TAGTGAAACTAACCTCTGATGTATGGTGAGAGAGCAAAAGAGAAAGGATTGCAAAGAAAC
TGGAATGTAGAGGATGAACATATTGGTAATAATAATACTGGTGGAATTGTTATTCAGGAA
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ACATGGTAGAAGATATCAAATATAAAAA
Sequence 942
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CTCTGGATTTTGCATGTGTGGGGCTTTTTTTTTTGATAGTTATTTGTTTTTTATTTTAAAA
ATTTATTTTGCCAACCCAGTAGAGAACAGCTGAGCATCTTCTCATGTATTTATTGGCCAT
CTGCATTTCTGCTGCTTATTGGCCATGTATTTATTGGCCATTTGCCGTCTGCTGTGAAAT
GTCTTAAATTTTTTGCCCATTTTTCTAGTGATAAAACACTGAAGCACATTTTTAAAGACT
TCTGATGATTTTTATTGT
Sequence 943
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ACTGATTAATGTGTATATACTAGTTCTGTTACTAAGGAGGGATGTTAAATTAATCCCTAG
CTGTAATTGTGCATTAGTTTGTCTCTTTTCAGCTGTTCTAGCTTCATAAATTTTTGGAGC
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TTAGGAAAC
Sequence 944
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AGGAAAATGTTCCATTCACTATGGTGACAAAACTGTAAAATAGGAATATATTTCTGAGGA
AAGTATAGGTATTTACAAATAGATAAACTATATTCTTAGATGAGAATACTTAATACCCAC
TTTACAAAATTAAAAATGAATTACAGCTTTTTAAAAAATAGATTAAGCTGGGTGTGATGAC
ATGGCACCTATAGTCACAGCTACTCAGAAGGCTGAGGCAGGAGAAGCACCTGAGCCCAGG
AGTTTGAGGCTCTAGTGAGCTAT
Sequence 945
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CGCCAAAAGAAGGGTAATCGATGGGACACCAAAGTTATCAGTCAAGTAAGGCAGAAATGC
TTGAATGAATAAATGTATATAGATAGAAAGTAGAGACCTTGATAAAGTCAAACTCCTTGC
CTTTACAAGTGTGTGTTCAGCAGCCATGCAAGGGAGATGCCCATCTGGCAGTGGCCCAGG
GCAAGGTGTCAGAGCCCTAGTGGCAGGGAGATGGCATCCACATATGAGGGAGGGTGACAT
GGTGCTAACTGGGCATCTACATAGGGCAGGG

Table 1

Sequence 946
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGCATATTTAATGAATTATTTTATAAATTGC
TGTTGTGAAGCATTTGTGAATGACCTGCCTCCTAGCTTTCAATGCTATTGCCCAGGCTNG
ACTTTTATTGCAACTGTTTTATGATACAGTTTTGCATTGTATGTGTTTACTTTTTAAAGA
AGCATTTCCTGGGAGGTTTCTTTTTCTGGTTATGAAAATAATATATGCTTATGGGGAAAA
ATTGGAAAATAGAAACNAGTATCTAGAAGAAAAATCACTCATAATTCCANCACCCTGTTA
ATACTTTGTCTTTTCTTACAGTTTCTAATA
Sequence 947
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGTAGATGAGAACTACTTATTTAGAGTGGCAG
AGCATGCTATAGAAACAAAATATGAGTAATTCTAACTGTAGTTATGTTATATTAGCATAG
TGAGATAGTAACATTAATAGAATTCCTTAGGTGGAATTTCTTTAATGC
Sequence 948
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGCATATTTAATGAATTATTTTATAAATTGC
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CTTTTATTGCAACTGTTTTATGATACAGTTTTGCATTGTATGTGTTTACTTTTTAAAGAA
GCATTTCCTGGGAGGTTTCTTTTTCTGGTTATGAAAATAATATATGCTTATGGGGAAAAA
TTGGAAAATAGAAACAAGTATCTAGAAGAAAAATCACTCATAATTCCAGCACCCTGTTAA
TACTTTGTCTTTTCTTACAGT
Sequence 949
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCAAGAACTAAATTGTGATACGATAGGTGACT
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TCAAGGTAGCTCGGAGAGACGGTGTCTACTTATTCACCACATCATGAGATCACCTCAAAC
TGAGCAGGCAGCCAATGAAAACCGTGAGCTTTCTTTACATTAACTTTCTGAAAGTCATTT
TTTCTTATTCCACTTTGTGCCTTTTTTTAAAAGCTGCAGCTTCATGGAATTTAATCCTGG
TATTTAAAACACT
Sequence 950
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TTAATTACCATCTATTCACTGATTACTCCCAAAACTGTATCTATAGTCCAAGACTGTTTC
TAAAAGGTCTGCACCCACATATGCAAATAAATA
Sequence 951
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CATTAGGGAAGAAGATTCTGCAGCCTACTCAGGTGAGCCAATCTCATGGCATTGAACANA
NAANATATGTTTTCACGTCTTTAACCANTGTTTTTCATAGTGNAAGTCAGGCCTTTCTCC
TTTGATCTAAGTGGAACCAAGAGGTTAGATACTCCCTTTNCTTTAGTTATATAATGGGCT
TCATGTAACT
Sequence 952
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TGCAGGTCAAGGGGCTAAGAAAATTGCAACACTAGAAAACCAACAAACTTAGGTTGTTCT
AACATACATACACAAATACAGGAGGGACGTTTATGGGTCACATCTGCGAAACATTTTTTC
CCAAAAAGCTGAATTTT
Sequence 953
CCCTTAGCGTGGTCGCGGCCGAGGTACCACCAATAATTATGCCCACAATTTTATCCTAAA
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AAAACATGACCCCTCCATCCAGAACCAAACTAAACTCAGGAGTGATTAGAATCACCTGTG
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ACAGCTCTTCCCCATTCCCTATCTGAAAGCAAGGAACCACTGGCTTTGGTCAGGAAACAG
GCATACAACATCAGATGTGATTATAA
Sequence 954
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GTGCTATTTTGTTNCTCCTACATTTACTCCATAGTAAGCTNTTGTTTGAGAAAAAAAAATG
CCAGTTTGGTGCGTAGTAGATACGCAGAGGCCTGNGAAAGGGACNGATGACNCCATTACC
CCATGGGTACAGAATGTATAATGCTTCCCCTCTCAAACTTGGGTTGNTTTGGNTTTTTTTT

Table 1

TACA
Sequence 955
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTAAGCCAGATTCATGGTATGAAGGCAGCAG
CATAGCACCTCCATTGACCCACATGGGGGCCTGCCTTGGGCTTCATCAGCCCTTTGGAGT
CTCAGATCCCTCACCTGTTAAAGGAGAGTAATACTACCCACTTACCTTTTTGGGTTGTTG
TGAAACACACATAAGACAGTATTAGGAGAAGTAAGGTCTGAGGGCTGGGCTTTGGACCCA
GCGGCCCCTAGGTAGAGGCCTGTTGAATTGGATGACAGTGAACTTTGCAGCATTTCCTAA
CCTCAGAAGTTCAAGA
Sequence 956
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCTGCTTTATTCAGTCTAGGTAAGAAATGTAA
TGGATGTGTGCAGGTGACATAATTTCAGGGGATAAGGTAAAAATTAGATGAAGCCCAAGC
AAATATTCTTAAAAAGAAAAACTTAGGATTTTTTTTTTACAAAAGTTAACTTAAAATGCAT
TATCTAGAATAATGTTATAAATCAACGTATAGAGACGTTAGTGAATAGTTCCCTTCATTA
GGATGTTGAAGGAATATGGTTTCAATATTCAACAAATGTCGTGATGCCTATAAATTTTTC
TACAAACAAGAGTATTGT
Sequence 957
CCCTTAGCGGCCGCCCGGGCAGGTACTTCAGGAGATACATTCTGCTAGTTTGGGGTGGTG
TGTTCTATAAATGTCAATTTAATCCAGTCGGCTTATGATTTTCAGTTCTATATTCTTACT
GATTAATGTGTATATACTAGTTCTGTTACTAAGGAGGGATGTTAAATTAATCCCTAGCTG
TAATTGTGCATTAGTTTGTCTCTTTTCAGCTGTTCTAGCTCCATAAATTTTTGGAGCTGT
TAGGTGCATATACGTTTAGGATTATTTTGTCTTCTTGGTGAACTAGACCTTTTATCATTA
GGAAACTGTCCATATAACCAC
Sequence 958
CCCTTTGAGCGGCCGCCCGGGCAGGTACTCCATAATATAATCTTTTAAATGGGCAACTTC
TAAATATTGATACAACCATTAATAATAATGCTTATAGGGTAAAAGAAAATTTTTGAAGCA
CTGAATTCAGTAACCTGGGTCATGGTCCAATTTTGCTCACTACTTCATATCTTTTATGTA
GATTATTCCTATAAACATGTTCCCTAAATTCCACATCAGTTTGTAAAGTCAATGGATTAA
ATTATTCAAATGTAGCTATTTAACGGTCAGTAACAATGCCTAGAAACCTAT
Sequence 959
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAANA
CAGTCTTGCTATTTTAAGTCCAGGCTGGACTCAAACTCCTGAANATTGCTCAAGCAATCT
TCCCACCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGATGTCCAGCTTAGGTTCCAG
CTNTTAAAANANTTGTCAGTGTGGTGGGCGAGGTGGGTCACATACACATATAATTATAAG
GTAAAAAATCACAACTACTACAAGAAAGGTGCAAACATTTATGAGAAAACCAAAGAAGGG

Sequence 960
CCCTTAGCGTGGTCGCGGCCGAGGTACTCCAGCCTGGGTGACAGAGTGAGAATATGTCTC
AAAAAAAATTATCAGCANAAGATAATATAGACCCCAAGGCTAAAGGGAACCATTATCATC
TCTAGGCCTGAAAGCCTAGGAGAGGGTGCTGTATGGAGAGGACTGCTTCTGACAGAGGGA
TATAGCCAACCTTGGTGGCCTAATAGAGAGGAAAGTAGGGAATAGCTTCACCTTCCTTCT
CTAATCTTCTGCTAGTATCCCTATTAATTTAGCCTAATTAGAAGCTGGAAGGTAGGAGAG
CCTCCATGGGCCAAAAAAGCTGTTGTAGAGAACATGGATCCTTGAGGGGGGTAAATGGGC
AGATAATTCTAGCCACAGATTG
Sequence 961
CCCTTAGCGTGGTCGCGGCCGAGGTACTCCAGCCTGGGTGACAGAGTGAGAATATGTCTC
AAAAAAAATTATCAGCAGAAGATAATATAGACCCCAAGGCTAAAGGGAACCATTATCATC
TCTAGGCCTGAAAGCCTAGGAGAGGGTGCTGTATGGAGAGGACTGCTTCTGACAGAGGGA
TATAGCCAACCTTGGTGGCCTAATAGAGAGGAAAGTAGGGAATAGCTTCACCTTCCTTCT
CTAATCTTCTGCTAGTATCCCTATTAATTTAGCCTAATTAGAAGCTGGAAGGTAGGAGAG
CCTCCATGGGCCAAAAAGCTGTGTAGAGAACATGGATCCTGAGGGGGTAAATGG
Sequence 962
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ACAACATTTCAATGATGCATATTTTTTTTTTCAGATGCATTCCTTTGATTGAATTTAAAGT
CAAGCTTGTGCTTCTGGATGGTTGCTTTGTCAGTGAACACTTGGATTTGGAAAAATACAGC
ACCTGGGTTGGTTTTGAGAGAAAATGGTTTCAACTTTATAATTACAGTTTTAACCACCAC
AACAACAAAATTAGGATGGTAGTGAAATGGAACTAAATCAAATGCAAGGTTTTAGTTTAA

Table 1

TANAACAATGTCATCCTTTAATAATCTTTAAAAGAAGAACAACTAAATAACCCAATNACA
AAATTTGAAAATTAGGGTCAAACCT
Sequence 963
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ACAACATTTCAATGATGCATATTTTTTTTTCAGATGCATTCCTTTGATTGAATTTAAAGT
CAAGCTTGTGCTTCTGGATGGTTGCTTTGTCAGTGAACACTTGGATTTGGAAAATACAGC
ACCTGGGTTGGTTTTGAGAGAAAATGGTTTCAACTTTATAATTACAGTTTTAACCACCAC
AACAACAAAATTAGGATGGTAGTGAAATGGAACTAAATCAAATGCAAGGTTTTAGTTTAA
TAGAACAATGTCATCCTTTAATAATCTTTAAAGAAGAACAACTAAATAACCCAATAACAA
AATTGAAATA
Sequence 964
CCCTTCGAGCGGCCGCCCGGGCAGGTACACTGCATAAAGCCAGAGTTAAAACTTCACTGC
CAGCCTCTGAACAGAAGGCTGTTCTATCCACACTATCACAAGACCTGGTGGAGTTGAGGC
AACTGCTGAATTACCATACAGGGAAGAATGAATTCAAGAAAATTCCCATGCAAGATAGGC
TCTTAAAAAATAAATTTACACAAGAAAATCAGCACTGTAAAGGTAATTGATAAGCCCAAT
AGAAGGGAAACCTATACAAAGAAATAGAAATAACTAAGCAATCTGAAATGGACTTTAAAT
AATGATG
Sequence 965
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CCAGCCTCTGAACAGAAGGCTGTTCTATCCACACTATCACAAGCCTGGTGGAGTTGAGGC
AACTGCTGAATTACCATACAGGGAAGAATGAATTCAAGAAAATTCCCATGCAAGATAGGC
TCTTAAAAAATAAATTTACACAAGAAAATCAGCACTGTAAAGGTAATTGATAAGCCCAAT
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AATGATGTTTACAATTCTCTAAGAGGAAAAGGAGCATTANCATCAGTGAAACAAAAGTAG
GGCTATAGAAAAAACAATACTTATGAAAAAACCAATTGGAAATTTTTAGATGGAAAAGCC
TGAAAGTAAAAAATTCAACACATGGTCTAAAAGAATAAACTGCACACAGCTTGAAGGGAA
AATTAGTTAATTTTACCNAAGAAA
Sequence 966
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AATCGCAATGTCTGGTGTCCAGTCAGTTACCAGGCATGGAAAGAGACAGAAAAACATGAG
CCATCATGAGGAGAACAATTAGCAGAAACCAAACCAGAACTGACATACATACCAGAATTG
GCACACAAAAGGATATTAAAACAATAACAACTGCGTTCCATATGTTCAAAAAGTTAGAAA
CATGAAAGA
Sequence 967
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGTCAAAAGGATGAAAATGTTTTCTGTC
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AATCGCAATGTCTGGTGTCCAGTCAGTTACCAGGCATGGAAAGAGACAGAAAAACATGAG
CCATCATGAGGAGAACAATTAGCAGAAACCAAACCAGAACTGACATACATACCAGAATTG
GCACACAAAAGGATATTAAAACAATAACAACTGCGTTCCATATGTTCAAAAAGTTAGAAA
CATGAAAGATACAAAAATAAAATCAAACTTCTAAAGATGAGAAACTGTAGTGTTTGGAGG
GGAAAAA
Sequence 968
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AGCACCCTACCCTCATGGCAGTGTCCCAAAGGAAGGGGTTTCCATGGTAACCTCAATGGA
TACAGTCAGCTGACGTCTGGCACCGCCTGTGCTGGTGTGCGCTAGCCTACTCACTCCCTC
GGCCCTCCCTCAATCCTTTCAACTATATTTATTAGTTCTCTTTAATGGAAAGTATATAAT
CCCTTAATGTCAGACCTTGAGTGGGCACTCAGCTTTATTAATTTATTTAGGTAATAAAAT
TTACCTTCCTAATTAAATTCTCAGTAAGTCCTGGGAAGCTGTATTATTTTAAACATNTTG
CACAATTGT
Sequence 969
CCCTTCGAGCGGCCGCCCGGGCAGGTACGCGGGCGGTCTGTGCCCCATCACCATTTCTAA
AGCACCCTACCCTCATGGCAGTGTCCCAAAGGAAGGGGTTTCCATGGTAACCTCAATGGA
TACAGTCAGCTGACGTCTGGCACCGCCTGTGCTGGTGTGCGCTAGCCTACTCACTCCCTC
GGCCCTCCCTCAATCCTTTCAACTATATTTATTAGTTCTCTTTAATGGAAAGTATATAAT
CCCTTAATGTCAGACCTTGAGTGGGCACTCAGCTTTATTAATTTATTTAGGTAATAAAAT

Table 1

TTTACCTTCCTAAATTAATTCTCAAGTAGTCCTGGGAGCTGTATTTATTTTAAACAT
Sequence 970
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GGTTATAACCTTTTTCTATTCTCTGCAACAGTGGATATAGGATTGGAGTTATTTTTTTCT
TAAGTTTTTGGTAGAAAACTAGCCCANTNGAAGTCATGTGGGTTTGGGATTNTTCTTTGT
ANGANAGGNTCCTAATTACTAATNAGCTTTTCAAAATAN
Sequence 971
CCCTTAGCGTGGTCGCGGCCGAGGTACCAAGATTATGATAGCCTCTTAAAACAAATTGGA
GGTTATAACCTTTTTCTATTCTCTGCAACAGTGGATATAGGATTGGAGTTATTTTTTTCT
TAAGTTTTTGGTAGAAACTAGCCAGTGAAGTCATGTGGGTTTGGATTTTCTTTGTAGGAA
GGTTCCTAATTACTAATTAGCTTTTCAAAATAGTTATGAGAATATTCAGGTTTTCTATTT
CTTCCTGTGTCAATTTTGTTGTCTTTTTCTATAAATTTGTTCATCTATAATTTTAATATT
TTTGGTATAATTTTTTTCAAAAATAATCTTGTATTTATTTTACAAGGACAGGGATCTTTA

Sequence 972
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AAAAAANNTTTTTTTGNNTNTGANNNNNGANTAANGAAAAGAAAAGGAAAAGAAAAAACA
AGAAATTAGCTCATGATAGNCAGCTTTATATTATNAATTATGTGACACTTTGGATATTTC
AAAAGCACATTCACAAAGTGTATTGTCACTTAAATACCTCAAAATTTCCCTGTTATACAT
GCAGATCATTCCCCATTCANCCCTGGGTATGGGACTGAACTGTGTACCTTGCCCGGGGCG
GGCCCGCTTCGAAAAAGGGGCGAAATTCCAGCNACACTGGGGCGGGCCGGTTTACTTAGT
GGGATTCCCGAGNCTTCGGGTTACCCCAA
Sequence 973
CCCTTAGCGTGGTCGCGGCCGAGGTACTCCAGCCTGGGTGACAGAGTGAGACCCTGTCTC
AAAAAAAAAAAAGAAAAAGAAAAAGAAAAAAGAAAAGAAAAGAAAAGAAAAAACAAGA
AATTAGCTCATGATAGCAGCTTATATTATAATTATGTGACACTTTGGATATTTCAAAGCA
CATTCACAAAGNGTATGTCACTTAAATACCTCAAAATTTCCCTGTTATACATGCAGATCA
TTCCCCATTCAGCCCTGGTATGGACTGAACTGTGTACCTGCCCGGGCGGCCGCTCGAAAG
GG
Sequence 974
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAAGCTAGAAGCAGCCTGGTCCAGATGGCTA
TACAAACCCNANACTGTCTACACCCAGACTTTATTCTTCTACAACCAAATTCCTCAAACA
CACAATCTTGACCAGTANCAGTTGAAANGGGAGTTTAAGGTGGGGGTGA
Sequence 975
CCCTTAGCGTGGTCGCGGCCGAGGTACGCGGGCTACCAAACCTGCATNAAAAATTTCGGT
NGGGGCNAANAAANGNNNTTNNCCNANCCTCCGAGCAGTACCATGCTATATTGGTCACTG
TAGCTCTGGTACATANTTTTNGAAGATTGGGGTAATGTGGATTCCTCTAGCTTTGTTAAG
CTCTGTTGTTTTCACTTAGTATTACTTTAACTATTAGGGCTTCTTTTTTTGGTTNCATATT
AAATTTGTAAAATAAAATTT
Sequence 976
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTCTCATTTGTCACTTTTCAACACTTCCTGG
CANGCAGGCANCATAACTGGTCCTGCTGGGTGATCCAGACCACACTCTGCAACTCTTTCT
TTTGAGCCAAGGCTCCCCTACTGTCTTTTCATTTTATGTCAAGGCAGGGGGAAGACCTCA
AAGGGCTCTTGCATCCCAGTCTCACTTCCCAAGAGAGGCACTGAGGCCCTCCAGGATGTG
GGGACAGGAACTTTGGGGCCAAGCCGGGGCTGTCCAGAAGATCACCAGGAGGGGCTTAAA
TTAGTTNGAAAAGGGAGNAGGTCCTTT
Sequence 977
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTAAAAAGTAAACAAATTTAACTGAAGCATGG
CTATTAGTTAGTGATTCTTTGTAGATTTTCTGGAAAGTCTTGTTTGTTTGTATTAAACAT
TAACTCTGCTGTATGCTGTAAATACACTGCTAAGATCAATATTGAAAAACGAACAATAAT
ACCAATTCATATGGACCTTCAAAATTAGTCTTATAAAATTTTTATGGATATTGGNATTAT
CCCAAGCCAACCTGACTTTTGAGGACTGACAAATAATATCTTAACTTTAACCCAGGGGTG
GATTTCTTGCCATTTNCCTTTTGGNTTT
Sequence 978
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGACTTCACAACACCAACCACAGGTCTCAAGG
TCAAAAAATGAGCTAGGAGTAAAGTATCTGCTCCAGAATCTACCCCCATCCCAGAAAGAG

Table 1

CAACCCAACTGTGTCCTGAGTGGCTCTTAGAGTTTAAGACTCTGAATGAATGCCTAAATT
TANAAAGGGTGTGGACCAAGGGATTTTTNGGTTAATGTATCNCTAAAAGCANGCTGACTGC
CAGGATTTCAAGT
Sequence 979
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTGGCAGCAGAGTAGGCACTAATATGTGTTG
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CTTCATTATTGCTGAAAATACCGCAGATAAATAGAGGGAGGCAGTGTAATAGAGTGGAAA
GAGCAGTAGACCAGGAGTCAGACAGTCGAGGATCTCATTCTAAATTTGAAGGTGAATAGC
CATGTGGCTTTAGACAGGACTCTGAACCACCTTGTTTTCTTATCTGTAAAAGGGGGGAAG
TCATAATAGCTACTCCTGCCTAACTCATANGTTGTTGAGAAAATGAAGTGATT
Sequence 980
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TAACCTATGGGGAGTGATGGCCACTAGATGACTGGGGACAGGGGCTGGTGAGTGAGCGCA
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AAGAAATTCCCCACAAGCTCTGCAAAATAAGTTCTGTCAATCAAATCTTACATGATGCAT
TAACTGAGCTATTTTAAAATACTACCATGGAATTCATCTTTAAAGGGTGACCTTTGTAAA
AG
Sequence 981
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GGAATAAATGTTTTCCAGTGAGGAGACTTCTCTGGTTTTCAGAACACCTCTGGCTGCCCC
TGCCCACCCCATAGAAGGGCTATCCCTCCAGGTCAGGTTAGCATCATCACCTAGAGCCAA
CAAGTCAAGGAGGTGATGGTTTGCCTTTGACATCTCTACCCAGACCAGACTCCACTGGAG
AAGACTCTCCCTTTTTTCATCACTGCCCTACCTAGTTAGGTTGGTCCTGC
Sequence 982
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CATTCAGTGCCAGCTCTCTAAAGTGTGGATTCTGGATTCTGGTAGAAGCCAGTAAAGAAA
CGTTTTTCTCTGGAGTGGAAGCCTAGTAAGATTTATTT
Sequence 983
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GAAACTTATCTTTGTATTACAGCTAGCCTTCAATCAGTAGGTGTTGAGCTGATTTTCTTT
TTCTTTTTTAAACTCAGAAGTTAAGTTCCAGCTTCAGTGGCTATGCCCAGATGGTCTGAT
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CAGTAAACTTTANCTGGCGGGA
Sequence 984
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AAAGTGCTGAAATTACAGGTGTGAGCCACCGCGCCCGGCCGAGGACACTATTTTTTTGCT
TTGGAAGAAATGAATCCTAGTTTTGGTTCAGAAACTGTCAACAGCATTGTGCCTCTTCTA
TGACTACTAAATTTCAAGCAAAGAGAGCTGAGTTGGGGGTAAAAGCAGGGCTATTCCCCG
CCTTCAGACAATGCTTGTCCCTTATCAAGGGCAGACTGCTGTCTGG
Sequence 985
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CCTCAGCCTCCCAAAGTGTTGGGATTACAGGAGTGAGCCACCGCACCCAGCCTGTGTGTG
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ATTGGGGTTGTATACATTGGGATGTATACCATTGAAATTATTTGNATCCAGAAAATTAA
Sequence 986
CCCTTAGCGTGGTCGCGGCCGAGGTACATGGAATACATAATTTTTGAAATGGAGTCAGGGC
TTTCCTAATGATCCATTTTGTAATTCACCTAACAGCTGAGGGAAGGTCCAGAGAAGGAAG

Table 1

AACTCAAGGTTAGTAGACAAACTTGATATTGAGTTGCACTGGCTGCCTTCTCTTTTTGGT
CCCCTAAAGAGTATTTATCATCTTAGATTCAGCTTAAGTTGTGGACAAATATCAAGGGGA
AAAGTATTTACAGTTAACGTTGGAATCACACGGTTTTCCGGGGTTGTGCCTCTTTACCCT
TCAACTTTGGTGGTTTCTAAAGAGGGACCGATTATTAGTTGCTTTCACTAAGGAAGGGGA
AG
Sequence 987
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGGCCTAGAAAATATTTTTTTTTTTTGAAATGG
AGTCTCACTGTGTCGCCCAGGCTGGAGTGCAGTGGCNCAAATCTTCNTCTNAAAAAAAAA
AAAAACAAAACAAAAATAAACTTTACTCAAATATCACTTTCTGTTAAATGTTCTTAATTC
CTTCAATCATCCCCCTCTTCTAACTNTNACAGCACTTTCTTCCACTACGGCACGCATTAC
ACGCCAACTACTCACCAGTTCACGTTTTCCGCCCTNTNTCCCACTTGCCCAATCACAGAN
TTCCTAAAGAACCAGGACTATGTTCTACTAGTCTTTGTAGCCACTGCACT
Sequence 988
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCCTGTTTCTACAAATTTATCTTATAATAAT
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ATCCAATAATTGAATATTATGCAAGTATATAAAAAATAAGAATCATGAATATGGAAAGAT
TTCGAAAATATATTGCTAAGATTAAAAAAAAGGAAGGGGCAGAAGAAAATAAGTTGGGTA
AAAAAAACCCCAGAAATGTTTACTAATAATTATATTTAAAAACTCATAGGATAAACAAGG
AAGGGTAATGAAATAATTAAT
Sequence 989
CCCTTAGNNTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTAGAN
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CCCGTGTTAGCCTCCCAAATTGCTAGGGTTATAGGTGTGAGCCACCCTGCCCAGCCTATG
TTTATTTCAGATGTTCAAAACAACAAACAAAAATAACACACTNGAAAAAATGATCAGAGA
ATACGTGTTAAATGAGAAATNGTTCAGGGCTTTTATAAATTTGTGACCTCCACCCTTCCC
CTTANTCCTTTTTTCTCCATAAACTCTAATTNCAAATTTTACTACCACAGCAAAAAAGAGG

Sequence 990
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AAGAAAGTTGAGTTTGGATGCCACAAGATTATTGGAGTNATAGGNAGCTGGGCACAGTGG
CTCACACCTGTAATCCTAGCACTTTGGG
Sequence 991
CCCTTAGCGTGGTCGCGGCCGCGGTACCCTAAAACTTAAAGTATAATAATAATAAAATTA
AAAAAACCAAAAACAAAGATTAACAGAAAACAAAACANCAAAAAAACTCCCAGCATATAC
ATTGAGTCATTTGCAGGTTTGGGAGGGGGGGAAATGCTTTTTTGTATTAGGAGAAAGGGA
AGCTTTCATTTTAAATGGCTATATTACTTAAAGTTTGCANTAAATATTTATTACTTTC
Sequence 992
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GGTGCTTGCCCACGCNTTGCACCCGTTCCCGAANTAAAAAGTCGCCGGTCCTANAAGGCG
NCGAGNTCTTGGTNGACCTTTGNGCANCCCCACCCGTTGCCAGTCTTGAATGNGGTTACC
CCANAGNCGCCNCAGGCTGACATGGGAAAGGATGTTCTTTGGGAAAAAAAAAAAATGGAAC
CCCGGTGGGTAGNCCCTTGNGGGGGCNTGGGNAGCCCCCCGGANGGGGTTCCCCGNCNGT
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TGGCCGGGGCNCAAAATTCANAAGNCAAGGGTTGGGGGNATCCCCGNGGGGAACCTTGGG
G
Sequence 993
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TCCCTTTTAAGNCAAAAAANGGGANGNAAGTAAGTTGGNNATTTGGNGTTTCAAAGNGNC
CAATTGNCTTTTGNCTTTTTTTCACA
Sequence 994
CCCTTAGCGTGGTCGCGGCCGAGGTACCAAGTTGTTCTCAAACTTTCATGTTTGTGTATA
CAAATCAGCTGAGGCCTTCACTAAACTACAGATTCCATGGCCTGGCCCTCAGAGATTTTG
ACTCAACAGGTCTGAGTTGGGACTAGAAATATGCATTGCTAATAGGCACCCTGACAATTC

Table 1

CGATGTAGGTGGTCCTTAGAACATATTTTGAGAAATATATTCTGTAGTCTGGCAGATAAA
GAATTCTTAACAAGGAGGTCCTGCCCGGGCGGCCGNTCGAAAGGGCGA
Sequence 995
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ATGAAAACGGATTTAAAAAGTCACATTATGATGCTCGAAGCTCTGACCTCTCATCACAAT
GAGAAGCAAAGACATGCCATAAAGATGATATTTCCCACAGGAACGATATTAGAATTATG
TGATGCAATCTCATCCAAGGTCATGGTATCAAACCAGACACAGCTAAAAATGTATCATAA
TAGCAAGGATACAGTAGCAAGGATGGGCCTCAATAAACATTTAAAGTGGAAAAATTCTTC
TCTAACTCATATCAAGTACCTGCCCGGGCGGC
Sequence 996
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GAACCCCAGTTGCGCCTTAGGCATTGTGAGTTGGCTCATTTCAAGCCAGTTGTAATATGG
TTTTTTATTCTCTAAATTTCGGGACCTGATGCTAAGGAATGTGAATATACAGTTAGGTTC
CTGCGAACCCTGTGTTGGTTCAAAAAGGCTGGTGGAGGGAAATTTATGACACTAAATGCT
TATATTAGAAAAGAGGAAAATTGGCCGAGCACGGTGGCTCATGCCTGTAATCCCAGCATT
TTGGGAGGCCGAGCCAGGTGGAT
Sequence 997
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AAACTACTCCAATTTAAGTAATGAGTTAGAGCTTTGGCAACCATTAAGGCTCTCTTTTCC
CAACTCTAACAATATGTGGTAATGTCTTCCCTGACTTCATTTTATGTTTACACAAAATCA
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NNTTATATGTCTGGATTACAAAAACATATNATATTCAAAGAATTTNTAACACTTAGAGGT
AGAAGTGAAATTACAGGTTGAAGAATTATTTAAA
Sequence 998
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TTATATTCTATTAAATAGATATGTGTGTATAAACTTATTGATATAAAAATGTGGTCATGA
TCCACTAAAGTGATTTTACAAGCCACTAATGG
Sequence 999
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AANCNAACAAANCTGNAAAAAAGTAGGGGNGGGGGTNAAATGGTTNATTTNAAATGTTTG
CCTTCANTANCATGAGAGGG
Sequence 1000
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CCATTTCTTGGACTAAATTAGGAA
Sequence 1001
CCCTTAGCGTGGTCGCGGCCGAGGTACCCAGAATATGGTATATCTCTTCATTTATTTAGC
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TCTTACATCTTTTGTAAAATTTATTCCTAATACTTTGGATTTTGACATTATCATAAAAGA
AAATTATTTCACTGACTTTTCCAGTTTGCTGCTGGCCTAAACATATANTTAATTNTTTAT
ATTTTAATCTTGTATCCTATNACTTTGCTAAATTCATATA
Sequence 1002
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACTTGGCATTAATTAGATTGTGATCATAAG
TCAAAATGTCATTGGTTATAAAGTGGTCATCAGACCATGCAGACTATTACTAATATTGGT

Table 1

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TATGTTTTAGTTTATTGCAGTGAAAATACAAAATTTAAAAGTTATTGTAGAGAATTATCA
TACCCCCCAAAAAGTGTCATTGGTCCTCCAGGACTCTGTAGTCCCCATCCAAGAAAGACT
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GTAGGACAAATGCAAAATAAAATAACACATTTAGCTATACTTTTAAGTATTTTTTATT
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Sequence 1003
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TTTCAAGCCTCATACCAGTCATATAAAACCATGATAAAACTTCATCAAAGCATACTTGGG
CAAATTTCAATTATCAAGTAAAATTGTAAAGAAAAATTTTTTACTAGTTTGGAAATAGAT
CTACATGTTTGATTTTCTTTCCTTCCTCCCTCCTTTGTTTCTTGTCTTTCTCTCCCCTTT
CCTAAAAAGTTAATGGCTATCATTATCTTCACCAAATTAGTGTTTGGTATACCCATAA
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Sequence 1004
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CCCTTAGCGTGGTCGCGGCCGAGGTACTCCTGAACTTAAAAGTTGAACAACAAAAAAAGA
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CAGAAGAAGTGTCAGAGTCAGCAGAAAGGGATTATTTCTCCATTTACCTACAACAATGGT
TTTAAATGACTGGATAGATAGAAATCTCTTTCAACTTAACTGCTTAGCACATTGCATTTT
TCTCTGTTTCAAGTTAGTTTTCCAAAGGATTACTGACTTTTTACCTAATTTGCTAAGGGA
TGTCAGGCCTTAATGACATATTTCTCCTCAAATAAAGGATACAACATGC
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Sequence 1005
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CCCTTAGCGTGGTCGCGGCCGAGGTACTTCGGTATTACAGCGCCACCCACTGGCTAGAAG
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AACACTTGACTATTCTGATTCAGNAGAACATAAAAAATGTTCTAACAAAACAGAACCAGA
CACATTTATATNTATTTCTACAAGTNAACAGAATATCTATTAGA
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Sequence 1006
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TCTGTGAAGATGGCAAATAAAATGAC
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Sequence 1007
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NTNTTNGNNNAATNCNCNNTTAGCGNGGTCGAGGGGCGNGGNNCATNTAAAANGTGATGC
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TTACACTTACATATGAATAGCTGAAATGNGCAACAGTGGACGCAANTTTTTTNGTTCTTC
AAGTTTTANTAATTACCCCAANAANACCTATTTAACNAGGCTGATNCTAACNTGGGGGAT
ATTTAATGGNTTTCTTATTAATTTGGACCNAAAAAANTCTTTTTGGAATTAANCTTGGGCN
ANTTCGCAACCAAAACCAAATTTTAAT
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Sequence 1008
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CCCTTAGCGTGGTCGCGGCCGAGGTACACTGGCTCACCTCTCAGGGCTTTGCTCCTTGGG
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TGCTCTTATAGCTGATTTTAGCTATTAGGAAAAACATCCCAAGTTGAGCTTTTCTATTCCT
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Sequence 1009
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ACCTTCACTCTATTGCAGTCATTTTCTCCCACTCTCCCCCCTCTCTCCCACTTCCTCTGA
GGATTACCTTCCCCTCTCTCANCATTCCTCTGTCAGTGGCTTTTTTTTTTCCTTTGGCATG
CAAACATGCTCAAGTCTGTCTTATA
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Sequence 1010
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CCCTTAGCGTGGTCGCNTNTCGAGGTACTCTTTTCAGATGAAAGTGTTCGGTCACCTGGA
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Table 1

CTCCGTCAAATATCAACATTTTACCAGGTTTCTCTGTTGTTGCCAAACCTGTCATTTTTA
TTTGGTGTGGCTTCTTGGGAAACTTCCATGGCCCATTTGATGGGAATCAAACAGTGAAAA
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CAGCAGCCCCAGAATGGTNAGGAGGAAAGGCACTNTAAGGTATCAGAAGGTAGAAAGGAN
AGGTTGGATNATAGNAATGGGGGAAAGGG
Sequence 1011
CCCTTNTNNTGGTCGCGGCCGAGGTACTGAGACACTGGATCCTAAGAAAATCAGAGTTAT
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TAGGATAGATAGGCGATGTGGCAGCAACAACTCCCAATTCGTAATGTCTTAAAACAAAAA
CAAGTTTTATTTCCCATTTATGCCATGTTTCCAGCACAGTTTCTCAGAGGGCTGTGCTCC
ATGCATTTACTCAAGGTCTGGGAATGATCATGGCTACACTATCTTGCAGCCACCATATTT
GGAACCTGTTGCCACTCTGATGGCAGCAGAGAACAAAAGAAA
Sequence 1012
CCCTTTCGAGCGGCCNTTTNNGGGCAGGTACGGGCTTTTTTGTTCTTGTGCAGTAACAGTG
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TCTAACAGGCCCGTGTCAGCAGCTCCGCTTCCTCCTGACAAGCTGCGAGCACAGGGGACA
GCACAATCTGAAACTCTTACNGATACCAACAGCAACAAAAATGAAAGCAGTTATGGTGGG
CAAGCATTAATCTAAAATTTTTTTTTAA
Sequence 1013
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CCACAATTTCACCATGCATAAATCACAACGGTTAACAATTTAGCATCTTTGCCTTCTTTT
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TGTTGAAATTTTTAGGTTACGTATATTTTCTCTTATAAATATGTAAATATGTTTATAAAA
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Sequence 1014
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TCAAAAGTCAAGTGACAGACTCAGTACCTCGGCCCGCGACCACGCTAAGGG
Sequence 1015
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CGTCTCTACTAAAAGTACCTCGGCCCGCGACCACGCTAAGGG
Sequence 1016
CCCTTAGCGTGGTCGCGGCCGAGGTACTATTATAATAAGTTAACATATTTCCCCTATATG
CGGAAAATGCTGACTATATCTTTTGGTTGCTTTGGAACACTATCTCCTCACAACAGTCCT
TGTCTACAGAAATGGGAAAGGGAAGGACACATTTTGGTTTCTGCAACATGGCAACATTCG
TAAAACCAGAAATGATGTGTGACAAGAAACTAAAGAACTGGACGAAATTCACTTCCATTC

Table 1

ACCCTGGTTAAAGCTTCCTTGAATCAGAGATAAGAAACAACATGAAAAATCTATTCCTTT
TAGAAAACAAGTCTTTAACCCAGAGGTTGGTTTATTTTGAAAAGGAATTAGACTCTGGGC
CCACATACCGCTCGTTCAAAATATAATGCTGTGGTTTCAACTCCTGCTAAATGTTGCTGT
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ACATCAATAATTCATTTTATTGGAAATAGGAGTAGTAGTATGAAATGCTAGCANACTGTT
TCATTTGCAGGGAGGCATTTTCTA
Sequence 1017
CCCTTAGCGTGGTCGCGGCCGAGGTACAATTCAACTATCATTCTGGTTGCGGTGGAAGAT
GGAGACTGGCTATAAGGTAGAAATATGGTTTGGGGTCTTGGATATAGTCATGGGTTGCTT
TGAAGGACTGGTGACAAAGTTTGGACTTTACCTTGCAGACAGTGGGGAGCCATTGAAGAT
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CTAGCAGGATTCAGTTTTCAAACTGGCCAGCTGTGGACTAAATCCAGCCTACAGATACAT
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Sequence 1018
CCCTTGAGCGGCCGCCCGGGCAGGTACGCGGGTCCCTTATTTTCTGGTGTTTACTTGGGA
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GACTGGAAATGAATAAATAAATAAAGAATGGAGTTTGTTGGAAGGTAATAAGTTCTGTGG
AAACAAGGAAAACCAAGGCATGGAGGTTTGGAGTGCTAAAGTGAAGGTGTGAGAACAGAT
TGCTCTTGCTCAGTTTTCTGTCTTCTTTTGTTTAGGAAATTGTCATTCTCTGTATGCTTC
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ATTATAA
Sequence 1019
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAGTTACTCCTTGCCCATAGACGTGTTTGA
CCTAGAAAAATTTCTTATACGCAACAGATATTCATAGAAATATATATTAAAATAAAGCTT
GAAGGGTGAATTAAATAAATATTTACTTGGAAGCTACAGTGGGTGAATTAAACAAATATT
TACTTGGAAGCTACTTTATAGCCACTGGGCTGGATTTCATATACAGAGTTCTTGCCCTTG
GGAGTTNTACAACTGCTTAACACTTTGTCTATGCTAGAATACA
Sequence 1020
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TGGGCTCTTTGCTTTGAGAGTCTCTGAAAATTTTCAATACCCTGGGACAAATTAAATGAG
GTAGATCCTTCTTTGAATTTGTTAATAAAGCATGCTTGTTTTGTCTCCATAAAACAGGCT
TTGACCATTAAGGTTTATATTTTAAATGGGTAAATTTTATTGTAATACACTAATTTTAAG
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AAGGCTGGTCATTTTAACCCTGATTTGACACACTCTTATTATGGTGTCTTTTCTCCTTAT
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CTAGAGTGAAAATGTTAAAAACAAAACAAAAAAGACAGCATACTGGCTACCAGTTTTTCT
TAATTAAGATGATCTGTTTTCGCAATTGCGTAAATTAGAATAAAATGTTATTTAACTCAA
GGATATTTCTTCACTGAAAGAAAACT
Sequence 1021
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TAAAAAACCCCTTCTGGATTCAAAGATGAAGGCCTCACTTACTTTATTTTTGTCATTTTC
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TCCAATGGCTAACAAGGAGCCTGACATAGAAGTAGCTGCTTGGTAAATATGTGTTCATTC
ATTCAACAAATACCCCCCAAGGGACCTCGGGCCGGGGACCACCGCTAAGGGCGAAATTCC
AGCACACTGGGCGGGCCGGTTACTAAGTGGATCTCGAGCTCGGTACCAAGCTTGGCCGTA
ATCATGGTCATAG
Sequence 1022
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TTGCAACATCTCTTAAAAGCTTGTCATCATGTTACTTCCTATTTCTTTAGAGTTCATTTG
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Table 1

TTCTAATTANCCCCAACACGGAAAAGAATGTAACACAACTGTCTTAGTTGTGCCATAGAG
TTAGAATCTATCTATTAACATGTTTTAGGTNATAACAAGAAAAATAATAAAAACAAACCT
ATTATGAGAAGCTGCCCATGCCAATAAATTTTGAAACATTACCAGGAAATATAAAAGGAA
NG
Sequence 1023
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AATGTTTTCACTCATAATTATGTGTTCTTCCCACTTCTATATTCTCTATTTGGGGAAATA
ATCCCATCAACCACCCAACGGCCCAAACCAGGAACCTGAAACTAACCATATTTCCCTCCC
ATTGCACATAAATTAACTTCTAATCCTACCTACTTATCTTTGAATCCACTCTTCTATTTG
CAGTGGCAATACTTAGGGCTTNCCTTACTTTTTACCAGGACTATTACTAGAGCTNCCTAA
ATGCTTTCTATCTGTAGGCTTACTCTTCTGCATTTCTAT
Sequence 1024
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AGGTTGTTCTCATCAACCAAGCCTGCAATGACTAGACATTCTAAAGAGAAGAGTGATGGC
AATGGAAAGAGGACACATCCGCTTGCCAGGTCACTTCTATCAGTTGATGACATGCCATAT
TGTTATGGCTAGGTCAGCTTTCCACAAGTATGCACATGCAAAATAGAACTTGGGAAAAAA
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GTCAGAGTTTAA
Sequence 1025
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TGGCGAAACCTNTTCTTTACTAAAAAT
Sequence 1026
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TGGGGAAGGGGCAGGGGGAGATGATGAAATTCATTTATCCTCTGTGATGCTATGGAAGAA
CAATTAAGATCATGTTTCCTACTTGATTTTAGTTGCTAGTCATTTCTTAATCTAAGCACC
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A
Sequence 1027
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CCCCCTGCATGCTGGGTGCCTGGCCAGCTGCCAGGGCATAAAGACAGAGACGATGTGGCC
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Sequence 1028
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GATAGNCGNCTGTNTNTCTTTAGGTGCCCAAGGCGACGGC
Sequence 1029
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TGTGATACATAGAAGTTGGGAGGAAGATGTCGGAAAGCCCTAAGAGAGCTACTTGCCAAC
CCCACCATNAGGTCTNCCTCAGTGTTCCTAGTCAGGACAGACGAGGCCGAGTCTGAAATT
ACGATAAGNCTTTGAATGCAGCATAAACAGACC
Sequence 1030

Table 1

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CCTCATAGCTATGCTATTGGCCTGGACACTCAAGGGAGTATAAGCTNGAGGCAAACATGG
ACTCATTTGTNTTTCTAACTTTCAGGGGATTATTTGNCCATCATTGCCTGATGTCCAGTG
TCT
Sequence 1031
CCCTTAGCGTGGTCGCGGCCGAGGTACCATTGTTTTGTTCAAAATCACAATTTAAATACT
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ATACATTTGGCACTGTCCATAGGTTTATGGCTTCCAACTTGTTTAAGACCATTCCCAGAG
TGAGAGCTGATTTGCCATGGTTATGAAGCTTTCAGGATATAAACTATAAGAATGACAAAC
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Sequence 1032
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TTATTTATAAAACAGGTGTTGGGCTGGACTTGACCCGTGGGCCACAGTTTGTCAACTGCC
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ATGAGGTGGTGAGACATGACCAGCAGATAAGCCCTGGGCAATGGTCCAGAGCTGGAGGGA
GTGGAGAACTAGCCATTTGTGACTTTGTGAACAATCCCTGGGGGAGTCTGGAAATTA
Sequence 1033
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GGGGAACACTTAGAGAAAAATGCATTTGGAAAGCAGAAATACGATCAAGACTTCCATTTT
TGATACATTAAGCTTGGTATGTTTAATTCATAGCTATATAGAGGTATTAAATTGGCAGGA
CAAAATCATAGCTAGAGATAAAAATTTAGAGTTCACCAGTGTAAAGATGATATTTGATGG
CACAGGATGGACTTTCTTCTGGGATTTGAGTATACATAG
Sequence 1034
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AAGATTTTCTGTTCAACAAATTGTTCATTTTCTTTGCCCGTNTTTTCTTTNTGAGTAATN
CTTTGTATATTCNGGATGTTGATCATTATGGATTATAAAA
Sequence 1035
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TTTGATAACAAAGACTTCAAGGAAGAATTTGCTCAAAAATCTCTGGGAGACAGTAATAGC
TTCTTGGGCCTGACTGATAAACTTTTTGCCTCCAGCAATGGAAATGTGGGAAAATTCCAG
ATGCTAAATGATCTGGCTTGGACCCAGCAGGTTGAGGTAGTGGAGCCTTTCGATTGAGGC
ACAGCCCAGGACTGCTGCAAGGGAGAGGCACAACAGAT
Sequence 1036
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AAGACGTGGCAGGGCCTGAGGAGGCCGCCCAGTGTCCTGGGCCACGCTGGCAAGGAGAG
C
TGTCCTGTCATCTTTGGCCACGTGCAGGGCCACGAGCGGAGCCTGCTGGTGTCCACGGAC
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CCCGCACCTGTGCCAAGAGCGACCTGNACCANCNGGCCACCAAGAGCTGGCTCAAGAAGT
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ANGGGCTCTGNCTGATCNGAGGACCACCTTCTTNTTGCGCTTGTTGCCCCCTTTGGCCGT
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Table 1

CCTTNTTCAGGAAGGCCAATNTGCCTTTCTGAAAAGNCTTTTCACCTGCAAGNTGCCAGG
ACTGGGANGGGAAAGTTNAGGGCCCCCC
Sequence 1037
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GGGTTACTCATTANCAGGACCTGGGTTTTGTTTTTAATCTCATTAACCCCTTGTTACCCA
TTTGATAACAAAGACTTCAAGGAAGAATTTGCTCAAAAATCTCTGGGAGACAGTAATAGC
TTCTTGGGCCTGACTGATAAACTTTTTGCCTCCAGCAATGGAAATGTGGGAAAATTCCAG
ATGCTAAATGATCTGGCTTGGACCCAGCAGGTTGAGGTAGTGG
Sequence 1038
CCCTTTCGAGCGGCCGNNCGGGCAGGTACTTTGACTATTTTTTAGCAACAAATTACTTTT
GACACACAGCACAATTGATTTAACACTTCCAATTTTGGAACTATTGGATAAATAATGATG
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TACAATGCAGGGATTGAATCAAATTCACACATTTTTTTTTCCTACGGAAACAACAACCTTT
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TTTTTTCTCAGAGTAGAAATCAGGTTTATAGGCTAAAGAATATAGGCTAATTT
Sequence 1039
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CATTCAGTGCCAGCTCTCTAAAGTGTGGATTCTGGATTCTGGTAGAAGCCAGTAAAGAAA
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CTTACAAGCAGTGTGGTTGTATCAGCATATGGGAGCTGACTGCCTCAGGACTTTGGAAGC
CTGCTTCTCTGTGCCTCANCCGGAACTCAGGTTACTCAGTAGTCATTTGCTAATTTCTGA
GAACGCANCACTCCTGAAGGGGATAGAAAGCATGAACAATACCC
Sequence 1040
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ATACTTTCTGGAATTGAAATGATACATTATATATACCTATAAAGATAATTGGCTATAGCT
TCCTAAACTACAAATTGTCATAAAAATGACTTCTGTCCTATATCAATTAGAAACTGGTAT
TAAAATTGAGTATTATAAGACAATAGAATGT
Sequence 1041
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GGACAGGTTGTCCCCCCTTCCTCATTAGCG
Sequence 1042
CCCTTAGCGTGGTCGCGGCCGAGGTACCCTGCTTTGATTATTTCCGAATCCAGTGGGTAG
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AAATCAGATATTTTTCTATTCCATATCTTAAACTTT
Sequence 1043
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TATACCAGAAGCAGTGGAGTTAGGACCAAATTAAGATTTGA
Sequence 1044
CCCTTAGCGTGGTCGCGGCCGAGGTACATAATGTAATTGTTACATATAATTGTTGTATAC

Table 1

CATAACTTACTATTTTTTTCTTTTTTTATTTTTTATATATAATTTTTTTTTTGGTTTGTTTGTT
TGTTTTTTAATAAACTGTTATCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANGTCCC
TGCCCGGGCGGCCGCTCNAAAGGG
Sequence 1045
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTTTCCTGGGTTGTGAATCTTGGAGGTTGCCC
TGTCAGACTGGTGAGATCCCAGTTTAGCTGTGCTAGCTAAAGCAAGGAGAACAGAGAGAG
CCATAGATACTTTTTGCTTAGTAAAATCTTTCTTTGAGGGTAGGGACTGGAGTATGGAACC
TTTTCAGAGGAATGAGAGGGGCTTGTGACGAAAGGGTAGAGGAGGGAATACCTCCCTGCA
AAATCTTACACAACTAACTAATGTCATAAGGCCGAGGATGAGAAAGTAGCACTTAACTGT
TTCATCCTCATCACACATAAAGCATTCC
Sequence 1046
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGCACTTTCAAAGTAGTGGAATATAAATCTT
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ATACATAGAAATATAGGAGCAAACACAGCAATGCAGGCGCTCTATGATCTGGTTTGCTCA
CATAGATCTTAAAAGGAGAAGAATGAGGGATTTGCCTACAAACCCACAGCCAATCTATGTG
GACACAAAGGGTGACTTCTTCCTTCTATTACGTTCCTTGAGGTAGAAATGGTAAACTAGC
ATGACCTCGAATCATAATTTAATATCATTCTA
Sequence 1047
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATTATTGGTAGTATCTCAGAATCCTGCTTAG
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TTGAACTGCCCAGTATTTGCCTTTTTCAATATTTACTTTGTAAGAACCTGACACTGTAGG
TCCTCACCACACCAAAACCTGCAACATAAACTTCAATTTTGGGCAACTCATAGACCAAAA
AAGCTAAACAAAACAAAAAGGAAAAAACCCTCTATATACAATCACCCTGCTTGTCTACAT
TTAATTTGCTTCATTCAAAATAAGCA
Sequence 1048
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GAACATAATTCAAAATAATTTATGGATCAAAAAATAAATCATATAAAGATCTGAGAACTA
CAATGTAAAAATATAGAAAAAAGTCATAACAATATTAGANAAAAATTTGAGCTGGATAAC
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Sequence 1049
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GGCGTTTGGTGGCCCTAAAGATTGTAACGGCCCCCATCCTCTTGGTTAAAATGGCAGGTG
TGTTGACAAGAACTGTCTTAGGTACCTCG
Sequence 1050
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TACCTTGGCTATTTTTTTCAATGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1051
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Sequence 1052
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ATGCTATTTATTTTAGCAGATATCTTCTTAATTAAATGTTTGACCCATGTGAAGTCATTT
AACAGATCTGTTACGCATTATTCACATATGCAAAATAATCTATATGATCTGAATACCATT
TCCATCTTTAAAATTACATATTCC
Sequence 1053

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATCAAAAAAAGACAAAAAAGAAATGGTGTT
AAAAGCCACAGTAAACATAAACCTCATATCAAGTATAAAACCACACACACTTTGCTCTTC
ATCCGGACAATGCCCAAAATTATACTGAGGTATTGGGGTGGGCTGATACCTTCAAACAGG
GAGAGAGGGACCATGTTCAGGAGGTGTATTCCTCGATTTAGGTGGTGACTGAATTTTTTT
TTTTAAGACAGGGTCTCACTCTGTCACCCAGGCTGGAATGCAGTGACGTGATCTCGGCTC
ACTGCAGCATCAACCTCCTGG
Sequence 1054
CCCTTCGAGCGGCCGCCCGGGCAGGTACAATGAAAATTACAAAATACTGTTGAGAGAAAT
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ATTAAGATCTCTTCTCTCCCACGACTCTATAGCTTTAAAGCAATCAAAATCANACTGGTT
TTGTCTGAACGTTTTTGAATAAGTCAATGGCTTATTTCAAAATTCATATGAAATTTCAAA
TGCCAAAGANTAGGCAAAATATTTCAGAAAAGAAGAAAGATTGAGGATTTGCAATAACCT
GACTTCAAAACTCACTAGAAGAACGAGGCCAGACTGCCCAGGGG
Sequence 1055
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AGTGCTTACACAGAAATGGCCCTTGATAAAATATGGGCTGAATGAATGAACATATGAATT
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ATAATGAACTCAGTGAACCTTGNCCCACCTTTTT
Sequence 1056
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AATAAAAAATTCTTAAATCTTTAGTGTGGTGTCTATTAATTTTTTATGATGATTTACAAGT
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Sequence 1057
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GACTTTTGTCTTCCTTCTGCTTATGTATTCCTCGTAAATGCTTTTTGTGACTTGTCTAAG
TATAAACAACTTTACTATTAGCTGTAAAATTTTCATTTTTAGTATGTCATCAATCTTTTT
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TTGATTTTTTTTTTAAAGTCATTTTCATTTTTT
Sequence 1058
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TGAGATCTCATTCAAAACAAAATTGCCCACAACCATTTGGAATATGTGTTTAAATTAGAC
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GAGTGAGATTCTGTCTCAAAAAATAATAATAATTAAAAAATAATAGTTGGTAGATTGAAC
ATAGAAAACACGTTTTGTAGATAAAAANTGGCCAAGTNTTAGCCACCTTTGACAATTTTT
TAAAA
Sequence 1059
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Table 1

Sequence 1060
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GAAAGATAATGTTGAAGAAAATAACAAAGCTTAAGGACTTAAACTATTACCATCAAGACA
TGTATAACTACAGTAATTTTAAAAACTGTTTTCTTGCATAAGTATAGAGAAATGTACCTC
GGCCGCGACCACGCTAAGGG

Sequence 1061
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTACGCTTTATGATCTTGAATATTTTCAGNGT
NTAAGGAATCTCTTCCTTCTTTGATCTCCACTGCATGAAGAACTCTGTTGCAGGTGTTAA
CAAGGAAGTTTTGAAATACAAAGCCAGAACCTGCCCCCCAAAGATCTGACAGTAGTANAA
GGAGATCCATTTTGAAGAAGGTATAATGGCAACC

Sequence 1062
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTAACAAATTAAAAACAAATTTTAATTTAAA
ATATTTTAGAAATTTTACTTAATACATTTATTTAATGAAGGCTGCTTTTAAGAACTTTAA
ATCCTCACGTAAACACCACCACCTGCAAAGTATTAATATCAACTTTTTCAACAAAATGCC
TGCTATGTATAAGCTACTGAAAGAAGACAAAAATTAATAAAATGTGTCCCTCCTCTTAGA
TATCTATAATCTANGAAAATGAACA

Sequence 1063
CCCTTTCNAGCGGCCGCCCGGGCAGGTACACAAATTCTAGGNAATCTAAATTATTTAAAT
GTCTAGAATTTTTTTTCTTTTATGAACCANATCACATTTCTGGACATGCTAACCATTAAA
ACGGNGAAGCTTCAGCTTGGTTGTTATTCTTCCATTAAACTGTTTCAGAAACATTCAGGC
GGCAGATAACTCATTTGGATTGTTAAGAAACACCAGGTTTTCCAGATGCTACATTAACAC
CTCATAGAAGTGGTCTTTCATATGTATGTTATGNATGATGTNAACCATAATATATATGGN
TAAAATTTTAGTAGGAGTTATCCTTTGCTTTTTATAATTTCCAGTTTTNNCGNNAACGTA
ATTCCTTTTTTCGGATTCATTTTTTAGGTAAAAATGGTTCCCCATTANTTTAAAGGATAA
AAATAAAGTCTTACTTTTGAGTCTTTTAAGNCGTNNATTTTNGCCANTNNTGTTCCCGTT
GGAACNAGAAAGGTNNTAAANCCNTAAATTTTTGGAAATTAAAACNGCCNTTTNAAAGNN
ATGGAAAGATTCTTCGACCACCNNGNTTTTANTAAAAAACCNTAAAANTNGAATCCNGAA
NNAANGGGGGGGGGGNNGTACCCGNGGGGNTTATTNAAACCTTTAGNANGNTTTTNTTTTNT
TCTGGCTTTAAAAATTANTGGNNTTTTGCNNTAAGGGCCAGGAAACCNTAGGGTTTTGGA
AAAANCNAAAANTGGCCTTNGGGGGGCTTNTTCNAAACCCGGGGCNCCAAAAAAANAAAAAA
AAAAAA

Sequence 1064
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTACTACAAGCAGCAAAAGGAAGCTCTAGAA
CAAGGAATTAAACACAGTGTTTGTTTCCAATCGCAGAAGAGGCCATGAGCACCATATGTG
TGTCAGGCTTATCATCTGAACCAAAGAAAGGCCAATCCTTCACCTTTCTTATGACTCTTA
TAGGCTGCAATATTTCACTTGGCCATAAACAACTTAATATCTCACACCTAGTAGTATTCA
GTGACACAGAAAGGGAAAGAGAAAGGATGAAGAAAAGAGGAAAGAGAAATAATTTNCCCA
AGATACAAATTTAATATTCTTTCCAAAGCATAAGAACAATTAAAAATATATTTCTCTGNT
GNAAGTGGAGGATGGA

Sequence 1065
CCCTTAGCGTGGTCGCGGCCGAGGTACATTGAAACAATATAGTAGTCTTCCCCTTTACAA
AGCTGAATTAAAGTAAAAGTGTGTGTTGGGAATAATAGGGGAATGTGGATTGTAGCTGTT
TAATAAAGATTTAGATACATATAAAATTGCTTAAGGCCAGGCGCTGTGGCTTACGCCTAT
AATCCCAGCACTTTGGGAGGCTGANGTGGGTGGATCACCTGAGATCAGGAGTTCGAGACC
ACCCTGTTCAACATGGTGAAACCCCATCTGTACCTGCCCGGCGGCCGCTCGAAAGG

Sequence 1066
CCCTTAGCGTGGTCGCGGGCGNGGTACCCACATGATCCCAAAGAGGAGGGGCCCTGTAGA
AACAAGAACCAACCACANAAAGCAGTGNCTACAGGCACCATGACAACAAAAGGAGTTTT
AAAGTGCATCTTCAAATAGCACACAATTTTCCAATTTAAATAGTTTGGAATGAATCAAAN
GGGAANAAAGCATTANTTAGATACAACTGAATTTCTCAAAAGTATATTANCACAGCCTAC
AAATAAATCCTTAAATGTA

Sequence 1067
CCCTTAGCGGCCGCCCGGGCAGGTACCCTCCGTGACTTTTCAGGGTCTCCTGGTTGAATG
AATTTGCANAAGGATTAAAATGTGTGTTCTTATTTGTGCTTTGTATTCTCCCATAANTAG
TGTGTTGGAGGCTATTAGAATAGCTGAGAGGGTAAAACATAAACACATACGTANGAGCCT

Table 1

GACATAAACACATAGGTAGGAGCCTGCCATAAGCACCGTAGGTAAGAACTAAAAGGGTGT
GTTTCCATTTCANGNGGTCCAGNCCTTCCTTNCATACTCTNAGATGACAAAAACACAAAG
TTGCTGGAGCTCACACAACTAATGACTAAANCCAGAAAGTTTGGACATGGAGAAACATTT
TT

Sequence 1068
CCCTTAGCGTGGTCGCGGCCCGAGGTACTATATTAGTGTAGCAATTTTCCAAAAGCCATT
CATCTTAGAGGGCTAAATGATTTTTACCTTATCAATTCCTCCTGTGAAAAAATATCTCTAA
AGAGGTTTTCTGCTGGAAAATATTGTTGCTGTCACATTGATATGCCAACAAAAGCTAAGC
AGGGAAGTCAGGCCAAGAAATATCTNCCTGCAAGAGAAGGCATCGCACATGTATCTCTCC
ATGCTATTTAAAATTTGCATTCTGCAACATAGAAGGGATAGGCCATGCTGCAGAAGCCAG
GTCCAGGAAAACTGCTTTCTTTGGCCNTTACACATCCTTTTTGGAGAAGATGCTGGTGAA
AGCAGCAACTACCATCTGCCTCCTGTTGACTTAAGTGCAACAGGTGGAAGGGANGAAGGA
AGGGCATCGCAAACATCATTCTATTATCTCAACCTTGCTTTTCTCGG

Sequence 1069
CCCTTAGCGTGGTCGCGGCCGAGGTACCCTGCTTTGATTATTTCCGAATCCAGTGGGTAG
AGAAGGTAAAGGCAAGGGCTCACTGGATATTTTTAAATTGTAGGGATGTCCTTTGCTCTG
GGTCAATTTTAGGATCAAATATAAAAGCACCTATAGCTCAGAGTATCTTCTAACATAAAA
CTTCTGAGATACCAGAAATTTTCCAAAACATGGTATAAACAGTATGAAACACTGGGTAGA
TAAAAGCTTTCTCTAAATCTTAAAGTGCTCAAATATCATGACCTGATTTTTTAGTTTTAG
AAATCAGATATTTTTCTATTCCATATCTTAAACTTTCATGTTAAATTCTAGTTCTGACAA
TGTAGGGTTCTATTTTTTTTCAGGTGATTGTTGGGAGCGTATAGAAGCATATATAAATATG
GAATATGTGTTTCTTTTTTCCCCTTCTGAAAGAAAGTCAAGCCTCTAATCAAATAGATTG
ATGCTTCAGAAACTTAACAGAATATTATCTGCAATTTGGCATAAATGCATTTTTCTTGGG
GAAGTTTCCATGGTCAAAATTATTAGTCATTGCAAAACAGAAAAGTTTGACACCTGGAAA
TGCAGACCCTTTTGCTT

Sequence 1070
CCCTTTGAGCGGCCGCCCGGGCAGGTACATTATATTAATGAAATTTATCTAGTCCTTGCA
AACTTGTGCCTATTGATTTTTCATTAGTGTAAACTAAAGAGAGAAACTTCACACTGACATT
TATAATTGTAAGAACTAAGAACCAACCATCAGCTTTTCTATGCCAATCCATGCCCTTCAG
GAAGTTCTTGAGGCCTTGAGGTTGCTAGTTTAGTAAATTGCTTACTGGGACATTAAAGCA
GCTACATTTTTGGAAAGANGGAGAATTAAGTTTTTGGTG

Sequence 1071
CCCTTAGCGTGGCCGCGGCCGAGGTACCAAAACTGAAAAAAGATTGTGTATCCAAACATT
ATTTCACATAAAATGTATTTTGATAAAGTAAATTCCCAAACCATGGTGCTCAGAGGTTGT
AACAGTCCATGTAAGTTGAAGAAAAAGAGTTATCAATCAATACGTGACTATCAATCATTT
ATTTAATCATTATTTAGTTTTCACATATCTAGAAATTTCAGTAGAAGAACCAGCCCTTCA
TAAANGTGGCCATTCCCTATACCTGCCATCGATTACATTATTTTACT

Sequence 1072
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTTT
CACTCTTGTTGCCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACCACAACCTCTGCC
TCCCGGGTTCAAGAGATTCTCCCGCCTCAGCCTCTTGAGTAGCTGGGATTACAGGCATGT
GCCACCATGCCTGGTTAATTTTGTATTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCC
GGCTGGTCTCGAACTCCCGACTTCAGGTGATCCTCCTGCCTTGGCCTCCAAAAGTGTCAG
GATTACAGGCGTGAGCCACCACGCCCTGCTTAAGTTTTAATAAGATCTCTTGGCAACTTT
TTACGACTGGCAACTTAGGTCTCACAAACACAGAAAAGCTTGTCTTTAAGTATATTGTCT
TTGAAAAGTTAATACACTCTCTAAATGCTCCATTTAAAATGATTTACTTTATAAATGCAT
GCACTGAGAGAAAAGATATTTGAATGATATACACCACAATGTTAAATTAACTGNGATTGT
TTCTAAGTATTGGCACTATGGNCAATTTTCTTTTTCTTGGTTATGCTTTTCTGAGTTTTC
AAAC

Sequence 1073
CCCTTAGCGTGGTCGCGGCCGAGGTACCTATTGTATCAGAAAAATGCTAATTAATTTTTT
GCACATAAAGGGCATTTTAAACTTGGTTTTATTCTTTGTGATAAATATGGATGATGAATG
GTAATGTTAAACAGAATTCAAAAGTTATCAGTTTGGCTAGCCAGACACAGTAGTATATGC
CTATAGTCCTAGCTACCCAGGAGGCTGAGGCCAGAGGGAGCCCGGAAGTTCACGTTTAGCC
TGGGCAGCATAGTGAGACACTGTCTTTTATAAAAACAACAGCAAAAATGATCAGTTTGGG
ATAGTAAGACAAATGGCTTTCTTTTGTTAGGAATTTCTCTATTTAAAGGACTTTTAGGCC

Table 1

TAGAGTGGTGGCTTACGCTTGTAATCCCAGCACTTTGGGAGGCCAATTGCAGGAGAATCA
CTTGAGGCCAGGAGTTGGGGACCAACCTGGGCAAAGTANGGGAGACCCTGTCTTTNCAAA
AAAAATTCAAAAAAATTAGCCCAGTGAGGGGGGGNGCTTGCCTGNGGGTCCTAGCCACCTGG
GAAGGCTTGGGGGTGGGAANAATTACTTGGGCCCANGAATTTGANGGTGTAGTNGAGCCT
TTGATNCCCCGTNAACCGAGTANAAGACCCTTNTTTTNTTNAAAAACTTTAAANTTNAAC
NTTTTTTA
Sequence 1074
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGGTCACTCTGCCCCAGCTCTCCAAAGGCATC
AAGATCCGACTGCTAGGAGCCCCGGCTTCTTCCCTGACCTGCCCGTCTCCTACACCCTCT
GGTCCTGCTCCACACTGGTCTAATAACTGGTGTTCCACATTCCTCTAACGTGCACAACAC
AGTCCTGCCCCCGTGCTTTTCACCTCCTGTCCATTCCTCTTATAACG
Sequence 1075
GATATCTGCAGAATTCGCCCTTCGAGCGGCCGCCCGGGCAGGTACTCTTCAAAGAGGATA
AACTTAAAGAAAATGACTAGATACACATCAAATTAAGCTGCTGAAAACCAAAAACAAAGA
AAAAATTTTTGAAAGCAGCTAGAAAAAAATTACACACCACACAGAGGGGAATAAGGTTTA
CATTACAAAGATTTTTCACCAGAAATCAGAGAAGTGAAAAGACAGCTAAATGGCATCATT
GAGGTGCTCAAGGAAGCAAGCATCTACTCGGAATTATATATCCACCTAAAATATCCTTTA
GGAATGAAAGTAAAATAAATACATTCTCAAAGAAAAACAAAGAGAATGTATCCCCAGCAG
ACTGATCTGCTAGAAAAGCTAAGGTCAACATTAGGCTGAAAGGAAATGCTGCATCTTCAG
GAATGAAGAAAGAGCAATAGAAACAATAAATATATAGGAAAACACAAAATAC
Sequence 1076
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTCACTGATTTATGGCAAGTCAGCCAATCCA
TCAGTGCTCAAAGCTCCTTGTATTGTCAGGNATGNNTNNCATTATTTGTCACTCATTCAG
AATTAAACTGCCAACTAGTAGCATTTGTTTTGTGTCTGATAGATTCTTCATGCAGAAAGA
ATAAGTAAAATGAGATGGGACACAAATCTGAGTATAGCATTGTCATTACTTTTTGCTGCA
CAGATTACTTGCAAGAAATATTCTAGTCTGGGGCATAACAAAATCCACAAATTCCAGATT
TAAAAAAGTAGGTCTATATAAAGCCTTATTTAATATTTGGTATATTTTTTAGGTACCTCA
TTGGGNGNNCCTTTATNATGCCAAGGCATTTTTTGGGGATCCTGGGTTTCTTAATTAAAA
ATAGGAAGAAAATCTTAACATTCNCGTGGTGGATTAAGAAACNCCNCCCCACCCTNTTTT
TTGGATTAANGGNGNTTATTAAGTAAAAGCTTACCGTTNAAGTAAGCTTCCCGAAAAGAA
AATNTTTA
Sequence 1077
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAGTAACCATGACTTACTAGGTGTTATGATGA
AGGTGTATGTGTGTGTATATGTGTGCATGCATGTAGATAAGTGTGTGCATTTGCACACAT
AAGAGTTTTAAGCTGCTCCTGTCATTTATTGATGGTCAAAGGTTTCTTTTGGCTATTGCT
GGACTCTTAAGATTGTCTTGTAATTGTCTTTTTGTTGTTGTTGAAAAATTAAGGGTGTATA
TTAAAGGTAGTTTTTTACCCAGATCTTATATGTGTGATAGCTCACGTCTGTAATCAGAAAC
CTACTGTTTAATGGCCACCCAATTGCCATTAGCTTCCTAGAGGGTGATTTAATAAACTAT
CTTCTTTAAAACTCATTTAAAATTAAGAGACATGTTTGCATACAATGGATTAATGACGTT
TTCACACTAACCCCAAAAGTCTGCTTGCACTTTCTTTTGTAGGCCTAACATTCATTTCAT
ATGCATTGATTATTATTGTTGAACTTGCATTAATTACATCGNGCATATATGGACATACAA
TGTCATCTGCAGAAATTAAGGATTTTTTA
Sequence 1078
GAATTGGGCCCTCTANATCNTTCTCNACCGGNCGCCANTGTGATAATTCTCCTNTAATNN
GCCGCCCGGGCNGGTACAGACTTTNGTTCCTTTGCTTTTATTTTTTTTTTTTTTTTGCATN
GATATGAATAGTTTCACTAATTCCATTCATGGTTCTGTAAACNTTCTTAAAACTTTGTTT
TATGGGATTATCAGAGTAACAAAATAATGTAGTCCCTTTATGGGACTATAAGTAACTTAA
TGCTTTTCTTTCCCTATTTCATATCCCCATATTTGGTGCAATAATTTAATTCA
Sequence 1079
CCCTTAGCGTGGTCGCGGCCCGAGGTACAGCTCACATTCATGGGGAGGAAAATCAGGGCC
TGTCTTTAGATAGGAGATGTATCAAAGAATTTGTGGACATATTTTAAAATCACAGCACTA
CTCTTGATGTACCTGCCCGGGCGGCCCGCTCGAAAGGG
Sequence 1080
TAGGGAGTCGACCACGCGTCCGCTGCCTCGCCCAATGGGCTCATAAACAAAGTGGCCATG
GTGGCAGGGATAGACTTTCTCAGCAACATGGACTTTCACTCACCAAGGCAGACCTGGCTA
CAGCCACTGCTGAGTGCCCCATTTTCCAGCAGCAGTGCCCAACACTGAGCCCTTGATATG

Table 1

GATCATTCCTTGGGTGATCACACAGCTACATGGTGGCAGATTGATTATATTGGACTTCTT
CCATCATGGAAAGGGCAGAGGTTTCTCCTCCCTGGAATGGACACTCCAGATATGAGTTTG
CCTATCCTACACGCAATGCTTCTGCTAAGACTACCATCTGTGGATTCACGGAATGC

Sequence 1081
CCCTTAGCGTGGTCGCGGCCGAGGTACACCGATGTGGCTGACATTTGGCTGGAGTCTGCT
AAGATGTTTTCTTATNCTGGATGGACGCAGACCTGTAACACCCTGTTTTTTCATCTTCTCC
ACCATATTTTTCATCAGCCGCCTCATTGTTTTTTCCTTTCTGGATTTTATATGGCACGCTG
ATCTTGCCTATGTATCACCTCGAGCCTTTCTTTTCATACATCTTCCTCAACCTACAGCTC
ATGATCTTGCANGTCCTTCACCTTTACTGGGGTTATTACATCTTGAAGATGCTCAACAAG
ATGTATATTCATGAAGAGCATTCCAGGATGTGAANGAGTGATGACCAAGGATTATGAAAA
GGAAGAGGAAGAAGGANNAAGAAAGAAG

Sequence 1082
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTNGCTGGTTA
ACAAATATTTTAATTCATTAAAATAAAACTTAAAAATTCATGCTTAGTCTACACAAGTTT
AACTTACTTTAGTCACTTAGTGAATTGTGAATTGGCTCCCATTAGTGGTCAGGANAATGT
ATTTGGTGTANAAACCAAATAAATCAAGCTATTATCGCCTTGTGAGTACCTCGGCCGCGA
CCACGCTAAGGG

Sequence 1083
CCCTTCGGCCGCCCGGGCAGGTACTGGGAAGTGCACTTGGACGAACAAAAAATAAAAAAA
AAAAAAAAAAAAAAAAAAATTAAAAAAAAAANGGAAAAAAAAAAAAAAAAAAAAAAAAAAT
NNNTTGGAAAAAANAAAAAAGGAAACANNNANNGCGGGTTTTTTAATTTTNAANCATTNN
AAATTTTTTTTAANNANNCCNTTNAANNNTNNNTGAAAATGTGANNTTTNNNNNNGAATNG
ANCNTNNNTCTTNTNTGGNTGATTTTTTATGTGTTCCAAATNGTTTTTTTTTANNGAANA
AAAATTTTTTTTTTNNGAAGNTANACNTNNATTNAAANNATTTATNCNTNNTAAAAATTNN
AANAAATTTTAAATNNTTAATGGNNTTNAAANTTTTAAAATTT

Sequence 1084
CCCTTAGCGTGGTCGCGGCCGAGGTACACATTTTTTCTGAAATGTCCCCCGTGATTAAGTT
GTGAACAAATGAACATGCCACATGTCAACAAACTGAACAAACATGGATTGTTAGTGACTT
ANAGGTGGAGGGAGGGCTAGAGAGAGGCTAGCTGTGTTGGTCTGCCAATCTCCTGTGTCC
CACACTGGCTACAAAAATACAACCACTGGGTAGGTAGGGCTCATCTAGAACCAAAATTAG
GAATAAGGATTGAGAAGAAAACTCAGCAAGGGTGATGAATGAGTTTCAGCTCATTGCTGG
AGTTAGCTGAAGAATGAATAGGACACAGTGGATGAAGGAACAANGCTATTCCNGGGACCT
TTTGAAG

Sequence 1085
CGGCCCGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCGAGG
TACCACCTAACAAATTGGAGGAAATGAAAAGACGAATCAACAACATTTTGGAGAAAAAAT
TTATTCTACTTCTAGAATTTCATTACTACAAGTGCTTAGTTCTTGGTTTGGTAGATGAAG
TGAAATCAAAATTGGATATTTGGAACATTAAATATGGGAGCAGAGAATCTGTGGAATTAT
TGCTGGAAGACTGGCATAAATTTATTGAAGAAAAGAATTCCTAGCTCGACTTGATACTT
CTTTTCAAAAATGTGGAGAAATTTATAAGAATTTGGCTGGAGAATGTCAGAATATTAATA
AACAGTATATGATGGTGAAATCTGATGTTTGTATGTATAGAAAAAATATATATAATGTGA
AGTCCACTCTACAAAAAGTGCTGGCATGTTGGGCTACTTATGTGGAAAACCTTCGCTTAC
TAAGGGCTTGCTTTGAGGAGACCAAGAAAGGAAGAAATTAAAGAGGTACCTGNCCCGGGC
GGGNCCGNTCTAAAAGGGC

Sequence 1086
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTTGAGAC
AGGGTCTCGCTCTATCACCTAAACTGGAGTGCACTGGTGCAATCTCGGCTCACTGCAACC
TTCACACCCCAGGCTCAAGTGTCAATCCTCCCGCCTGAGTAGCTGGAACCACACGTGCGC
ACCACTAAACCCAGCTGTTTAATACACCATTTTTAACCCAAAACATTAAGAAAAATATAG
GAACAGTAAGTAGATTCATTTTGTAAACAGACAAGCTTACAAGTTTTCTCAAATATGAAA
GTCATACTAAACTGGGAGACTGTTAACTTCTTGATGGGGTTAATCTCTAATATGAAGCCA
CAGTCATAGCTAACTACAAATTACATATACAATGCCAAAAATAT

Sequence 1087
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTAC
CCAGAAGGGCAGACTTCAACCCAGAAACAACTGTGAATTGTGATGGAGAGATGGGCTCTA
GTATCTGAACAACGAAATTATACTTATAGACTACTTTCTTTTCACAGAACAAATGAGCTT

Table 1

TCTTGGCTTTTAACAAAATTATCATTGAAAACTACAAAATTAAGATCACCCATAATCCCA
GCATTCAGAGGGTTAATCTTTTGTTTAAAATCCTTCCAAAAGTCTTAAATGTGTTTATAT
GCCTTTTGGAAAAAAAATTTATTTTTATAATCATTTNGGATTTACAGAAAATTGACAAAGA
TAGTACCTCGGCNCGCGACCACGCTAANGGCGAATTCC
Sequence 1088
CCCTTNCNAGCGGCCGCCCGGGCAGGTACATCCTTTTGCATGCTCAAGAGCCCATTCTTT
TCATCATTCGGAAGCAACAGCGGCAGTCCCCTGCCCAAGTTATCCCACTAGCTGATTGCT
ATATCATTGCTGGAGTGATCTATCAGGCACCAGACTTGGGATCAAGTTATAAACTCTAGA
GTGGTAAGTGTCTTCACATTCTTTAAGCACTAAAGAAAACTTTTAATTAGCTACCTTGCT
TCCAGTAATCAAACTAGAGCTCCTCTGCCTTGTGTAAGTTGCTATAAAGTATTGACTATT
AGAATGTCTTGAACTTTGGTTACTGTGAGCCAAGTCGGTGCTCAAAGTATATTTCATAGT
CTCAATTATATAGTAATTTAAGTTCTGAAAAATAGGTTCTGGCTTTGCTATGGAAATATT
TTGNGAGTATTTACTTTGGAA
Sequence 1089
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACATATCCCTATCTACTATGTAAAGACAAAAA
GGCAAATGAAATGATGTAATACAATGAACTCCTCAGAAAATAAGCTCTGTAAAATCTCAG
ACTGCCTGTTTATCATATGCTAGAGTAAACTTACATTCCTTTCTTGTTAGAGAAAAATGA
TGGTAAAATCCATGCATTAATCAAAACTAAAAACATGAAAAGGCAAGCCAACTACAAGAG
AAATACAGTTGGCCCTTGAACAACACAGATTTGAACTACATGAGTCCGTGTACCTCGGCC
GCGACCACGCTAAGGGCGAAT
Sequence 1090
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCGTGCAGAAGAAGCTACCAAACAGCAAATAT
GGAAATAGTCAGTTTTTTTTTTTTTTAAAGCCTCAGTAGAAGAGTGCAGAGTTACACTGTC
CTGTTTGGGGTGCCCCCCTCCCCCTTNCGACCTAAGTGCTGCCAAGG
Sequence 1091
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTGCAGTTTTCTAAGGGCTCTTAGTGCTTTT
AACTAGAAAGGGGTTTTTCGTTTGTTTGTTTGTTTTAAAAGGGTCCTTAGTGCCTCTTAC
TCCCTTCCTGTAAAATCCTGTGTAAAATGACAAAAGTGCACAATTGATCATTGTAAGTTC
TAGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1092
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGATCTAAAGTTGGGGTGGGAAGGAAGG
AGAAAAGGGGATTGATTTTAGTGGAAGAACAAGAATGTTCTGAAATTGATTGTGATGGCT
GTATAATCCTGTGAATATACTAAAACATTGAGTTGTGCACTTTACATGAGTGAATTGTGT
GGTATGTGAATTTATATCTCAATAAAGCTATTTTTAAAACGAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAGGTNCCTCGGCCGCGACCACNCTAAGGG
Sequence 1093
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGGTCACCTGTATCTTGATCACCAGAGAGCAC
ACCAGCCTGGACAGCAGCACCATACGCTACAGCTTCATCTGGGTTTATGCCACGGGATGG
TTCCTTGCCATTGAAGAACTCTTTAACCAGTTGCTGAATCTTTGGAATTCGAGTCGAGCC
ACCAACAAGAACAATTTCATCAACCCGCGTACATGCTAAGACTTCACCAGTCAAAGCGAA
CTACTATACTCAATTGATCCAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACA
GCGCAATCCTATTCTAGAGTCC
Sequence 1094
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATGCCAAAGACTTCGCCATAACTTTTCAAGT
TAATTACACCTGCTACTGTTTCACTTAGTGGCACTTTGCTTAACCTGTTATACACAGAAG
GGGTTGAGAAGACAAAACACTGTTAACTTCATTATACCTTTGACAAAGTAATATTATGTG
ACATGATGTGTTTTCCCCAAAATATTAGAGCTGCAGATTTAGCTGATTCAATTTATGGGA
CAATTTGTTATGTGATCTAACAATTTGGCATATAATCTAGAAAGCAGCTTTATGATCAAA
AATTGATTTTATATATATACATATAAAT
Sequence 1095
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAC
TTCAAAATAACATTTTTATTATATAAAAATGTAAAAATCCAGCAAAACCAGAAATACGGA
ATATATTTTTCTGGGCTTTCACATTTGTTGATTTTTATTCGCGATCTTTTTCAATACAAT
TTACACCCTCATCCCCATTTCCAGTCTGATTATACAAGNGCTAAGTGGCANAAAGGTCTG
GAATAAATACATCAAAAAGAAGAGGCAAAGCTGTGAAACTAAGTTGCA
Sequence 1096

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATCTGATACAAAATCTGAAAGAAAGAACAG
TCTTGTAATCTTTACATACTTGTAAAAGCATTTCTCAAATTTCAGCTTACTTTCAAAATA
AAGTTCTTACTGTCTAATATGCTCTCTTTAAATTTATTAAGTATTTTAAAAATACCCTGG
CTCTTTATCTAGTTTCAATCTAAGTATAGAAAAGCATTCTCTGTAAGGCTGTCTTAAAAA
AAAGAAAAAAAAAAAAAAAAAAAAGTACCTCGGCCGCGACCACGCTAAGGG

Sequence 1097
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATCTGCAGACATACTGAGTGTCACCGTTGAA
GAGAGTGGAGTGGCTTTTGTAAAGAAGTTCAGGTACATGTCCAGGGGCCCAGCCTCTGGG
CCCAGTAACTCAGCTACTCTTTGTGGCTTTCTTCATGGCTTTTTTTGTGGGCTGCCACGC
CCATCTTTATCACCAGAATGAGGAACTCCTGGAAGTTAACTGCACCATCAGTGTTGATAT
CCAACTCTTTGAACCAGACGTCTGCACCCTTTTTCCTGATATACTGAGGACACTCGGTCT
CTAGCAATTTCTTCAGGTCATCC

Sequence 1098
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACCATTCCATACAATGGAATATTACCCGAT
GAAAAAATAAAGTTGAACACATGCTACAACATGGATGAACTTTGCTTATAAGAACATTGA
AAAGAAAATGCCAAAAGAAAAATGAGTTTTAGCTCAAATTTTTTTAAGAGGCCTAGCCTG
CTCAAGATATCCTGTTAAAAAAAAAANAAAAAAAAAAACTCTTCCCATATCTAAGGTGAAA
ATAAAAAACATTTTTAAAAGTTNAATATAAAAGAATGAAATAATTTCAGGTCAAGTTTAT
TATACAGAAATTATATTAATGGGTGG

Sequence 1099
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGGAGGTCTCCATTCAGTAGGTGGCCC
GGGATGAAGGCCGTGTTGGGGCTAAACCACACTCTGGAATTCTGTCAGCAAATTCCTCGC
TGTGTGAACTTGAGCAAGCCATTCACCTTTCTTAAGCCATTTTCTTGATATTTCACAGAG
CCTCACCAAGTATTCAACGAGAACATGTAAGTGAAATGCTTCACAAAATGCCTGGTAAAT
AATAGATGCTTAGAAAATGGTAGAGAGAGAAAAGAGCAGTCTCTGCCCTTTAATGTACCT
CGGCCGCGACCACGCTAAG

Sequence 1100
GGGGNCCCGGGGAAAAATNATTTTGGGGGGGGGGGGNCCCCCCCCCCTTTNCCTTTNANNA
NNTTAAAGGGCCCCNNTTGGGNCCCTTTCCCGGGAANGGCCCGGGGGGCCCCCCCGGCC
C
CCCAGGTTNGGTTTGGGANTGGGGGNANTTANTTTCTTTGGCCAAGGAAAATTTTCCCGC
CCCCCTTTTTTTCCGGAAGGCCGGGGGCCCCGGCCCCCCG

Sequence 1101
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTGTTGGCTAGGAGCTGAGCTTATCACAACAA
ACAACAGCATTACAGGAATTGTCTTATATGTGGTCAGTTGTAAAGCTGATAAAAATTATT
CTGTAAATCTTGAAAACCTAAAAAAATTTACGCAAGAAAAGACATCACTTGTCTACTGTAA
CATCCAAAGGCTTTGCCCAGTATGAGCTCTTTAAGTCCTCTGCCTTGGATGATACAATCA
CAGCATCACAAACTGCGATCGCTTTGGATATTTCCTGGAGTCCTGTGGATGAGATTCTTC
AAATCCCTCCACTCTCTTCAACTGCAACTCTGAATATTAAAGTGGAATCAGGAGAGCCCA
GAGGTCCTTTGAATCATCTCTACAGAGAACTGAAATTTCTTCTTGTTTTGGCTGATGGTT
TGAGGACTGGTGTCACTGAATGGCTCGAGCCCCTGGAAGCCAAAATCTGCTGTTGAACTT
GTCAGGAATTTCTGAATGACTTAAATAAGCTGGATGGGATTTGGTGATTCT

Sequence 1102
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACGCGGGATTCCCCCAT
GTTTTCTTCTAGAAGTTTTACAGTTTTACGATCTACATTTTTGGTCTATGACCCATTTTG
AGTTAAATTTTGTGTAAGGTATGTTATACATGTGGAAGTTCATTTTTTTTGCATGTAAATA
TCCAATTGTTTCAACACCATTGGTTGAAAAGACGGTATGTTCTCCTTTGAATGCTTCTGC
GCCTCAATTAAAATCAGTTTACTCTATCTGCATAAGTCTACTTCTGGGCTGTCTACTCTC
TTTCATTGATCTGTATGTCTGTCCATTTTCCAATACCACTGTCTTTATTACTGTAGTTTC
ATAGTAAACCTTGAAATCATAATTCTATAGTAAGTCTAAAAAAAATCACACAGGTTGGAAA
TGCACAATTAGTATGCTAANATCAGAGCAATCTTGTTGGTTCANAATGGTTTATGGGAGA
AATATTAGCNCAGTGNNCTTCACATGCCTCATTGATGATAACTGGAGCTTAATGTGAA

Sequence 1103
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTGTTAGCGTCTGCGTGTGTATGGAAAGTTGA
CAAAAAATGGCATGAAAGATCATGATTGGATTTTCTTTTAAACCTGCCCTTCTGTAAAA
AATAGTTTATATATTTTTAAATTAGTAGGTATGTGTGGCTTCCTTTTTTTCCTAACATTCC

Table 1

CAGCAAATTTTTGCTGCTAAGACTATCACTGTTAAAGTGAAAATTACAGGGAAAAATGTG
ATGAATATACCGTAACTCAAAATGTGATATTTTCTTAAAATCACTCTTTTATGCTTTAGG
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ANCNAAATATTAGAAGTTATTGCTTTTAAAATGTTTAATGTGGGACTGAAATTTTCATCT
TTTNNTTNAGAAATCTATGAAGTGTATTCAAATAACGTGGGCCTAAAGGCAAAGGNGGGG
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GGCCCTTTTTTTTTTTTTTTTT
Sequence 1104
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T
ACTTGCAATGTTTTGACATTAAGAGAGAGACTATACATTCACAGAGGTTGGGAGCTTCTG
TCTAGCCTGTTGTCCAAAACTGCTTATAAAATTTAGCAACTAATTTTCACTTTTGACAAC
TATTTTAATTCTAGAAAATAGGTTTATAAAGATTTTCTTAAAGTGTTATCTATCCTTCCA
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AATTGAACAGTTTTCATGAAGAACATGTTACACCATGTAGAAACATGGGTACCTCGGCCG
NGACCACGCTAAGGG
Sequence 1105
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGNACT
TTTTTTTTTTTTTTTNTNTTTTTTTTTTATATGGCAATATTTATATTTATTTTTGCAATTCC
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AAAATGAAGGTTTTTNTATTTTCCACAAAAGTTAAA
Sequence 1106
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AGAACCATTGTTCTGAATGCTGCTTCCATTTGACAAAGTGCGTGATAATTTTTGAAAAGA
GAAGCAAACAATGGCGTCTCTTTTTATGTTCAAGCTTATAATGAAANTCTGTTTGTTGAC
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AA
Sequence 1107
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AGCCACTTGGGGAGGCCAAGGGCANGGAGAATCGCTTGGAACCTGGGAGGGCGGAGGTT
G
CAGTGAGCCAAGATGCAGCATTGCACTCCACCTGGGCAACAAGAGTGAAACTCTGTCTCA
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Sequence 1108
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CCAACATTATACAAAAAATGTGTGGCACCGTGCACATACNTGTGCATATGTGTATGCAAT
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ATTATATACAAAACCTTTTATATAAAAAA
Sequence 1109
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Table 1

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TTGCNTGAGCCTTTGATCAAAACTTTACTTTAACCCTGGGGTGGACCANAACCAANGGGG
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CCCCGGGGGGGNCCGGGGGCCCCNGGNTTTTTTTGAAA

Sequence 1110
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CCAGTTCCCAATAAGTTCCTCATCTCTGTTGGAGACCACCTCAACCTGGACTTCATTGCC
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CCCACATTTTCCTGTCTTCTTCTGCACCCTTCAAACTATTTCAACCTCTTCCTGGTACCT
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GTACCTGCCCNGGGCGGGCGNTCGAAGGGCGAATTCCAACACACTGGGCGGGCGTTACTA

Sequence 1111
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CCTCAGCCTCCCAAAGTGCTAGAATTACAGGCGTCAGCCACCACGCCCAGCCTGNAGCCT
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TATNGGCGTGGGCCCGCCCCACCCGGGCTAAATTT

Sequence 1112
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TAAGTGGGAAAGCACTTTAGGGCTGATCCCATATANGTGGTGAACACTGCACTTNTGGCC
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GGCGAATTCCAGCACACTTGCCGGCCGTTACTAGTGGATCGAGCTCGGTACCAAGCTTGG
C

Sequence 1113
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Sequence 1114
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Table 1

Sequence 1115
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ATCACTTTATATTTTCAAGAAGGTGGTGAGGGTGTGTTGGTGCCTGGGGTCTCTAGCTGA
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GGAATAGCTATGGAATGTATGCTTCTGGTTAACTAAAAATTAACCAGTAAACACTCTGTA
NTAACCATTACAGAAAATACTTCTGCTTTAAAAAAGTACCTGCCCNGGCGGGCCGCTCGA
AAAGGG
Sequence 1116
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TGTTACATCTGGACTCTGGATTGCAAGTGTAAGGAAGAAAGTGAAAATGAAAGAGAAAGT
GGAACAAATATTGGCAACAGAGCCCCCAGAGGACAGTTGTCCCTTTTCCAACAAGTTAAG
TGGAAAATGCTGTTGCCATGGGAGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1117
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CCCGGGCGGCCGTTTNAAAGGG
Sequence 1119
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Sequence 1120
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Table 1

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Sequence 1121
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ACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCGGGCTGAAAAAT
AACCCTTTAGATATCTACAGCTTTAAACTGTGTGCAGTCATGAAAAGCAGACATTAGAAG
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TGGTCTCAATATGGTNGCTGCTCTTCTTATCAAATCTATAATAAAACTATNTGACTATNA
TATAGATTTCAGGAGCTAAAAAAAGCCTTATATTTTCAAAATTAAAGAACNATTTTAATT
TTGCNAAATCAATNAGCATTACTGAAGTTTAAGGAAATTTTGGAATAAAATATATGGCAN
TTANATNCCGCCTAAAAAGAATGNAATCTTAANGATTNCTTTTTGGCTCAGGGGCNTAAA
ATTCCA
Sequence 1122
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CCAGTTGCCTGACGAGAGCTCTTCAGCAAAAGCCCTTGTCAGTTTAAAAGAAGGAAGCTT
ATCTAACACGTGGAATGAAAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1123
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTAC
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TTTAGTGAGAGTANATGCCAAAAAAAGTGGAGGGG
Sequence 1124
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Sequence 1125
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AA
Sequence 1126
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CACACTGGCGGNCG
Sequence 1127
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Table 1

TTGGCTCAGTGCATGTCACCAAAAATTCTCCAGGGATTTCATAGTCTCGGTGGTGTGGCT
GGCCCAGGACTATCCATGCAGGGAGGCCTGCACCTNTGACAGTCGGCTGCANCTGGGGGT
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GCCTGAGTTGGCTTTANTATTAATGTGCAAATACAGTTTTCTATACCAACAAACCC
Sequence 1128
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TATGTGAAGGAAAAGGCATANTTATATGGTCATCCATGCTGGGGAATATTTNGNAGNTNT
NTTTTGTTGAGAGAAATNGNNCATNTTGGATCAATAGNATTAGACAAATATCTTGNGCAT
CAAGAGACCTGGAAACATG
Sequence 1129
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CAGAAAAAAAGGCCTTAATATCATAAGGTTTTTTTATAGCCCTCAAAACTGATTTTTAAA
TGGAGGTAGGCAACTGAGAAAATAAGCATTTAAATTAGTTTTCACCCCAAAGCCCCCCAA
AATTTTGCTTACAAAATTAGGGTACCTCGGCCGCGACCACGCTAAGGG
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Sequence 1131
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Sequence 1132
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CATTGCAAAATATAATTATGCCTTCCTAACAGTCCCCAAAAGTCTTAACTCATTCCGACT
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TGG
Sequence 1133
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TGTAGTCCCACCTACTCAGGAAGCTGAGGTGAGAGGATCACTTGAGCCCAGAAGTTCAAA
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GAACTTCATTGATTCATCAATGCTGNCTGGTTTTTTAAACCCA
Sequence 1134
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Table 1

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AAATGTCATTTTAAGTATAGGAGACAGGTGAAATTGTTCAAGGTTACTACTAAACCAGGG
AATAAGGGAAGCTTAGATTCTTGGNCTTTTTTCAAAAAAGAAAAATTTTA
Sequence 1135
CATGCTCGAGCGGCCCGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTAGCGTGGTC
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Sequence 1136
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Sequence 1137
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Sequence 1138
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Sequence 1139
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GATATATTAAAATTGAAAACTTAATGCTGTTTAGAAGGCTATTAATATACTATTAATTTC
TGAAAGCTTTGAGTTTTCTGAAAAGGCTTTTAAGATCAAAATTTCTGAAACACTCCACAC
ATTCTTCCTCACCCACATTTA
Sequence 1140
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TTTTATTTTGCAGATTCATGCATTGATCACAGGCCCATTTGACACTCCTTATGAAGGGGG
TTTCTTCCTGTTCGTGTTTCGGTGTCCGCCCGACTATCCCATCCACCCACCTCGGGTCAA
ACTGATGACAACGGGCAATAACACAGTGAGGTTTAACCCCAACTTCTACCGCAATGGGAA
AGTCTGCTTGAGTATTCTAGGGTAAGAGGAGACTTTTAAGTAGCCAAGTCCGGTTGTTAA
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Table 1

ACAGAAAATGATTGAGTGACTCTTCTCAAATCTCCTTCAGGATGGTATGTGACTAGTATC
ATTCTAGATGCANAGGGGGAGAAGTTAATTTATTACAGTGGTAACCTTTAGAAGTGGTCN
CTTAAGANTGTGGGCCCTGAACCATCTGGGGAACTTGTAGCCCAGCCNGTTTCTGGGGCC
CTTATCTTAGACCTACAAAAAGAAACTTTGGGGGTTGGGG
Sequence 1141
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TCTTGCCCAGNATGGAGTGAAGTGGCACGATCTCGGCTTACTGAACCTCCACCTCCTAGG
TTCAAGCAATTCTCCTGCCTNAGNCTNCTGAGNAGTGGGGATTACAGGTGCCCGCCACCA
TGTCTGGCTAATTTTTGTGTNTATAGTANAGACGGGGNTTTACCATGTTGGCCAAGGCTG
GTCTTGAACTCCTGACCTNANATGATCCACCTGCCCTGACCTCCNACAGTGCTGGGATTA
CAGGCATAGCCACCGAGCCNGACNAGGGCNNTTTTTANCAAGGAAAACGTGTGGAATGAAT
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GNTNNGATTTNGTATGANGAATGANNNNCGGACNCAANCACCCNTAAGGGGNGAAATTNC
AGACANANTGGACGGGCNGTTACNTATNGGGATCNNNATNTTNGGTAACAAAANNTNAGG
CTGNANTACNTGGTGNAANGGTCATGTTACATTGTNTGNAAAGTTGGTAATCNCANTTCA
NNATTTNTANANANCATACTANNNNNGNGGCTTGTTTTGGNNANAGGAGGGGGGGGGGGCC
AAACCCCCCNCCCCNCCCCCCNTTTNNCCCCCCCC
Sequence 1142
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AAAAATAAACCATGTTTGCATCTTGGTCTTCTTTCCATTTGGATTCAAAAGTTNTATAGT
GATTCCTCCTAGTAAAATTGCATTTTCTCCCTAGGAGTACCTCGGCCGCGACCACGCTAA
GGG
Sequence 1143
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTACACACATATATGCATATATGGTATAATG
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GGGAAATAGCATTTAAATGGTAAATATGGTAAAGATTGTTTTATGGTTTTTGGGTTTTTT
TTTTTTAATGATCATATTTTTAATGTTACTTTAAAATAGATTAGTGGAATGTGATTCAAT
T
Sequence 1144
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTATAAGTAGNTGGTTTGTATGANATGGTTAA
AAAGGCCAAAGATAAAAGGTTTCTTTTTTTTTCCTTTTTTTTGCTATGAAGTTGCTGTTTATT
TTTTTNGGCCTGTTTGATGTATGTGTGAAACAATGTTGCCAACAATAAACAGGAATTTTA
TTTTGCTG
Sequence 1145
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AATTAAAACGAAAATAAAGTAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCGGGCGGCCGNT
CGAAAGGG
Sequence 1146
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TATTACCCAAACTGTGAAGTTGTGGTTATGGGGATGGCAAACATTCATTCTATTCGGAGG
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CTT
Sequence 1147
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AAAAAAGAAAAGTCAGCCCCTCCTGCACGAGTNGGAGCTGCAACCCTTTANAATTGATAA
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Table 1

TCCAGAACCAGNNTTNCAGACTTTNTATGATAANCTAAATGTGCCANTCCTCGGCCNNTG
ACCACNCTAAGGGG
Sequence 1148
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TCTAATTGATGGAGATGCGGATCACTCATCTATAAAAAATGACTTACAGCTTCAGCTTAA
TCAGTTGCTATAATGTGAAAACAGGAATGTGTATTTTTTTCAACTAGGTAAAAGGTGCAT
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ATTACTGGTCTTAGGTGTTTGAAACAAGGTAAAAGTATACATTCCAGTTTTGCCCAAAAG
TCACTTAAAATATCTACAAATTATTTAATCTGTGTGTGGTAACACCATTATTGCTCCAAT
TTCTGGAAAGAGTCTATTTTCAAAGTTTAAAAAAGAGGAAAAACAGCAAAGTGGCTAACC
TTTGCAGTGGAAAGAAAAAGTGTCCTTCATGGGTTACACTTTCATATTTTTATGCAGCAT
TAAGTTATCTACCGTTATGGGGGAACTTGGGGTTT
Sequence 1149
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GNTATAATTTTGCAATGGCGGTTTCNCAACTNGCCTGNCCNNACCCNNNTGTNTCATAAN
TAATCTACGTAAACAAGTTAAAATAGGTAAATGNAATGTGATNAATACTTGNGGACAACC
TGGTCATAATTTANAATCTCAAGGCTATATTAAATAATACATATTTCATTATTNGGGTAT
TTTCCAATANAAATGTATTGGAGGAAAACCTTTCCCANAAAAAAGNGTAACCTTTTTAAN
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TNAAAGAACCNTNAAATAAAGAAAGATNTAANATAAAACGTTACCAAAAATAAAGTG
Sequence 1150
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GAGGCCAACTCAGGAGGATTGCTTTAGGCGAGGAGTTGAANACCAGCCTGGGCAACAAAA
AACAAAAAAATTACCCGGGCATGGTGATGTGTGCCTGTAGTCCCAGCTACTTGACAGGCT
GANATGGGAGGATCCCTTGAGCCCTGGAGTTCAAGGTTGCAGTGAGCCATGATCTCCCCA
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ANAGAGGTGGAAGGGCTCANCAAGTGCTTTCCACATTCGCATTCCCTTAAAATCGGGAAT
GCTCTAAAGCTAGAGGACTTTTA
Sequence 1151
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GCTGGGACTACAGGCACCCACCACCACACCTGGCTAATTTTTTTGTATTTTTAGTAAAGA
CGGGGTTTCACTATGTTGGCCAGGCTGGTNTCGAACTCCTGACCTCGTGATCCACCCACC
TTGGCCTCCCAATCTTATTTGCTTTACAAGTCCTGCTTCAGGGTTACCTTCCCTGACCAC
TGCTGCCTCCCTCCCAACATTTCCAAGGGACTGTCATTGCCTTAAGTTATTTTTTCTGTT
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GCTTGGAAATCANTGCCCAAATTAAAAGCNTTGTTGNAGCCTTGAACTTTCTGGGCTTA
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GGCCTTTAAAATTAATTTNTGGGTAACAAAAAAAAAAACTTAAGCCCTANGNAAANCTTTG
GTTTAAAAAATNACAAGAGGGGACTTNNATNTTNCATTNATACAAATGGAAAANATTAANTT
TCNTCNTTANNANGANAAAGGAAAAAAAAAAAAAAN
Sequence 1152
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CCTCTAAAAATTGTTCAATANAATATATATTCATTTATTCACTTTACTTATTGTTTATTT
ATTGCCTTAGAGTATACCCAAACACNGGAGGATTCAATAATGATCAAGACAGGTCTAATT
TCTGTCCCAAANGAGCTTAAATATGNGAATTAGAAAAGGAATTTT
Sequence 1153
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AAGGAAATCAGGAAAGAACAAAGGAAATGAAGGAAGAATAAAAAAGAAGAGAAGTCATTG

Table 1

AAAAAGTATGAAAAAATATGAAACAGATAACAAGAAAGTAGAGGAGATTCCAAAAAATAC
AACCCAGGTTTTCTGCCCTCATTCTATAGAGTCTTGAGAATTGTAGGGTGTAAGAAATAA
AGAATCAAGTCTGAGAGATCCCTTTTGCTTCTTTCTTGTCTCACTGATCTGGAACCCAGG
TTGCCAGCTGGCTATTCACAGGCCCCGCGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1154
CCCTTAGCGTGGTCGCGGCCGAGGTACTGCAACTATCACTTGTCATTTGTCTAGGAAGGT
AAAATACAGGAAGTTCCCAACTTAAAAATGGGCTTGACGTAGCAGTCATTTGTAAGTCAC
TTGCTTGGAATTTAGAATGCTTCTTCCCTCTGCAGAGACAGCTTCCATATGGTGATTAGT
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TACTTCCCCTTCGAATAGACCACCTACTGTTTCTTCTGAGTGTGGTCTTTTTCTTTTCTC
CTATTCCCTCCTCAATCCTCTTTTTTTTTTTTTTTTTTTNCTGGGTTTCTTCATTATTCTC
TAATTTCTTCTTGGCTCAAAATACTTCAAGTTCTATTGNGGTAGCCTAGATTTAGGGACT
AGTTTGG
Sequence 1155
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGCAGGAACAATATTCCTGTAGCCATGGAAGA
GGGCCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAATCTCCCCGTGGCAACAGGTCCA
GGAGAGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGGAAGGGAGCATGTACTTGCG
CTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAGCAAGAG
GTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGCTCCTCTAGAGGGATATGAAG
CCCCGCGTCCTGCCCGGGCGGCCGCTCGAAGGGCGA
Sequence 1156
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TTATCCACAATANTAATACCAATAG
Sequence 1157
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AGTGAGCAGTTGGGGGTCTGCGTGACTCGCTTTCGTGCTTAATCTACTGGTGGTCGAGCT
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TAAGCTTCCAGTGTANNTGAGTGTCTGGTGAAAGGGAAGGTAAAGGTTATGATTGCATTT
TCTGAAAGAGCTAAGGTANGGAAATGGGGAACATAAAAAAAAAAAAAAAAAAANAAAGTC
Sequence 1158
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GGCGAATNCCAGCACACNGGCGGCCGGNACNAGNGGANCCGAGCTCGGNACCAAGCNNG
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CGGAANCANGGCATAGCNGNNCCTGGGGGAAAANGGNAN
Sequence 1159
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CGACCACGCTAAGGG
Sequence 1160
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Table 1

TATTAATAGCCTACTGTTGACCGGAAGCCTTACAAACAGTTAATACACATTTTGTATGTT
GNATGTATTATATAATGTACCTGCCGGGCGGCCGCTCAAAGGGCGA
Sequence 1161
CCCTTAGCGTGGTCGCGGCCGAGGTACTATAAAGCTTTTGTTCACACACACTCTGAAGAA
TCCTGTAAGCCCCTGAATTAAGCAGAAAGTCTTCATGGCTTTTCTGGCTTCGGCTGCTCA
GGGTTCATCTGAAGATTCGAATGAAAAGAAATGCATGTTTCCTGCTCTTCCCTCATTAAA
TTGCTTTTAATTCCAAAAAAAAAAAAAAAAAAAAAAAAGTACCAGTCTCACATTTGGCCCAA
ACCTCAGGATTCTCCCTCTGCCTGTCTTACTTCATGGTACCTGCCCGGGCGGCCGCTCAA
AGGG
Sequence 1162
CCCTTAGCGTGGTCGCGGCCGAGGTACCAACCCTATTTTACAGATGGGAAAACTGAGGCT
CAGAGAGGTTAAATCACTTACACAAAGCCACACAATTTTGAGTGGAGAGCTGGAATGTGA
ATCCAGGCAGTCTGACCCTGCAGCTTATGTGCTTAACGATACTGCCTCTCATGTGGGCAA
AGGATGGCCCAGGAGAAAGGCAGGCCCAGATTCCAAATCTGGCTTGACCGTCTAAGAGGC
TGAGTCTTAACCTCTCTGAGCCTTTGCTGTTTCATCTGTAAAGTGGTCCTCCTGACAGCT
GCCTCCTAGGGTTGTTTTGAGGATAAAGTGAAGTAATGGAGGGCCCTTGGGATATGGTAC
CTGCCCGGGCGGCCGCTCAAAGGGCNAATTC
Sequence 1163
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTTTCACCCTCTGAAATTACTAAGCAGGCTG
TGGGGTGGTGCTCTGAAACTAGGTAGAAGTCCTCACCCCCCAACAAACCTTTACCAGTGG
TTTTAGCATGCAGAAGATTCTGGCCTGAACCAGTTACTACTACAGAGGCTGCAAAATGAT
GATTTTTTTCATTCATTCTTTNGTAAATACCCGGTATTTTTCACAGGATGAATGTACCTGC
CCGGGCGGCCGCTCGAAAGGGCGAATTCCA
Sequence 1164
ACTTTNTTTTTTTTTTTTTTTTTTTTTTTTTCTTCTTAGCAGGGTCTCACTCTGTCACCTAGGC
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AAGACTTATATTGATTTTTTTCCCCAATTAACATTAAACGCCTCCACCTGCCCCGTGGGAA
ATTGGGTTGGCATGTCACTGAAAGGCAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1165
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Sequence 1166
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Sequence 1167
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TTGACATAAGTAGAGTTCATTTATTTTCATTTATTCTTGTATAATAAAATTACTTAAGGT
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ATCTACTTCAAAATTTCAAGCTTCCCCTTTTAAAATACTGTTTAAAAAACTTTATGAAACC

Table 1

AGTATTTCTCTCAACCCTTNGTGTAATACCTGGTTTTACTTTAAATGTGGTCAAGATAAT
TTAACCTGT
Sequence 1168
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACGCAGGGATATACAAAGGTGAAAAGAAACCT
GAAATATTTGTTGATGGCTGGAATATTTATTTTTTTGATCAAATAGATGAACTGCCTACC
TATTGGTCAGAATGTGGAAAAAATACAGAATCTGTTGGGCAGTTATGGTTGGGCCTTCTT
CGTTTCTACACAGAGGAATTTGATTTTAAAGAACATGTTATTAGCATCAGGAGAAAAAGT
CTGCTTACAACTTTTAAGAAACAGTGGACCTCAAAATACATTGTTATTGAAGATCCCTTT
GATTTGAATCATAATCTCGGAGCTGGATTATCAAGGAAAAATGACAAATTTTATAATGAA
GCTTTTATCAATGGTAGAAGAAGTATTTGGGATTTCCTGGTCAAGGGGATTTCAAANGAC
TACCCCTCAA
Sequence 1169
CCCTTAGCGTGGTCGCGGCCGAGGTACACCTGGTTTCACAGAAAACAAAGCAACTCTTAA
ACACCAGCTGGCAAAATGATAGGGCTTTTCCTTTGAATTANTCACCACAGGTGTGAAAGA
CAGAATGACTAATCCATCTGATTAAACATANACCTTTTAGAAATCAATAACCTTATTTAC
ACAGATGACAACTGCTACTGTTCCAAGGC TCCTAATCATGGTTCAGTTCTCAGGGCCTCA
AGTCTTTTTCCATTCCATCNCANAGTANTACCTGCCCGGGCGGCCGCTCGAAA
Sequence 1170
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TGCAGTGAAGCCGATATCGCACCANAAGNGCTCCAGCCTGGTCGACAGAGTGAAGACTCC
NTTCTTAAGAAAAAATAAAAATAAANGTTGTTNTCTTGAAGAAAAAAAA
Sequence 1171
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GGAATCCATTACCATGTCCTATAAATGACCTCTAGCCATTTTATGATTATTGTTCTCTGT
AAAACTCTTCAAGACTTCAATGAGAAGTTTGTTTATAAGAATTATCTTCTCATACCTTTC
CTTGTGAAGAGCGTATTCTGTTTTTTCTATCAGTTCGACATGAAGTCCACATCACATGCTG
TTCTTTTCTAGTTACATGATGTGCCT
Sequence 1172
CCCTTAGCGTGGTCGCGGCCGAGGTACCAACCCTATTTTACAGATGGGAAAACTGAGGCT
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AATCCAGGCAGTCTGACCCTGCAGCTTATGTGCTTAACGATACTGCCTCTCATGTGGGCA
AAGGATGGCCCAGGAGAAAGGCAGGCCCAGATTCCAAATCTGGCTTGACCGTCTAAGAGG
CTGAGNCTTAACCTCT
Sequence 1173
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CTGCTAAATCACCACGGCTAACGGATAAGCAGAGACGGACTACCCGCGTACCTCGGCCGC
GACCACGCTAAGGG
Sequence 1174
CCCTTAGCGTGGTCGCGGCCGAGGTACAGATTGCATAATAATTTTTAGATAAATGTCAGG
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GAGCAGCTCTGCAAAGATGTGTATAACTGCATTTGAAAANGACAGTGAAAATTTTGGGTT
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NTGCTCCAATTTTGGTTCTGNGGGGTACCTGCCCGGGCAGCCGCTCAAGGGCGAATTCCA
G
Sequence 1175
CCCTTAGCGTGGTCGCGGCCGAGGTACATGGTCACAACAGATGAGCAACTGATATCACTC

Table 1

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ACACATGCTATTAAGAACTGTCCTGTGATAAATAACAGACAAGAAATTCAGGCATCAGAA
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GTCTCAGTGCCATTGATGTTCAGAGAGGAAGTGGCTGAATTCCCACAGGAAGAGTTGCCC
GTTAAACTGTCTCAGGTGCCAGACCCTCCAGATAACATGAATCTGGCCAAGAATTTTCCA
GCACATATTTTTTGAGCCAGCTGTGTTGTTAACACCAC
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Sequence 1176
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Sequence 1177
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GGCAAATCACTTGAGGTCAGGA
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Sequence 1178
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TTAGCACTCTGAGTACCTCGGCCGCGACCACGCTAAGGG
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Sequence 1179
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ANTTTTNAAANAGGTTTTTACNCTTTTTTTGTTAACAACCCCNGGNAAAAAAAAAANAATTT
TTTTT
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Sequence 1180
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CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCCNANCTNNTTTT
TTTNCNTTTTAAAAAAAAANTTTTTNNNAAAANGGTTTTTTTAAAAAANTTTNNNNGGNNGGA
AANTTAANANNATNANNNGGNANAATTTTTTTTTTTTTTTTTTTNCCCCAAAAANTTNTTTTNGG
GGCNTTAANTTTAAAAAAAAAANTTTNNNNCCGGNTTTTGGNNNNGNNNGGNGGGGAAAAAA
AAATTTAAAAAA
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Sequence 1181
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CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAGGCTTTCATAAAAATACAGCAGGGCAAG
AGGACCAAGATGGAGGCAGTGATCAGGGAATCTCAATGAGGGTGAGACTGCGACAAAGAC
TTGAAAAAGGTGGAGAAGCAAGCCTTGTGGGTATTTAGGGTAGCAGTAGTCCAGGCAAGG
GGAACAACTAGTGCAAAGGCTCTAGGAGGCAATGTGTTTGAAGTGTTTTAAGAACAGTAA
GGAGGCTAGTATGGTTAGAACAGAATGAGCAAAGGGGGCCAAAGTGGTAGAAGGTGGGGA
TCAAAGAGGTAATGAGGCCTTTG
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Sequence 1182
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CCCTTAGCGTGGTCGCGGCCGAGGTTCTAATGAAAGCCAGATAAAGGGATGGACGATCAC
AAGGTGAAGTCCCACANTAGGCTATCTGCAAGCTGAGGAGCAAGGACCANTCATCCAACC
TCAAATAGNANAAAAANGGNNNGNAAGCCCGACAGGGCAGCCTTCAGTCTGTGGCTGAAGG
CCCTAGAGCCCCTGGCGAACCACTGGTGTAAATCCAAGAGTCCAAAAGCTGAAGAACTTG
GAGTCCAATGTTTGAGGGCAGGAAGCACCCAGCACGGGAGAAAAGATGGGCCGGAAGACT
CAGCCAGTCTAGCATTTNCACATTTCCCCCGCGTACCTTGCCCNGGCCGGG
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Sequence 1183
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CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTCTTTTTTGTGTATTACTTTTCACTTAGC
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Table 1

ATAATGTCCTCCAGCTTCATCCATAGCAGCTTCATCCATAACTTCTGGGTGTAGCCATGG
CAAGGGTAAACTGATATGGCACACTGGTGGGCATGTCTTCTGGAGAGGTGCTTCCAACTC
TTCCCTGTTTTAGCTAGTCCTCAATTTGTCTGATGTCTGAACCCCACTGCCAGAGTTGAG
TCTTGCCTGCTGAGTCATGTCCAGACTCCTACCTCAGAAGTATGAAGCATAACTGGTGTT
ACAAACACCATCTTCAGAACA
Sequence 1184
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GTCTCAGAAAGCAAGATTACTTTTGTGTTTTTTAAAAAATGATTCTTTAATGTAANTTTT
CTAAACATTCTGATTGGAAGTAGTGGATTCCTAAATGATTCCAAAGTCATCTGTAATTCT
TCTGTTTTTGTTTTGTTCTGTCTTTTCTTCATTTTGGCTTTGGGTGGGGGGAGGGGCAGG
TGACACAAAGGATTTTTTTTTTTTTTTTTTTTTTTTAATTTTTGGAATCTTTTNCCAATAACCCA
GCTAAAGATTTGCACTGAATACAACTTGTATGCCTTTTGCAT
Sequence 1185
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CCTTCTCGTATCTAGTAAGATTGGCTGGCTCAACTTTCTTCTGTCAAATTATATGGTTAT
TTTTTATATTACCACATCAGCATTATATTAAAAGTGTTTTTAATAGTTGAATGTATTTTG
CCAACTACTAGTATAGACTCAAATTTGCTATTTAATTTTTAAAATACAATTTATTTTGTA
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TGAAGATGAAATTG
Sequence 1186
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GCAAATGAAATGATGTAATACAATGAACTCCTCAGAAAATAAGCTCTGTAAAATCTCAGA
CTGCCTGTTTATCATATGCTAGAGTAAACTTACATTCCTTTCTTGTTAGAGAAAAATGAT
GGTAAAATCCATGCATTAATCAAAACTAAAAACATGAAAAGGCAAGCCAACTACAAGAGA
AATACAGTTGGCCCTTGAACAACACAGATTTTGAACTACATGGAGTCCCGTGTACCTCGG
CCGCGACCACGCTAAGGGCGAATTCCAGCACACTGNCGGCCGT
Sequence 1187
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CTCCTCTTGAGGTCCCAAGATGGCGTGGGGGTTCCTGGGCCTGTCGGAAAGTGGCATTCTT
TACTAACCACAGGTCAGGAACCCTGCACAGGAACTGTGTAGACAAGGTATGAGGCCAGTT
TTCCCAAGGAACTTTTATTGGCTCCATAAGTCAAGTTTGAGTCCTTAAAGGAAAGCACAC
CATTCCCATCAAAGTCCTGGTAAAACAACTAGTTTCTCTAATTGTGTCCTGTTGCAAAAG
AAAACAGATTCTTATTGCACTTGTGCAAA
Sequence 1188
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CACCAATCCACACCTTCACTGGAAAGTAAGTTCCATAGAGGCGGAGACTTTTGTCTATTT
TGTTCAATGAACATCCCAAGCACCTAGAACAGTTTCTGACACATAAGAAGTATTCAATTA
TGTGCTGGCTGAATGTATGAATTAATAAGTTGAGATTCGATCACTAGTTGAAGTATAAAT
ATATATTTTTGCAAGAATAAATGCTACAGTAACTGATTATGACAGCTAATTCTGTGTACC
TCGGCCGCGACCACGCTAAGGGCG
Sequence 1189
CCCTTAGCGTGGTCGCGGCCGAGGTACAATGGCATAGTTGAGTAGTCACCACAGGACCTA
GCTGAAATCCTAAAATATTTATTATCCCTTTATAGGAAAAGTTTGTTAATTCCTACAATA
GACAACGAACTATCAGAATCTATCATACACAGCAATGGTGAACACCTATTCCAGTTGGGG
TGTGTGTGTGTTTGTGTGTGTGTGTATGTGGTGGGTT
Sequence 1190
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AGACAGAATGACTAATNCCATCTNGANTAAANATAGACCTTNNNAGAAATCAATNACNCT
TATNTTACA
Sequence 1191
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GCTTGATTACCAATGTTTTGGAGTTTATAAAGCTCAATTCTAACAGAACATGATGATGTA
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TACCTGCCCGGGCGGCCGCTCGAAAGGG

Table 1

Sequence 1192
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAAACAAATCTGAAATATCTTATTAAACAAG
AAAGTAAAAATGTTATCAAAAACTACTGTCGTCTCATCAAAAAGATTCAGAAGCCAATTT
AAAGAGTCTCACACTGGACACAAAAATAATTTGAGCTTCAAAATAAACTGCAAGGGATTA
AAACACATAAATTGTGTTAAAATCCACAAGTTCATAATGATACTAAAAAAAAAAAAATCTT
GTTGGTTTCCTCTAGAGGCTACTAGAAAATCAGCTCATTATTTCTGATATTGGTTTAAAT
AGAAGAAAGAAAACCAAGCAT

Sequence 1193
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TCATNCAANAAANATAATTTTACACTTATTCTTTGAAAGANAAATTCTATGGAATTTTNT
TNTTCTAATTNAATTCCAAAATACATTCTNTNANCCNTATGCCCTNATACTAGNAACTNG
ATGGTNAGCGGGTAAGTAGGTAGTAGTANAANAACANAANGGGAAATTNGGGGAGCANAA
AAGGGANAAA

Sequence 1194
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GTGTATGTATTAAAAATAATAGGTATATAAACAAATACANTATNTACAATNNAAACACCT
AAACGCAGAGGCTGCTGTTATC

Sequence 1195
CCCTTAGCGTGGTCGCGGCCGAGGTACATAGTGTCGCGAACTCAAATCGGCATTTAGATA
GATCCAGTNGGTTTAAACGGCACGTTTTTGCTTATAAAAAAAGTG

Sequence 1196
CCCTTAGCGTGGTCGCGGCCGAGGTACTAAAGGGAAGTTGCTAGGAAATANAGCAGGTAA
TTTNTCGTTAATTATGGAAACCATNGCAACACAGTAAATATTATGTCTCTNAATTTGTCT
TTCAGTGNTTTTTTGGCATGANTGTNATGGAANAGTAAACAAAA

Sequence 1197
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CTGTATACACTTGTACCTCGGCCGCGACCACGCTAAGGG

Sequence 1198
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TTGAGACCCGCCTGATTAATNTTGCACTANGAAAAACAAAACAANAACAAACAANNAACA
AAAACAAGACACTCACATACAATGTTTTTTTAATGCTTGAAAAGTACCTGCCCGGGCGGCC
GCTCGA

Sequence 1199
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TATTAGCATCCAAAAATGTGGAAGGCCTCCCAACCACCATTTCTNGCTGTGTCCTTAGGA
TGTGCAGNAAAAAATATAGACCTAACAGNTTATGTTATAGAATGGGTTTATTTACTTTGG
GTGACTGTTTATAGTTTTTAAATAAAAGACTGAACATTTTNTCGAAAAAAAAAAAAAAGA
ANAAGAAAGTACCTGCCCGGGCGGCCCGCTCGAAAG

Sequence 1200
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GATTTTAGGCAAATAACCTAACCTCGCTGTGCCTCAGTTTCATCATCTATAAAATGGAAT
TTATAATAGAACCTACATCATGAGTTGGTGTGAAGATTAAATATATTTATATCCCGGCTG
GGTGCGGTGGCTCAACCCTGTAATCCCAGCACTCTAGAAGGCCAAGACAGACAGATCACC
TGAGGTCAGGAGTTCAAGACCAG

Sequence 1201
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ACTTATTTATAGCCTTCTCTTTTAAAAAAGGACCCATTTCTCTCTTGAATGGTGTGGTGA
AAATTAAGAAAAAAAAAAAAAGAAAAAAAGAAAAAAAAAGTACCTCGGCCGCGACCACGC
TAAGGG

Sequence 1202
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Table 1

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNATTNAANAAANNTTT
NTTAAANNTTTNTNTNCCAAAAANTTTNNTTTGGAAATNCAAAAAANAAAAAGGTTNNTT
TTNNTNCCNTTAANGANCNAAANTTTNAANAAAAANTTTT
Sequence 1203
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAGTCCATTCTCACACTGCTATGAAGAAATA
CCTGAGACTGAGTAATTTATAAGGGGAAGAGGTGTAATTGACTCACAGTTCTGCAGGGCT
GGGGAGCCCTCAGGAAACTTATAATCATGGCAGAAGGTGAAGCAAGCATGTCCTTCGCAT
GGCAATGGCAGGGAGAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1204
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTCCTACAAATGAGTAATTGAAGAATTTT
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CATTCTATATTAAGTAACATTTTATTCAGATCCATATCTAAATAGCAATTTTGTGAGATT
TACTAAGAATTTTTCCTGGTATGTATGGTTTTGGTGTATTGGAATGTACCTGCCCGGGCG
GCCGCTCAAGGGCN
Sequence 1205
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AGGGACTAACTACTTTGGAGGACATGGAAGATACCTCAAGTTTAAATGCTTATAAACCAA
GGCTCAGCAATATTCTAGTTAATACTCTAGAGGAATGCTTGCACAGTGCCCAAGAAGGTA
TTAAAAGAATGTTTATTCAGGTGTTATTTGTCATAGTGAAATACTGGAAGCACTGTAACG
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Sequence 1206
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AACCCTGTCTGAGAAAAAAAAAATTAAACTGAGATGCATTTCCCCCCTTTTACACTAAGA
AACAGACCCTTCTTTGTTTCTCACTGGCCGCCAAAGGGAATGCTGTATGAGCATTTCAGG
TGCAGATGCAGCTGCGATATCAGAAGACCCC
Sequence 1207
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GCTTACATTGTCTGTCTGATTCTTCCAGGCATTAATTAGAATTTGCAACTCCTAGCTGGG
CACAGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCTGGTAGATTACTTG
AGGTCAGGAGTTCAAGACAAGCCTGGCCAACATGGCAAAACCGCATCTCTACTAAAGGTA
CCTCGGCCGCGACCACGCTAAGGGCGA
Sequence 1208
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ATATCGCAAAGGCTATCTCCAGGCAAGTATGTTCCTTTGCTTGTCATCCCCGCGTACCTG
CCCGGGCGGCCGCTCGAAG
Sequence 1209
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GCCTCACCAAGTATTCAACGAGAACATGTAAGTGAAATGCTTCACAAAATGCCTGGTAAA
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TCGGCCGCGACCACGCTAAGGGCGAATTCCAG
Sequence 1210
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NAGTTGAAAACCGTCTGTGAGAAGCTTCTCTGGCCTGGATGGAGATCCAGCGCTTTTTTT
TTTTTTGAGGCAGAGTCTTGTTCTGTCNCCAGGCAGGAGTGCANTGGCACGATCTNTGNT
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Sequence 1211
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Table 1

AAGGGGGAAATGAAGGAACTTNCGCACAAGGGGCTGCCCAGCTTTGTGGGGCATTCCAGA
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AGAAACCAGAGCCCAGAAGGGAAAAGTGATTGTCCCAAGATCACACAGCACTGGAGAAAG
TGGATGAGGAGGGGCTGAAGAAGCTGATGGGCANCCTGGATGAGA
Sequence 1212
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ATGCTATGAAGGCCCTTTGAATTCGCTTGACAAGAATGACAGAGATCTACTAGACCCAAT
TTTTAAATAATATTGCTGGTTTTTGCTCAACATGAATTAAAATATGGTGGCTAATGTGCA
GATTTTACATTTGGAGAACTTTAATTTTCAGTATTAATTAGAATTTGTTTAATATTACAA
ATGCATTTAATGACACTTAAAATTGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1213
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GGGCTGGGGCAGGGAAAGTGAAAGAGAATCACAGAACATCCTGTAATGACAGAAAAAAGT
CACAATAAATGGTGGGATTATGTCAAAAGGACATGGGATTCAACTTGAAAGATCTTCCAA
TAGCCAAATCTGAGAAAAGTTAAGCAACAAAAAAAATAACAAAATCTTATAATCTATAGA
AAAAATATGAATGTATA
Sequence 1214
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TCACAGGANAGTTGCATTTGGGAATANAGTGAACCANTAGGGGCTGTGGAAGGCAGGCTT
TGCAGTAACAAGAGGAAGAGGCGATTCCTGGCTCCTCCAAATGTGACAGGCTTGTTTGAA
TAATTTTCCAGGCTGGAGGGAAGTGAGCCACGTTGANACCCANGGAG
Sequence 1215
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TGTTACTTACACTGCCTATTCTTTATTTCTTTTTTAGTTCAAAGGTGAAATTTTGACCTT
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Sequence 1216
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AAC
Sequence 1217
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AAAAGCTGCATGCTTGNTTTTTGTTTTTAGTTATTCTACATTGTTGCCATTATTACCAAA
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TCCAGCACATTTTTAAT
Sequence 1218
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CTTTTTTAGAACAAAACANAGGTNTTTANAANAAACCACTTGCCCACANGGGNCTTTTGAAC
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NAGATAATAAAA
Sequence 1219
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AACTCTCTCTACAAGCCAGCTATTATGGCAAGGGAAAAAAGAAAGCATCTAGATAAATAT
CTATCAAAATTAACTTTAANAGAAATACTCTCTTTCCTTAAAAGCCCTTATTTTTTAAGA
CACTANAAAATAAGTTACTATAAAAAGTGGTGGTCTGGGGGCTAAAAACAAAACAAAAAA
AATCCTCTTTTCTACATTTTTTAGTTTT
Sequence 1220
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Table 1

ATGCTGGTTGATTTCCCTCATTGTGTAAACATTGACAGGTATGTGACAAATGGGGAAAAA
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NATGTNTNTTNTTTGNGNCCCCACCNTTTNNATGTTTGACCACCNNTACNACTNTNTCCT
NTNATAACATTNCCATACATACTTAAAAC
Sequence 1221
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TGTGAGCTGTACCTGCCCGGGCGGCCGCTAAGGG
Sequence 1222
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TTTTTTTTTTTTTTTTTTTTTNAACAAACCCTGTTNTTGGGNGGGTGNGGGTATAATACTA
AGTTGANATGATATCATTTACGGGGGGAAGGCNCTTTGNGAANNANGCCTTATTTNTNTTG
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AAAAATAAGGNTACCTTAACTTCCTTTTTTCCT
Sequence 1223
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AATTTAAACCTATTTAAGGGAGAGAGAGCTCTTGTAAAAATTCATTTATTAGTTCTGGAC
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GATAGAACATTTTTCTTTTT
Sequence 1224
GCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACTTCTCAAGACCTCACTTTTATC
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GNGCCTTGAAGTNATATTTGTGGATAGCTAAAAGCAATTTTTGGTTTATTTGGTTTATTC
TTTGGTTTA
Sequence 1225
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ACATATGTTGCATGGGTTTCTATAACATTTGAAATGACTGCCAAATATTTCACTGTATGA
TCATCATTTAATATTATTATCAATTTTGTATATTTAAGTTAGAACTTTTCCATTACCATA
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CTTAAAGTAATAA
Sequence 1226
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TAAACGCAGAGGCTGCGTGATATCCACAATAGTAATACCAATAGTATTAATGATGTNTAT
GTAAACACAAACAAAAGCAGCGGACCGTATTAATAGGCAAACACACAAAAGCACACAAAA
GCAAAGCAAAAAGCCCGCCAGTAATGTT
Sequence 1227
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TGTGTTGNTAATNGGAATGTCTATTTCTTTAAAGAGCAGAGAACTACAGTTACAGGGGTT
ACAGTGTGAGGGGTGACACATTGCTGGATTCTGAGCTCAGGCAAGTCTGTCTGTGTCTTT
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TCTNGATATACTGGGATTACAATA
Sequence 1228
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CTTGGCCTCCCAAAGTGCTGGGATTACAAGCATGAGTCACCATGCCCAGCCAATAATGAT
TTCTTGATTGAAGGAATGAATGAATTAAAAGGTTCATCTTTGGACACAAAGGCANACAAA
AGTTTGACAAAAGGCATTTTTGAAACTAGGACCTTTATTNTAATATTAGTCTAAACAGNG
GGA
Sequence 1229
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Table 1

GGATGCAGGGCTACATTTGCCACTGAAGAAACATTGTTCTCTTGCATCTGAATTCCAGTG
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ACACTGATGCATACACTATAGTGAAACACTGGCTTTAAGAAAACTGATTAACAGAAAACC
GGCAATTGTTATTTATTTTAAA
Sequence 1230
CCCTTTGAGCGGCCCCCCGGGCAGGTACAGGTTCTAAAACGAAAGTATTTGGGTAGTCCA
CTTAGTGATATTAGTGGATNGTGTAGACAATAATATTAGTCCTAGA
Sequence 1231
CCCTTTGAGCCGGCCCGCCCGGGCAGGTACTCCATAATATAATCTTTTAAATGGGCAACT
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CACTGAATTCAGTAACCTGGGTCATGGTCCAATTTTGCTCACTACTTCATATCTTTTATG
TAGAATAATTCCTATNAACATGTTCCCTAAATTCCCATCAGTTTGTAAAGGCAATGGATT
AAATTATTCAAATGTAGCTATTTAACCGTCAGTNACAATGCCTAGAAACCTATTTATTCA
TCTGTAATATTAAGAAGGCTGAATTTGATTGGATCTTGAAAAATCC
Sequence 1232
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CGGGCCCCGGCCCAGGTTGGTGGATTGGGGAATTATTCCTTGCCCAGGAAATTTCCGCCC
CCTTTTAGCCCGTTGGGGTTCCGCCGGGGCCCCGAAAGGTTACCATTTTTNAAAAAAAGG
GGGGGGATGGCCTTAAATAACCTTTTTTNAAAAAAAANAGGGTTTTTAAAAGAAAAATTTA
AAAATTTTTTAAAAAAAAA
Sequence 1233
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CTGAATTCAGTAACCTGGGTCATGGTCCAATTTTGCTCACTACTTCATATNTTTTATGTN
GGATTATTCCTATAAACATGTTCCCTAAATTCCCATCANTTTGNAAAGNCAATGGATTAA
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Sequence 1234
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NCCTNTTATAATTNGTTTNCTNNANTCCAATTGAAACCCCTTTTGGGGTTATTGNNTCCN
CNCACACTTTTTTNATTGTTTAAANNCCANTAAAAAACCANTNTTCNTCGGNTATATAAA
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Sequence 1235
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ATATAATAGAATTGGTTTCTATAAACCATTTATAGTATTCAACTTTTATAGTATTACTTT
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AT
Sequence 1236
CCCTTAGCGTGGTCCGCGGCCGAGGTACTCGGATCTNTTATNNNGTNNAATAANNCCTCT
TTCGTCTACAAGCCACACTTATNCAAAATTNTGTGGACAACTCACACTNGCTATNATACC
TGCTTANATTCTCCTANTTAGTCCCTGAGGGTTTATACCTTTTATTCTTTCATTGAAATT
TTAACAGAGGTTTCTGTCGGAAGCAGAGTTAAATGCCTATGTTNACTCCATCATGGTTAT
CTGAAAGTCTGAGGNGCAATTTCAAAAACTCA
Sequence 1237
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCTGACTAAACTGGAATTATGAGTGAGGAAGA
GNGNATTACTANATAAATGACTGGGGCAANGCAAAATTGAGGAGGAAATTANAAACTGTT
TGACAANACTTTTAAAGAGCCTACTTTGAAATNACAGAAGTCTTGATNAATNTTGCAAAT
AATGGCTAGAAAGTATGGTTTAACTGGACCCTATTATGCCTTTT
Sequence 1238

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAAGCTAGAAGCAGCCTGGTCCAGATGGCTA
TACAAACCCGAAACTGTNTACACCCAGACTTTATTCTTCTACAACCAAATTCCTCAAACA
CACAATCTGAACAGTAGCAGTGAAAGGGAGTTTAAGGTGGGGGTGAGGGAGAAGGGAGTA
ATATGGTTTTTTAGTAATATAGTAATTTACA
Sequence 1239
CCCTTTGGCCGCCCGGGCAGGTACGCGGGGCGGTATGTNGGGCCAGAGCATCCGGAGGT
A
ANANAACCTNTTTTNTNCTTAGGAGCCACTATGAGGAGGGCCCTGGGAAGAATTTGCCAT
TTTCAGTGGAAAACAAGTTGGTCCGTTACTAGCTAAGATGTGTTTTGTACCTCGGCCCGC
GACCACNCTAAGGGCNAATTTCCAGCACACTGGCGGCN
Sequence 1240
CCCTTAGCGTGGTCGCGGCCGAGGTACGCGGGGCTACCAAACCTGCATTAAAAATTTCGGT
TGGGGCGACCTCGGAGCAGAACCCAACCTCCGAGCAGTACCATGCTATATTGGTCACTGT
AGCTCTGTAACATAGTTTGAAGTTGGGTAATGTGATTCCTCTAGCTTTGTTAGCTCTGTT
GTTTTCACTTAAGTATTACTTTAACTATTAGGGCTCTTTTTTGGTTCCATATAAATTGTA
AAATAAATTTTTTCCAGTTCTGTGAAGAATN ı CATCGGTAGTTTGATAGGAATAACATTGA
ATCTGTACCTGCCCGGGCGGCCGCTCGAAGGGCGAATTCCAAGCAC
Sequence 1241
CCCTTTGAGCGGCCGCCCGGGCAGGTGGATCACTTGAGGAGTTACAGACCAGGACTGGTC
AACATGGCGAAGCCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCCGTGGNTGGGCG
TGTGCCCCGGTAATTAANTNCCCNANCTTACCTTTGNGGAAAAACTTGAAGGGCCAGGGA
AGAAAATTNCNGTNTTTGGNAAACCCCCNCCNTAAGGGTTGGGGAAGGGATTTGGCCAAG
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CCCTTGGGGGGNCCCAAAANNNAAGNTTGGANGTAACCTTTCCCCAATTCTTTTNAATNAT
ATTACANNTATNTAGATANACNNTATAANAGNGANNNGANANTGGGNTNACCCCCTTNNG
GAGGCNCCGGNCNGNAACCCCCANCCNNNCCTTTAANAGGGGGGGGCCG
Sequence 1242
CCCTTTGAGCGGCCGCCCGGGCAGGTGGATCACTTGAGGAGTTACAGACCAGACTGGTCA
ACATGGCGAAGCCCCATCTNTACTAAAAATCAAAAATTAGCTGGGCGTGGTGGCGTGTGC
CCGTAGTAGTCCCAGCTACTTGGGAAGACTGAGGCAGGAGAATCGCTTGAACCCGCGAGG
TGGAGGTTGCAGTGAGTCAAAGATTGCACCAGTGCACTCCAGCCTGGGCAAGAATGAGAC
TCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGTCCTNGGGCCGCGACCACNCTAAGGGCG
AATTCCAACACACTGGCGGNCCGTTACTAATGGATCCCAGCTCGG
Sequence 1243
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ATCTTTTTGCCACANTGGGATTNTCCCAGGCCTTTTTTCCCAACANCCCATTGTTATTTT
GGAAAAGGAAGNAACTTACTCNTTNTTTCCCCCGCTTTTTTGGTCGGGAANTATCCTTTT
GGGGNCAAAACCTCTTATGNTTTGGGNAAAAGAGNGCCCCTTTTCACCTTTTTTGNCCTT
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GAAACCTGGTTTTGGCNTTCCAACCCTTNGNCATTTGNCCATTGGAATACCCCCTCAAGN
AAAGNAAAAGGNCCTTNGNTTTTGTNNGGCCNTTNGTTGGCCCCAANG
Sequence 1244
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ATCAGTATATTCTGGGAAAACATANTANAGAATGAATNNATAAATTNCATTGAATTNGGA
ATATGTTGTCCATTCTCCCTGTAACTAATGCTATCAAGATANAGTAGAAATACCACATTT
CAAAANCAGCTGGAGTANACAGGTCTTCATAGGCTAGCTTGGAAACCTAATAGCTATTAA
TAATGAAATTTTAATTATACTCTGGATTCTAAACAATGAACACACANTGATCTTTTTGAC
TT
Sequence 1245
CCCTTAGCGTGGTCGCGGCCGAGGTACAGATGTGTCCTTTCTTATAGTCNGTCAATGCTG
GGAAGTAACAGGCAGATGTGACTTCACTTGANCATTTGGANGAANCAAAAAAGGTTGCGC
TTGNTCGNNCCTTAGGGTTTAGATGGGCAAGGACCTTGCTTTTTGCNTCCCCAATTTCTT

Table 1

AGGGTAGNTGTTNTTCTTTGNGTTGCANGGGGATNNGTANACCGGTACATCCTTCTTGNNG
GAACCAAGGGGGNNNACNTTATGAANTGNAAAAGGGGANGTTCCTTTGTAGTAAAANGGCCT
TGGATTGGTTTTCAAANNGGNAAGNTGGGGTTCCACCA
Sequence 1246
CCCTTAGCGTGGTCGCGGCCGAGGATACTTTTTTTTTTTTTTTTTTTTTTGNCTAATTACTA
CCTTNTATTCTAATTGTGAACCATGGCCCTGAAAGCTTGATAANCAAGACTTGGCTGAAN
CCAGAAGGGGNAACTAAGTGNGGTTCGGCCAAGNAAAAGGGATTANTTGGGGATGNGAAA
ANTCAANTGGNCTTNTTCCCTT
Sequence 1247
CCCTTGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTANATGA
AAAANCTGTAATTCTTTATTTGAAACAANTGCNTTCAAAAGAANTNAAAACACTTCAAGG
ACTTCTAGTAAACATAAAAGGTCNAACAAACTGTGGCAAAAANTTTTGCAATTNGTANAT
AAGCTAANATAGGGGTTAACNAGTACCCCAGGCCANAATTAAGGNGGNATNNCNTCAANT
ACTTCCANTCANNNAAAAAGGG
Sequence 1248
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CAATAGGCCCTTNGGNTAGTTAACCAGCCCATTTCTTCATTCCAAAACCCCNCCCTGNAA
AGCATTNNAACTCGGGNNGCCANNTTCAATNTCTTACAATNAAATCCGCCNCCCAACCGG
GGCCTTTTAACAATTNCCCTNCCAATATTACCTTAATTTNCTTGGGCCCTTAGGCCAAAT
AANCNTGCAAAAACCTTAACGGNAAACCGGGCAACCTTCCANCCCAAGGNTGCGGCCAAT
TTCNATTAAAATTNCCCTNCNTTCCTACCAANAGGGGGA
Sequence 1249
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AAACAAGATANNGAGATTAATATTGNAGTGGNNGTAATTTAATTAAAGTTATATTTTGGG
TTAATTTTTAACAACTGAAGTCTTATTGTTGAAACTTATTTTTCA
Sequence 1250
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TGGTCNGCGGCCGANGTACTTAGGTGCCTACAACATAAACAGCA
Sequence 1251
CCTGTAGATGCATGCTCGAGCGGCCNGCCAGTGTGATGGATATCTGCAAGAATTCGCCCT
TCGAGCGGCCGCCCGGGCAGGTACGCGGGCAACAGTTAAATCAACAAAACTGCTCGCCAG
AACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGGTGCTTCATATCCCTCTAG
AGGAGCCTGTTCTGTAATCAATAAACCCCGATCAACCTCACCACCTCTTGCTCAGCCTAT
ATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCTNGGCC
GCGACCACGCTAAGGG
Sequence 1252
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TTTTTTAAGAGATAGGGTATCACTATGTTGCCCAGGCTGATCTTGAACTCTTGGCCTCAG
ATGATCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCTCTTATTTGCTTTACAA
GTCCTGCTTCAGGGTTACCTTCCCTGACCACTGCTGCCTCCCTCCCAGCATTTGCCAGGG
ACTGTCATTGCCTTAGTTTATTTTTTCTGTTTTGTTTTTTTTTTGTCGTTTTTGTTTTTT
TTTGAGACAGCGTTCTTAGTCTGTCGCCAAGGCTGNGAGTTGCAGTTGGCCGCAATC
Sequence 1253
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TANTAGAGATGGGGTTTTACCATGTTGGCCAGGCTGGTCTTGAACTCNTGACCTCAGGTG
ATCCACACGCTTCANCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCAGC
CTAAATATTTNTTTATAGCAATGCAAGGATGGCCTAACACACTGCCTAAATCAAAATTGC
TATTCACTTCAAGGGTATTTCATTTACCTGACTAGCTTTTTTGGGTGCATNTGGAACATA
ATGTA
Sequence 1254
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GAGTATGGACAGGGAGGCAGGGCAGATACAGTCCTTGCTTCTGGTTTTAAGAGTTCTTCT
GAACCACAATCAACTTCTCCAAACACCCACCTTTGTCTTCTACCACAATAGGGGTCAGAT
CTATTGCTGACTTTTCCTCCACCTTCTCTACATCAGCAGCACCTAGGGGAAGAAATGTTA

Table 1

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TTGAGACTATACCTAAAGGAAGAACATTCTCCTCTGTTGCACACTATTATCCAATTGGAT
AGACCCACATCTAAATGTCTGCAATTACAGTAATGTCAGCTGGGCATTGGTGGCTCATGC
CTGTAATCCCANC
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Sequence 1255
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GAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTC
TTTTTTTTTTTTTTTTTTTTTTANAATAACAAAAAATTTTTTACTNAAACATAAANATTTN
CAGANGTTTCCNNACAANCCNTNCAAAATGGTCACAANCTTTTTTNA
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Sequence 1256
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AGGAAGTGGAAATAAAAAAATCTCAAAGCTATTTGAGTTCTCGTCTGTCCCTANCANTCT
TTCTTCANCTCACTTGGCTCTCTANATCCACTGTGGTTGGCAGTNTGACCAGAATCATGG
AATTTGCTANAACTGNGGAAGCTTNTACTCCTGCAAGTAAGCANANATCGCACTGCCTCA
ATAACTTGGTTATTTGAGCCNCGTNTTTTTGCAAAAACTACTTTTTCCTANTTTTTCAAN
AATTTACTTTCAATNGTTTTTAAAAAAA
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Sequence 1257
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TTAACTGATACAGACTTTTATTCTAAATGCTCACAAGCACAGAAACCAACAAGAAATCAG
ATCTTGAACGAATTTATAATGATTCTTCCAGGAAGCACCGNGGCAGCCACATAAGCCGCT
NTTCACACCTGGCTGCNTTCTGCCAAGTTTAGTCCTCAAAGAGAAAAACAAGGGAGGNAA
AAGACCNAAAAAAAAAAAAACAAAA
```
Sequence 1258
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GAATTATAACTTTTAGATGTCACAGAAAATTAGAGTATTTATTGTCAAA
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Sequence 1259
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ATACCTCTTCCTTCAAGTAAGTTTGCCATGCCTACCATATCTGTGAGTGGTATTCTGGAA
TGGCCAAATGGCCCTGGTAGGACTATGGGTCCTGAAGTCGTGCTGCCTGGCTCTGGCCAC
ATCCCTGTGGTGCTTTTCCATCCTGATCTACAGATATTCAGAACTGCAGGGAGTTCCTTT
TAGTCCTGGCAATCTGAACCTGATTTTTTGC
```
Sequence 1260
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CAAGATTGCCGTAAAAAACTGTGATGGTGTGCCTGCCCTTGTGCGATTGCTTCGAAAGGC
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AAGTCAGTGTTACTCTCTAGTGATGTTGAGAACTAGAGGGATTTCCAGACCTTTTACTTT
TTGATGAAAGGTTGTGAACTGGTGGCTGTGGGTCAAAATCCATCTCACAGNATTTGTTTT
TGGATC
```
Sequence 1261
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TGATCAACTCTGCTNTTAAAGGACTCTGATGCATTCTTCAGTATGTGAACTGCTTTTTTC
AGCTCCANAATTTCTGCTTCATTCTTTTAAATTCAATCTCTGTTAAATGTATNTGGTAAA
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AATTCTGTCTTGAAAGGTCACAATCNCTGTTTTCTTAAGGGATTGGGGCCCTGGGTAACT
TTATTTTAAAA
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Sequence 1262
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GCTGTAACTAGGAATGGGTCAGTGAAGTTCAAACGACTTTTCCTTGAGGGAGTATTTTAA
TCGGACAAGGGAACTCTTTTTTCTTTTGGGCAATGGCCAACAGGACTGAGAAGCCAGAGAG
CTTGCACCTGAGCCATCTCAGCCGTGAGAGTAACAGTCCTAGGAAAATAGATGGGGGCTG
GGGGTAAGGAAAT
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Table 1

Sequence 1263
CCCTTAGCGTGGTCGCGGCCGAGGTACTCTTTTTTTTTTTTTTTTTTTTTTTTAGGGGTT
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CTGACCTATATTTAATTTTTTTAAAGATTAGACTGGTGTTAGCTGTAAATAGTTTGAAATA
CCTCTCTGATAGGTGCTAGCTTATCGTTACTCTTAGTGCTTCTTGCATTTGCAT
Sequence 1264
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTGTGTTTAAGAGAAATTCCTAAACTGGAT
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GCTCATGCCTGTAATCCCAGCGCTTTGGGAGGCCCAGGCGGGAGGGTTGCTTGAGGCCAG
AAGTTTGAGACCAACTTGGGCAACATAGCAAGACCTCGTCTCTACAAAAGATCNNNAANT
NAATANTAATNTAAATTAAAGTTCCTTTGGGCCGNNACCACNCTAAAGGGCGNAANTTTC
CAGCCACCACTGGCCGGC
Sequence 1265
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTTATTGTTAAAGTGAGTCAGATAAATCTTC
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TGTTTCTAGACATCCTTGAATTACACCAAAGAACATGAAATTTAGTTGTGGTTAAATTAT
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GCCTCTAAAAAAATTTTTCACTGGGGGCCCACGTGGGGTCATTAGAAGCCAGAAGCTCTN
CTCCAGGGCTCCTTCCCAAGTGCCTANAAGGGGTGCTTNTAGGGAAACATTAGGATTCCCA
GCCCAGGGGGCT
Sequence 1266
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ACATGCAGAAGTAATGAGGTTTGACAGAGACATGAGACTATAAGATGTCTGTCATTGCTG
CCAACCATGGAAAAGATGTTAAGATGTCCAGCTGCCCATAAAATCATATTTTCAAAGTGT
GAGACACGAAGAATATCTTTCTCTTATTTGGAAATATGCTGAAGGATAGGAATAAAGAAA
AGGATTNCAGTAAAATGGGAGNC
Sequence 1267
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TTTTCTACAAAGGTTTACTTTGGTTGTAAAAGATGTAGTTAANAGGGGTANGAANAATTT
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GGGCCATTTTTTTNTTTTT
Sequence 1268
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GTCAGAATCCAAAGAGATGTGAGAATGAAAAGCACAAGTGAGAGCAGTGGGATAGCCAAA
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CTCTCGATCTCCGGGCTGTAGAAATAATACATCTGTGCTATTTTAAG
Sequence 1269
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTAAAAGGTGATGCTAATACTTTAAAATGTT
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TGGCATTTTGGAACAAGGNACATTAATTGGTT
Sequence 1270
CCCTTAGCGTGGTCGCGGCCGAGGTACTGCAAGCAACAGTTACTGCGACGTGAGCAGCAA
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CATACCAAAGCCGTCGCCTTGGNCACCG
Sequence 1271
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AGGTTTTTAAGACGTCCTTTGTTCTGGGATGAATCATAGGGAATGACTGCCTTTGGAGCT
CAGGATATTAAACTGAGTGGTGTCAAATATTNCCAGGATCAATTCGACAATGCCATGTGT

Table 1

ACCTGCCCGGGCGGTCGNTCNAAAAGGGCNGAATTTCCANCACACTGNCGAGNCGTTACC
TANTTGGATTCCCGAGTCTTCTGNTTCCAAAANTCTTTTGGCGGTTA
Sequence 1272
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TACACTATACACTTCAACCTTGAAATGTGGACCCAAAAAACATTCTATTTTTCAGTAATC
NATTGAATTTNGGTGAGGGGTCCNACACCCTCAAATCCTAANTTTATCACANAAAAAGCC
CNTNCTTGGCTGCCAAGCGCTGGCNGATGAACTTTGTNTTGCTGNANCTCTTNATGANTT
GGATNCCANAGTNTCNTGATGATCCTNTTCAATGTTTANGAGCATNTGACCNGNCATGNT
GTAGNGGANTGACTTTC
Sequence 1273
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTTT
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GNAAAAAAAAAAAAAAANNGNAAAANNAAAAANTNNNGNATTGNTTTTTTTGGCAANTNANC
AANATCNTCCCCCTGAAAAAAAAAAAAGTTTTTTTTTTT
Sequence 1274
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AGCAGAATCTGTTCCATCCCTCTCTTCTTGTCTTCATCTGTTCTATGTCTGTCTTTGTTC
AAATTTCCCCTTTATATAAGGATAGCAATCATATTGGATTAGGCCCAGTCCTAATGACCA
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TGTAGACTTTAACATCTTTTTGGGGGAAGACACAGTTCAATCCGTAACAAGATGTTAAGT
CCTTTCCTCTCCTAAA
Sequence 1275
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Sequence 1276
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTATAAAAGGTTGAGTAAAAACAGGAAAGCGT
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TTATACTTTTTTTTATTTGTAATTTGGTCTATCTAAAATGTTCGTTAGCTTAACTTAATGG
GCGTTATTGGATTCATATGACTAACGTTTCCTCAGTATTGTAATGCTTGAAATATTTGAA
AGAAAAAATGTTGTTTTTTAGTTGAAACTGGTATATATAATTTCAGTGCTTGGCAGGTTA
GTATATTTTTATGCATTTTT
Sequence 1277
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GGCTAGGACAGGTGGNGGNGGTGGCCGGGTTTNAGGNTCTNCAAGGGACCCTNTGCAGAT
GCCGGGGCCCTGTTTATTCTGAGCAC
Sequence 1278
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CTTAGTTTTCCAAAACAAAAATGTTTAGGGCAAGAGTAACATTATTTTACATTATTGCAT
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AGGGGGACTATTGTAACAGGGCTGTGCACATAATTGTGGATGATTTTCTTTGATACAACA
ACAAAACTTGGTGGAT
Sequence 1279
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TCATTAATAATTTGATAATTAAATGGTCCTGAATGGTTAGCCATGTTCTCCGCATTTAAA
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CATGTGAATATTGCTCTGAAAAACCAAAATTAAAGCTTTCTTAAAG
Sequence 1280
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Table 1

ATTTAATAAGATTTGAGCATAGATATTAAACTTAGCATGGACAGAGAAACTTATTTNTTG
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Sequence 1281
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AGAATATTTTTCGTCTACTATTGTTAGAACACCTTAGAACCATCAAAAATATAATTACAT
GGCTAATAGAAAAAAAAGAGCAGTTTTAAAATATGTTTTATGTAACCTATTTTCATTGTT
TTTCATTTTGTTGTTGCCGAATAGTAGTTGTTCTAAGTAAATACAGGTCTCAATTTCACT
ATGAATAAAAAAAAAAAAAANGAAAAAAAAAAAAAAGTACCTTGGCCGCCGACCACGCTAA
GGG
Sequence 1282
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GCTTTGGGTTTAGTTTGTTCTTAAGTTCCTTAGGTGTAAAGTTACGCTGTTGAAATGAGA
TCTTCTTATTTAATGTATGCATTTATAGCTCTAAATTTTCTCTTAGCACTGGTTTCACTG
CATGCTCTAAGTTTTGATA
Sequence 1283
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NNANNCTNGTTTGGCCNNCCAAANNNCTNGGATTANNNGNNTGAACCANCNNACCCANNT
TTTAAAANCNNAATNTTTTTTNNGGNAANNTNANANANANCNNNCCCAAGGANTTAAANGGGN
GGGAAAAACNTGGANNTTTGGNTTTTTTTTTT
Sequence 1284
CCCTTAGCGTGGTCGCGGCCGAGGTACTCACAAATAACAAGACAAATTTGACCTGTTCAA
TAAATAGAAATGAAGTGGCTAAAAATGTTTAAATGGAAGTGGAAAACAGTCGTCTTCTTT
GTACTTGGTCTCTACCTCAGATAATTCTTCTTTGAGCTTTTGAGTAGCTTCTCCTTTTTC
ACTTAGTTCTACATGTATTCTATGCAGTGAGGTTTCAGATGCAGACAATCTTGACTGAAG
CTGTTGACAATCTAGGTCTTTTTTGATGAAGGGTTGCCTGAATATTCTTTTTACTCACAGA
TTCTTCATTATGTTTCTCCT
Sequence 1285
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TGCAGTAAGTAGGCAACATGCTACCCTTCTATTCAACACAGCACTAGAACAAGGCAAGTG
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ACCTNCATCCACACCCACAGCTCANGTTAAGCTGCAAAAGTTACACATCTTCTCTAGGCC
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Sequence 1286
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GCCTGGTGCCTCATCAGGTGTAAGTTCTTATAACCACTCTTGGCAAATTTATTAAAGACA
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AAGTCACCTTCCACTNAAAAAGCAGCCAAACTCCCTCAAAGGAGTAACTTTTAAAACCTG
GATCTAACCTGGAANGGGCTAAAAANTGGCTTGGTTCTGAGTTTTTTTT
Sequence 1287
CCCTTAGCGTGGTCGCGGCCGAGGTACATTCCAGTTCTTTATCTGAATACAAGCGTTTG
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GTCATATACTATATAGAATAAAGAATTGTTATGTAAATTATTAAATGAGTATACAGACCT
TTACATAAAAACTAAGGTACTTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTTTTTT
Sequence 1288
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Table I

TTGCTACATTCAAGAAGGAATCACTCTGGTTCTAATGCCTCCGACAGAATGGTCAGATTC
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ACTCGAATGGCCTTGAGGAGCTATTATCAATAAAAACAGTATAACTTATAATTATCTGTT
GTGTTACAATGAAGTATATCATCACTGC
Sequence 1289
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AGAGGTTTAATGGACTCATAGTTCCATGTGGCTGGGGAGGCCTCACAATCATGGTGGAAG
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AAACCCCTTATGAAATCATCAGATCTCGTTAGACTTATCCACTACCACAAGAACAGTGTG
GGGGAAAGCACCTCCATGATTCA
Sequence 1290
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TAAGGGAGCCACTGGGCAGGAGTAGGCA
Sequence 1291
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Sequence 1292
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TATTTAACATCTACACCTTTTTNGTCAGTTGTGTTAGCGTGTTTTCCACCCCATTTTATTA
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AGAACCCCAATGGTTTTAGTTATNGCTTTGTAAATTTTTATTTTTTTANTTTTACCTAAAN
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Sequence 1293
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AGATAAAATTAATAATCTTAAATTCCATTCATGTTAAAGAAGAAAGACAATTAAGAAATC
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AAAA
Sequence 1294
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Sequence 1295
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TCAAAATACCCCTATTTGTTATTNTTTTTTAAAAAGTAAAGTGGGGGATG
Sequence 1296
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Table 1

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Sequence 1297
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Sequence 1298
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CT
Sequence 1299
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GAGATCAGGAGATTGAGACCATCCCGGCTAACACAGTGAAACCCTGTCTCTACTAAAAAT
ACAGAAAAAANAANAAAAAAAAAGAAAAANGGTCCTTTGTNTACTGCAGTTGTCNTNTAC
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TGATAGTGAATTGGCAAACGTGACCAATTTTTT
Sequence 1300
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AGTGTTTTAAAAACGCATACCTCGGCCGGGCGCGGTNGGCTTCATGCCTGTAATCC
Sequence 1301
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ATTGGACAGGACATAA
Sequence 1302
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GTGGCAACAGTGGCAGNAGTCTTGTCCAAGGGGAC
Sequence 1303
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GCCGCTCGAAAGGGCCGAATTCCAGCACACTGGCG
Sequence 1304
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GGAGCTCTGAAATTTAATTCGAGGCTTTCATGCCTATANAAAGGCTTCTGCCAANTGATG
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Table 1

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AATCTACCTTGG
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GAATGGGTTTCCTCTACCCCCGACACCACCTGATATGCTAAATCCAAGTTCTGGATCCTT
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Sequence 1308
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Sequence 1309
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NNNTTNTTANAAAAANNATTNNACCCCNNTNTNAAAAAAAAAAA
Sequence 1310
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Sequence 1311
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CGCCTGAAATCCTTTTGGGAGG
Sequence 1312
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Table 1

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CGCTAAGGG
Sequence 1313
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Sequence 1314
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CCTA
Sequence 1315
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CTAAGGG
Sequence 1316
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Sequence 1317
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CCCTTATGAAAANNCCCCTCNNTTAAAAAAAA
Sequence 1318
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CGTTT
Sequence 1319
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Table 1

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GGTGGCCTATAATGGGCCTTCACCTTGTGAACATGTGANCCAATTCTNCTTAACAAACGC
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Sequence 1320
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Sequence 1321
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AAA
Sequence 1322
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CGA
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Sequence 1324
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Sequence 1325
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Table 1

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Sequence 1327
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Sequence 1328
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Sequence 1329
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GAAGATGAGGATATTGTTCTTACACCTGATGGCACCAGGGAATTTCTGACATTTGAAGTC
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Sequence 1330
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CTAAGTGTGAATTTTCACAGGAGGAGAAATCTGGCAGATAGATCCTCACCATCATCTGAA
CACTCGAACTGGACTTCCTTTTCTGAATTGACCAGTCAAAGAGAAAGGAAAAGAAAAAAA
ATATGACCCGGTTGAATTTAGAGTATCAAAGCATGGAGTATAGAATAATTTTGTTTTTAA
AAGAGGAGCTATTAAGTTGAATGGAAGGAAAAAGTTCTGGAAAATGCGTTCCATGTAAGG
ATAGTAATCCCG

Sequence 1331
TATCTGCAGAATTCGCCCTTAGCGTGGNCGCGGCCCGAGGTACTGTTTGCATTAATAAAT
TAAAGCTCCATAGGGTCTTCTCGTCTTGCTGTGTCATGCCCGCCTCTTCACGGGCAGGTC
AATTCACTGGTTAAAAGTAAGAGACAGCTGAACCCCCCGCGTACCACTGTAATCATTATT
CCCAATGTTATGATTACATTGACAGATAACTCCAGTTTTGCTAACCTGAACTGATGTTAT
GGCCATAATATGTTGTTGATTCATGGCAAANGGTGATGTGTGAGTTATGATCCTGTTTTT
CTCAAAATGGTGGTGGAGGCCGGGAGCTTATATGTTTATTTATGTATGAATGANGATAGC
AAGAGATGGCATATAATCACCAGACTGATCATATTGGATTCTTTG

Sequence 1332
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGGATTTTTGCAAGCCCTCTATTTAAAATTC
CCCAGAAATTAAATAAGGAGGCTTTGGAGGGAGGAATGCCCTANACAAATTGTGGAGTGG
GTTTGTTTTGTTTATGGAGATGGTCTTTAAAGTCTAAATTGTCCCCGTTTTATTTTTGCC
CAATTGAAGAGGGGCTGAACTCAGCTGGGAGGGAGGGGATGGTTGTCAAGCCTACAGCTT
TTAGTTGAAACCAAGTCCATTCTGGGGCCAAGAAGCTTCCATTTTTAGCAAAGAGAGAAA
GGGGAAAAATATACANACTCGTACCTCGGNCGNNACCACGCTAAGGGGCGAATNCCAGCA

Table 1

CA
Sequence 1333
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAATTCATTCTACTTTGTGTTAACTATCTT
TTTATGTGTAGGTCTCATCACCCCAACCAGACTATAAATTCCTTTGTCATTATTTAAATC
CATGCATGGAACTCCCATAGACATCAACCAATCACCAATAGACAAGCCTTAGAACATGTA
TTACAGGAAAAATAGAGTAACACATACAACTAATACAGAGGAAGAACANTTGACATTAAA
ATAGAANAANAAATTAACACTCTTTGGANTCTATAAANAAATGNAAACAGAAAGAAAGAT
NGAAGGATAATNCGTNAACTTAGAATATTCATTTGCCTGCTTCAACATTCAATAATTAAA

Sequence 1334
CCCTTAGCGTGGTCGCGGCCGAGGTACAAAGTTCAACAAAGTTTGTTCTTGATTAAAAAA
AAAAAGAATGAATATCTAATGTATAAACAACTCCAACTTAGATTTCCAAAATCTTGCATT
CATTCACATTTGTGCTTCTTTCTACACAGCTGTCATTTACATTCCTAGGCTTGTATTTCA
CTATGTAAAATGGGAATTTAATCTTTATAAATGAGGCATTTATGTAAAAAAAAAAAAAAA
AAGTACCTGCCCGGGCGGCCGCTCGAAAGGGCGAATTCCAGCACACTGGCG
Sequence 1335
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATAAACCAGCCAAAGAAAATAACCAGTTAG
CACTTAAATAAGAATCTACCATGTAAAAAACACAGTATGGGACACTACAAGGTAGTATTT
ATATATTTTTTAAATGACTGAGCTACAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1336
CCCTTAGCGGCCGCCCGGGCAGGTACATCTATCTGACCCCAGAGTTACCCTTTTCTATCA
TGCCCCCGTAGGATATTGCCTGGGGACACCTGACAACAGAAAGTCTAAGGTTTTCATCTA
GGATTGGGAGTTACCCCAACACCAGCAGGATGCAGGAAAAAGTAACTGACCGGATGGTTG
CCTCAATCTGTTGATTCTTCAGTGAGTTAGCTCAGATTTTGTCCAGGAACAGCTTTCAGA
GCCAAAGATTACCGTATTGAACTCTACCAAGGCATCTGGTGACTAGAAAACTCCTGGAAG
GTGGTCATAGCAGAAATTGTTGGGAAAGTTCTCAGCATAATAAAAGAGAAATTTTTATTT
CCTTCATTGATCCACTCCTACAGGGAAAAATAAATGGCANATGAACCCATGTATGTCANA
CTCTGNAATAAACATCAGTGAGATCACAGTGTCAGNGAAATTTCAGCCTGAATTAAA
Sequence 1337
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAAACCTT
ATAAATAAAAGTGGTATGCCAGTAAAGTTTCAATTTACATTTCTCTTCTGAATGAAACT
GAGCATTTTCCATTTTCCTCCTANATTCTTAGGAAGCCTTTGTATCTGCGATATAAGTTA
CTTTCTCCTTCTTTGTCATGTTGTTTAACTTTGCACTTTCTTTTTAAAACCTGCAGTAAA
TTTTAAATCTTTTCATTCAGTGCTTCTGGTTTTCAAATCACATACAGAAAGAATCTCCCG
AGTCANAGGGTGTGACCACAGACTGTTCTGGTGCTTCTATGGCTTCATCTTTTCACATTT
GAATCTCTGACGTAGTTGGAATTTATTCTGGNCTATAAGGANCCGACTTTATTTTAAGAA
CAAAATTTTTTTNAACAAATGGTAAACTTAACTCCTAAAGGCAGATTNT
Sequence 1338
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTGGTAAAAGATTTTAAGAAGGCATGGGAAT
ATGAATTTCTCACCTAAGTTTAGAGGGTTAAAGGATTGTGTTAAGTGAGGAAGGAAAAAA
TCTAAAGGTTTAAACAAGTTGTGAAAGGTTTATAAAAAATTAATGTGTGCAAACATATCN
GGCTAAAGTTAAAGAGGTATTATTCTGTTTTTCCATAAATTGAACATTGGAATAAAAGTG
CAACAGAGTTTTCCTAAATCATTGNTCTGCTCTTTAACAAAAAAAAANATTGTAAANGGTT
ATAAAAGGNTTATAANAATCTTACC
Sequence 1339
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAAAAATTTCCACTATCAGAAGATCCTGATT
AAAATAAAGAAATACATAAAACTCAAACAGTAAGTCAATGTGATTATTTGTTTCATTTCA
GAAGATCTATGGGTCCCACTGCCCGCCACACGTAGTCTCCTGGGTTCTCAACGAAGTGTG
ACCAGCTCTTCTGAAGAGGTAGGGTGAATGGCGACTGTGTTGTCA
Sequence 1340
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTAACTATTTGTTTCTTCTACGATAATTGGT
TTGTTGTGACTTTATCTACCTAGAGTAAATTTTGGCAATTTGCATTTTTCTCAAAATAGT
TTTTGAATTTATTGTGTAAAATTGCTCAAAATAGTCAATTTAAACAAATTTCCTGTTTTA
CTATTTCCCCCTTGTCATTTAAATTTTTTGTATTTGTGCTTCCTCCCGCGTACCTGCCCGG
GCGGCCGCTCGAAAGGG
Sequence 1341

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTGACTATTTTTTAGCAACAAATTACTTTT
GACACACAGCACAATTGATTTAACACTTCCAATTTTGGAACTATTGGATAAATAATGATG
GGATTTAAATAAAGCAATCCGATTCTACTATTACAGCATAGGGTCTCTTGTAGTCCTCTT
AGTAAAAACTATTGTGACACTTCCTTCTTTCTCCAAATATTCGGCCTGGAAAGACCTAAA
TACAATGCAGGGATTGAATCAAATTCACACATTTTTTTTTCCTACGGAAACAACAACCTTT
CTTGCTTATATTTAACAAAAACTAGTATAGATT

Sequence 1342
GGTCCGTGGTGCGGGATCGAGATTGCGGGCTATGGCCGCCGAAGGTTTTTCGTCAGTACT
GGGATATCCCCGATGGCACCGATTGCCACCGCAAAGCCTACAGCACCACCAGTATTGCCA
GCGTCGCTGGCCTGACCGNCGCTGCCTACAGAGTCACACTCAATCCTCCGGGCACCTTCC
TTGAAGGAGTGGCTAAGGTTGGACAATACACGTTCACTGCAGCTGCTGTCNGNGCCCGTG
TTTGGCCTCACCACCTGCATCAGCGCCCATGTCCCGCGAGAAGGCCGACGCCCCCTGAAC
TACTTCCTNGGTGGCTGCTCCNGANGCCTGACTCTTGGAACACGCACGCACAAACTACCN
GGATTGGCGCCCGACGNCTGCGTTGTACTTTGGCATATCGGGNCTTCCTGGTCAAGAATG
GNCNCGGNTTGGAGGGGGCTGGNNAGGGTGTTTGNAAAAACCCAATGTTTNAGCCCTTGTG
CCTTGCCGGGGACCTTTCAGCCCTGCAATAATGCGTCCCAGAAATAAAATNNTGTGGTCT
TGGTGTNNGAAAAAAAAAAAAAAAAAAA

Sequence 1343
CGCCCCGCGTCCGAATGCAGTGAAAGTGACACTGCCTGACCTTCAAGACTAGATCATCAA
AGGTGCTACAGCTTCTGCTTTGGCTTACCCTCTCTGTCGTGGGACACTCACCCTTGGACC
CAATCTCCACACTGTGAGAACTTCTATGCTACCTGGAGAGGCCTTCTATAGATATTTCAG
TCAACAGGCCTAGTTAAAGTTTCAGCCAGCGTCAACCACCCAACATGTGGGTGAGTGAAC
CCTCAAATGATTGCAGCTCCCAGCCTTTGAGTCTTCAGTTGCGGTCCCAGTCATTGAAAC
AGAGTCAAGCTGCCCCCGCTGTGATTTATCTGAATTTCTGACCCACTGGGAGCATAATAA
ATGATTGTTTTATGTTNAA

Sequence 1344
GGGAGTCGACCCACGCGTCCGTCCAGAATTTCTAGAGTGGGTGGGCATGATTCCAGTCAA
TGGGGGACCGCCCGTGTCTAAGCATGTGCAAAGGAGAGGAGGGAGATGAGGTCATTGTTT
GTCATTGAGTCTTCTCTCANAATCAGCGAGCCCAGCTGTAGGGTGGGGGGGCAGGCTCCCC
CATGGCAGGGTCCTTGGGGTACCCCTTTTCCTCTCAGCCCCTCCCTGTGTGCGGCCTCTC
CACCTCTNACCCACTCTCTCCTAATCCCCTACTTAAGTAGGGCTTGCCCCACTTCAGAGG
TTTTGGGGTTCAGGGTGCCTGNTGTTTCCCTTTNCTGTNCCCAGGTCATTCCAAACCCTT
CTGTTATTTATTANGGCTGGNGGGGAAGGGTTTTTTTCTTCTTTTTTCTTTGGAACCCTGCC
CCTGTTCTTTACACTTGCCCCCATTCCTTAAANCTCATACAAGAATTTNCATCNATNGGG
GGGCAATGGGNTTGGAAGCAAAAAGGGGCTTCCNTTAACCCCGGGCAAGGCAAAANGCAA
TTNGGTAAAAANGGANGCACCTNCCCCCCTTTTCTTNGNCCCCTTNCTTAANTTTTNAATA
AAANAACCNGGGTTTTNTANTTTTTTAAAAAAAAAACCTGTTTTNTTANCANAAAAAAAAA
AAAA

Sequence 1345
TAGCANTTCAGCCCTGACCTGGGTCCGCAGCCTCCAGGGCAGGGGCTGGAGTGGGTNTCT
CAAATTAGTGCTAATGGTGGTCANAACTGACTACNCAGACTCCGGCCCATC

Sequence 1346
CCCTTAGCGTGGTCGCGGCCGAGGTACTAGATTGGGTGTGTGTATTAAGAGAAAGACAGG
AGTCAAAGATAGTTCCAAAACTTTTGAACAGAACACTGGATGAATACTGTTTACTGAGAT
GGGGAACACTTAGAGAAAAATGCATTTGGAAAGCAGAAATACGATCAAGACTTCCATTTT
TGATACATTAAGCTTGGTATGTTTAATTCATAGCTATATAGAGGTATTAAATTGGCAGGA
CAAAATCATAGCTAGAGATAAAAATTTAGAGTTCACCAGTGTAAAGATGATATTTGATGG
CACAGGATGGACTTTCTTCTGGGATTTGAGTATACATAGAGGAAAGATGTGAGGATTGAG
CACCAGGGGACTTCAACATTGACAGGCTCAACAGAGGAGAATTCCCAAGAGGATGAGGTT
CCACCTTTAGGACCCGCCAAAGAAGACTTCCCAGACAAAGTACCTGCCCGGGCGGCCGCT
AAAGGGCG

Sequence 1347
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTAACTATTTGTTTCTTCTACGATAATTGGT
TTGTTGTGACTTTATCTACCTAGAGTAAATTTTGGCAATTTGCATTTTTCTCAAAATAGT
TTTTGAATTTATTGTGTAAAATTGCTCAAAATAGTCAATTTAAACAAATTTCCTGTTTTA
CTATTTCCCCCTTGTCATTTAAATTTTTGTATTTGTGCTTCCTCCCGCGTACCTGCCCGG

210

Table 1

GCGGCCGCTCGAAAGGG
Sequence 1348
CCCTTAGCGTGGTCGCGGCCGAGGTACAAATTACTCTGTAATATTGCTTTCTATTAAAAG
GGTGTGGTTTTTTTTTTTTGTTGTTTTTTTTTTTTTTTTAGCTAGTCCAGTGGTCTTTTTGAT
GTTGGTTCAGCTTAGTGGTTCTCAACCCTGGAACAACCCGTANACCCACCTGGGGAGCTC
TTAAAATTATCAAGTGCCTACCCCACCTTCCAAGATTCTGATTTAAATCCTGTAGTGTTT
TTAAGGCACCCCAGGTGATTGTAATGTACCTGCCCGGGCGGCCGCTAAAGGG
Sequence 1349
CCCTTAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
NAAAAAAAANGGNTAAAANNAANTTTTTNTTTNCCCCCNAANGGGGAANGGGGNTNAANTNN
NAAAANNTTTANNTTTTGGNAAAAAAAAAAAAAATNNNANTTTNAAAAAANCCCNGGGGGGNGN
TTTTTTTTTAAAAAAAANNNNTAAANANNTTTTTTTNGGGGGGGGTTAAAANTTTTTTTTT
NNGGGGNCAAAAAAAAANNNNCCCCNTTTTNNCCNTTTTNAAAAAANNGGAAGGGGGGNNNNN
NTTTTANNTNNCNNTTTNAAAAAAAANTNNTNANGGNNTNNNNATTTTTTTAAAANNNAAN
NNNNNNNGGAAANNTTTTAAAAAAGGGAAAAAAAAAAAANGGTTTTTTTTTTTNNNGNGGC
CAACCCNNGGTGGGNGGAAAAGNNACNCCNCCNAGTTTTNCCCCTGGGNGGAAAAAGNTTT
TTTAAAAAAA
Sequence 1350
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCGTCTTCTAATTTCAAAAATATAACTTAAAA
ATGTAAATATTCTATATGAATTTAAATATAATTCTGTAAATGTGTGTAGGTCTCACTGTA
ACAACTATTTGTTACTATAATAAAACTATAATATTGATGTCAGGAATCAGGAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAANGTACCTGCCCGGGCGGCCAAGGG
Sequence 1351
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAGTATTATGTATCCATAAAAATTAAAAAAT
CTTTAAAAATGCATATGGGGGTCAGTAGGTAAAAGAAAAGAGAACCAAGAGAGCTGCAGC
GGGGAGCACAGCTTGCTTTAAACATGAGATCCAGCTCAGTGATCATGCGGGGGAAAAGGC
CCGGCATTGCTGGAACTCCTAATATTTAAAAAGATGATGGAAACTTGAAATTTTATATTT
AATCTTCTCATTTTTAAGTGTTGGCAATGTATTGAAGACTTTGAAGCCTCTCTGCTGGTC
AAACAAGATGTATCTGTAGGCTGGATTTAGTCCACAGCTGGCCAGTTTGAAAACTGAATC
CTGCTAGCCTTAATTTAAATTTTTTTAAATTTAATTTGCTTTGATTCCTGCCTCCTGCTC
AAAAAAATCTTCAATGGCTCCCCCTGTCTGCAAGGNAAAAGTCC
Sequence 1352
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACA
GNTATACTCGNGGAAAGTTATTCAAATTTCAAATTTATTTACAGNGTTTGAAAAGCACAC
AACAGAAGATCTTCATTTATGCAACAAGTCAATCATTTGCAGTATGTATGGAAAATAAAA
ATCTAAGGTAAGTCAAACATACAAACTCTACCTNTTGCTTTCTCCATTANAATATACACA
TTGGAAATCTAAGTTCCAAACAGTTCCTNTNTACTGAANATAGTGAAATTTAGTGCAAGC
CCCCTAATTACCAATTTTTTGG
Sequence 1353
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATTGGTTTGATCTGGAAAGGCAGGACAACCC
AAAGCGGGCTGGGGACAGTTCCAAGTTATAGGAGGTTTTCCAATTGGCAGTTCGTTGAAA
GAGTTTATCTTAAGACCTGGAATCAATACAAGGGAGTGTGTCTGGGTTAAAATAAAGGGG
TTGTGGAGATCAAGGTTCTTATTAGGCAGATGAAGCCTCCAGGTAGCAGGCTTCAGAGAG
AATAGATTGTAAATGTTTCTTATCAGACTTAAAAAGGTCCCAGACTCCTAGTTAATTTTC
TAGTGGATCAGGAAAAAGACCTGGACAGGGAAGAGG
Sequence 1354
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTNGTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTNTNTNTNTTTTTTTTTNANTTNNAAAAAAAAAAAAAAAAANNNANTTTTTTTTTANNN
NANANAAAANANNNNATNAAANNANTTTTTTTNANAAAAAATTCTTTANNAAAGGGGGGAAA
AAAAAAAANNTNNAAAAAAAAANTTTTTT
Sequence 1355
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAACCTGCCTGAGTATGACCTCTCCACCTTAT
AGTTTATGAATGTCTTGTTTGTGAAAGTGACTATAACCCAAACTTTTTTTTTTTTAAAGAG
GATTTGGAAGTTGTATGGATTTTTTTGTTATCTTCACTTTACTGCATAGGAAACAATCTAC

Table 1

CTCATCATTTAAAATGACATGGGTGTCGGTTTTGTAGATCTTTGGTTTTTTTGTCAGGTT
TAATTTCAGTTAACAAAATGTAAAACATGACATTCCCTGCAGATATTGTTGTATACCAGT
ATGGTTTCTTCTCTTTCTTTAAATGTTTTTGGCCATCAAGTA
Sequence 1356
CCCTTTCGAGCGGCCGCCCGGGCAGGCACTTTTTTTTTTTTTTTTTTTTTTTTTTGNGTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNA
AAAAAAAAAAAAAAATTTTTTNNAAAAAAAAATTTTTNTTNNNTNAAANTTTAANTTTTTNAA
AAAANCCANGGGNTTTTTTTTNAAAANNTTTTTNCCNGTTANGTTNTTNAAAANNANTTG
GGGGGGGGGGNCTTTTTTTNTAAAAAAANGGGNNNNNCCGNCCCGNAAAAAAAAAAN
Sequence 1357
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAACACTTTAAAAAGTGAATTTTAAGCTATGT
GAATATCTCAATAAAAACATTTTTTAAATAAAAACAATTCCCAAAGGCCTGGAAATTCAG
GAACATAATTCAAATAATTTATGGATCAAAAAATAAATCATATAAAGATCTGAGAACTA
CAATGTAAAAATATAGAAAAAAGTCATAACAATATTAGAAAAAAATTTGAGCTGGATAAC
AAAAATAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1358
CCCTTAGCGTGGTCGCGGCCGAGGTACTTACATGGAAATAAGTGTTAAGAAAAGGATTGC
TTATTGGTAGCATATAGATTTAGAGTCAGGAATGATGGTGATTTCAAACAACCACAGAAC
GTCCACATGGGTGGCTGGCCAGGATAGTGACACCTTTGCTTTCTAATGGCTTAGTGTACC
TGCCCGGGCGGCCGCTCGAAGGG
Sequence 1359
CCCTTAGCGTGGTCGCGGCCGAGGTACAAAGAAAAAGCTAAGGAACGGTATGTATATTAA
TCCCTTTATTAAAAATGTAAAAAGCCAAAAGCAAGATAGACGCAGATATGTGCCAAAATA
TGTATTTTTTTTTTCCTGGAACAAATCACAAGAAATGTAATAACAGTTACAGTGAGAGGAG
CCTTTGACATCTCTTTCTAAACTATTTGATATCATTTGTATACTAACGATGTACCTGCCC
GGGCGGCCGCTCGAAGGG
Sequence 1360
CCCTTAGCGTGGTCGCGGCCGAGGTACGCGGGATAGGCCTTCTTGTTATTATTTCAAAGA
AAGAGACTTGACGTTTTATGAGTGGGGTGGATTGTAGGTTGAGCAGAACTAATGGGAGAG
GTGCTGGCTAGAGAAAGTTAAAAATTTCTGTTAGCTTTGCATTGAGCTTTTTAATATCAT
TTGTTCATTTCACCAGTTCAGAGGATTGGGGGGTGATGGGCACAACAGAAATGATGGAATA
TAGGCCAAATGTTACAAAATAGATAAAATTACCTGACCAGTGAAGTGTGTTCCTCAGTCG
CCATGGANCCTCAGATTTGAACTCCCAAAAAAAAAAAAAAAAAAAAAGNN
Sequence 1361
CCCTTAGCGTGGTCGCGGCCGAGGTACTATAGCTTCAGTGTGGTTTAGTAAACTTAGCCT
AGGAGGCCAAGATGTCTCCCTAAAACTTAGTCTCTGTCCTATTTACTTTGTTTATAAGAC
TGTGACCTAACTTCCCATGGCCAATTCAATCGACTAGGTTATCTTTACTCCAATGGACCC
AGGCCTTTTCCCAGTCAATCCATGTCCAACCCTTCATCTCCAGCGTGATCACTCAACTCT
TCAACATGCCTGCTTGCTGCAGGNTTAAAACCACACCCACCATCCTGTGCTTNCCCCTTA
ATCGCCCATTGATGCCCCGCANGGTAAAATAAAAACTA
Sequence 1362
CGANGTACATGAAAATGGCTGTTTTTCCCCACATTANTCAGCTCTGGATTTTGCATGTGT
GGGGCTTTTTTTTTTTTTTTTGATAGTTATTTGTTTTTTATTTTAAAAATTTATTTNGCCAA
CCCAGTANAGAACAGCTGAGCATNTTCTCATGTATTTATTGGCCATTTGCATTTCTGCTG
CTTATTGGCCATGTATTTATNGGCCATTTGCCGTCTGCTGTGAAATGTCTTAAATTNTTT
GCCCATTTTTCTAGTGATAAAACACTGAAGCACATTTTTAAAAGA
Sequence 1363
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTAAAAGGTGATGCTAATACTTTAAAATGTC
ATAAGATATAGATTNAAAAAGCATTGTAAATTGTATACTAGCAAAAGTCGTCTANATGGC
ATTGNACAGGACATAATGTAAAACAT
Sequence 1364
CCCTTAGCGTGGTCNCGGCCGANGTACTTAAACTTTTTTCAGCCTACTACTGCACACCTAG
GCTATGTGGTATAGCTACCTTGTATATGTGGNCTGTCACTGACTAAAACTTNGTTACACA
GNGTATGACCCTACTATTCANCCTTGAGAAGATGGAAATGCTGNCATTTGCAACAATATG
GATGAACCTGGAGGACATTAAATTAANTGAAATANGCCAGGCACAGAACGACAAGTAACA
CATAATC

Table 1

Sequence 1365
CCCTTAGCGTGGTCGCGGCCGAGGNACTTTTTTTTTTTTTTTTTTTTTNTTTNACTTNATTN
TACTTTAAGTTCCAGGATACATGTGCAGAGTATGCAGGTTTGTTACAGGTATACATGTGC
CATGGTGGTTTGCTGCACCCATCAACCCATCACCTAGGTTTTAAGCCCCACATGCATTAG
GTATTTGTTCTAATGCTCTCCCTCCCCTTAACAGCAGTTTTTCTATAGGNCAAAACAAAT
TTGGGAACCAGAATNGNCTACTGTCTTTATATAAATGATCATTACGATTTGGGANGAGGG
TTTTTTT
Sequence 1366
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACAACGTTTCTACTCTATTGTGTAAGCTTT
AAATACAAAAATACCACAACCACTCCCGGACTCCTCCATTATTTCAGTAATACTGGCTGC
CCTAGTTTTTCAGGATACATCATGCAAATAAGTTCTTTTATTTTTCAAATTATTTTATTC
CTAAAGTATCTTTAATTTTTCTTTTTGGTTATACAGCTTATAGAATAAACAAGTCACAAG
AATCTTCATTTGTTTCTAAAGTATATAATTTTACAAAAGTTGTTTTACTCAATGTGAATT
AAAATTTGCAAGGTCTAAAAAAATAAAAAAATTTTAAAAAGTAAAAAAAA
Sequence 1367
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATATATTATGAAGCATGACCACTTTATTTT
GAAACTTAGCAATTGTATTGCTGGGGTTTATTGTATCTGTAGCATGTCACTGATTATTTC
AGTTAGTTTTATAATGATTTTTTAAAAAACATATCTATTTGGAATAAGATACAGCAACAAT
CATTGCTATTGACTTGTTCAACCCCTTAGTTACACTGTATGATCAACATATAACAAGATA
CAGTGGGAATGGCCCATACAGTATATTACTGTTGTGTGATGATTGGCTTTGGAAGCAGTT
TGATTTTGAAATGCTTTGATATTCTAATTGACATGGAACAA
Sequence 1368
CCCTTAGCGGCCGCCCGGGCAGGTACATATGATGGGGCCAATGCACAATACTTTTATCAC
AATCAACTTTTTCTTTGTATCCCTATTTCAATGAGCAGTCAGTCTCAAGAGGTTACTGCA
TTTCAGTTCTAACTAGACATTTGTACTTGTGATCACACTACGGGAATCTCTGTGGTATAT
ACCTGGGGCCATTCTAGGCTCTTTCAAGTGACTTTTGGAAATCAACCTTTTTTATTTGGG
GGGGAGGATGGGAAAAAGAGCTGAGAGTTTATGCTGAAATGGATTTATAGAATATTTGGA
AATCTATTTTAGNGTTNGTTCGNNTTTTAACGGTCATTCCT
Sequence 1369
CCCTTAGCGTGGTCGCGGCCGAGGTACAGCTTTCTCTGCCTCACGTTTCAAGCTTAATGC
ATCATCTTAATTCATCTTTCGACATCTATTTCTACTACATGCTGCTCTCTTTCTCTATCT
TACATCTCCCAGAATGTTTTATTTCAACAAATTGCTAATCTGTGCCAGGCATTGTTATTA
GCAAAATGATAAGCCCTGCATGTAGCAAAGTTCCTGCCTTCACTTGCATATGCATTAACA
AGCTCTGATTAGTCCCACTTAAAAACCATTTGTTCCCCCGTCATGCAGAACTCCATTGCC
AAGCCACACAACACCCCAGCCAGTAGGGTAGCAGCTNCCTGGAGCAAGGGA
Sequence 1370
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTTTTTTTTTTTTTTTTTTTTTT
TTTTNNCNNCCGGNNNAAAAAAAAAGGNCNAAAAAAAAAANGGNTTTTTTTTGCATAATNAAA
AANNNAAAAGGGGNTTTNAANGGANTTGGNNTTTTTTTTTTTTTNGNCCNNGGNAACTTTNA
AATTTTTTTTAAAAANCCNGNAAAAAAANTTT
Sequence 1371
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGTCGTTTCCTTCCTACCTCGTCCTCACCCC
ACCCCGAGTGAAACTTTTCGAGTGTGAACCTTACTTTTTTCCCGTTCTCCTCAAGGCAGT
TTGAACGACACAGGTTTGGAAGGAATAGTTAACTCTCCAGTATTATTGGAACATCTGGAC
ACCACCAACAAAAAATCTTAGAAAAGGGTCATTTAAGGCCTATAAAAAGTGCCACCTTTC
CCAGAATTAATTCAGAGAGAAAAATCTTATCTGCCTCCTGGCAGCTACAGCGCANAAAGT
ACCTCGGCCGCGACCACGCTAANGGGCGAATTNCCAGCACACTGGCGGCC
Sequence 1372
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTNTNTTTTTTTTTTTTTTTTTTTTAAAAAANCCGGNTNC
GCGGGNANANAAGGTNCANNATTNTTTNAAANNTNANTTTTTTANCAAAAAAAAACAAAANT
TTANCCCAACANNTTATTTTTAACAGCAANANGTAAAAAAANCCCAANCNACNTTCCANNT
AANAAAATTTTTTT
Sequence 1373
CCCTTAGCGTGGTCGCGGCCGAGGTACAGCTATTCTCAATGGATAATTCTATAAAATATT

Table 1

TAAAGAAGAATCAACACCAGTTCTCCACACTCTCCTCTAGAAGAAGAGGAGGATGGAATA
CCTTCCCCCTTAATTTATGAGGCCAATATTACCCTGATGCCAAATCCAGACAAAGATATT
GTCCCCCAAAATAAAACTAACGATCATAGATAAATACCCTCTTATAAATTTAGATGCAAA
ATCTTAAGCAAAATATATTAGCAAAATGGAATTCAACAATGGAATAAACCTATTATACCA
CCAAGTGGGAATTTATTTCTAGCTATTGCAAGACTAGCTTGGACCTTTTGAAAATTGATT

Sequence 1374
ATATCTGCAGAATTCGCCCTTTGCGGCCCGCCCGGGCAGGTACTGGGAATACAGGCATGA
GCCACCGCACCCGGCCAGAAATTATAAATCTAACCAGGATTCCAACCTACAATACAATGA
AATATCATTTCTCTCTTATAGGTTTTTGGTTTTAACCAATCTATTTTAAAAGGGGCAATT
CAAGGATTATGGTTTATATGGNGGGGATTTCTGTTTGAATATGATCAAATGTTCACTGGAG
AACAAGCAATAATTTGCAAAAGGCATATNTATGCCTTACATTAAATGTGGATCCTCTTCT
AAAACTAGAATAAGCATCAGTTCAGTCACCCAACGGTGGGAAG
Sequence 1375
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGGATATGATTGGCCGGCGAATCGTGG
TTCTCTTTTCCTCCTTGGCTGTCTGAAGATAGATCGCCATCATGAACGACACCGTAACTA
TCCGCACTAGAAAGTTCATGACCAACCGACTACTTTCA
Sequence 1376
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTCTTTTTTTCTTTTTCTTTTTTTTTTTTT
TTTTTTTTTGAGACAGGGTNTCACTCTGTCACCCAGGCTGGAGACAGAGCAAGATCCCGT
CAATTAAAACAACAAATAAATAAACAAAAATGCCCAACAAGGAAGAGAACGGGAAGTCAT
AGGCAATCTCATTCATGAACATAGATTAAAAACACCTGAAGTATATACATACCCACACCC
CCGACATGAATACATATGAGATGTGTAAATGTGAATACTTACATGTATGTATATGAAAGC
AAACCAAATCAAACAATGTAAAATAAAAATAACACATNATGACTGACTGGCATTTGTCCC
AAGAATGCAAAGCTACTTGAGAAAATCTATTAATTCATCAATTTAATACTTTAAAAGAG
Sequence 1377
CCCTTAGCGTGGTCGCGGCCGAGGTACCATATAAAAACATTCCAGTGTCAACAGCACTTT
AAATTTTCACAGTAATATATGAAAGAACAGACTTTACACTTCTTTTGCACAGAATTATCT
TTGCTATGTTTTAAAATACTTAAGAAATAGAAACAAATTTAAGAGAGTTTTCACCTTTAA
AATTTATTACATAAGCTATACACACAAAATGAAATCCTAGTTATAAAAGATGCATCTAGA
AGAATAATTTATAATAAACCAACAAAAATGAGAATGTGTATCTCCAGGAATATAAATATA
TTTAAATGTTCTCAGTGACTGGCATTGCTTTATGCATTACATAAGATAGTATGTACCTGC
CCGGGCGGCCGCTCGAAAGGG
Sequence 1378
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TGTTGGAGTCAAAAAGAACCACTTGTGGTTCTAAAAGGTGTGAAGGTGATTTAAGGGCCC
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CATGACATCAAGACTTTGCTAAAGACATGAAGCCACGGGTGCCAGAAGCTACTGCGATGC
CCCGGGAGTTAGCCCCCTGGTAATAGCTGTAAACTTCCAATTTCTAGCCATACGCTCAGC
TCATCCATGCCTCANAAGTGCATCTGGAGAGAACAGGTTTCTAAGCATAAAAGATGAAAG
AGCAGTTGGACTTTTTAAAAAATTCAGCAAAGTGGTTCCCTCTCTTAGGGACAGTCAAAAC
CAAGTCACTTAGGTAGTACCTGCCCGGGCGGCCGCTAAGGGCGAAT
Sequence 1379
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGTGAATGGAATGCCTTGCAATATGAA
TGTTAATATAATGTGTAAAGGGAGATTAAAAAGTTTGAATGATTATCCTAAAAAAAAAAA
AAAAAAAAAAANGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1380
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACAGTAATTTTGGAAACCTCTTTGATGTCTGG
CTTATAGAAGACACCTGGGTTCTTATATCTGCTTCTGAATCGATCTATTGTAATGNNGTT
ATTTTGGCTGAAGTATGTTGAAGAAAATACTACCTTACAAAGATATGTATTTTCA
Sequence 1381
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TATTTGTTGTANCTTGTATATGAACATAATTTTCTTTAGAGGTAGTCACTGTTCTCTCCA
GTATGACCCAGGTTTCTTGACTCTGAGTAATGCACCTTCTATAACTATCTAAATTTCTAT
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Table 1

TTAAATGTCATATCCTTCATGTCTCAAAGCCAAAATAGTAACATCTCATCTCAGAACANG
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Sequence 1382
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GGGCATGGTGGTGCACACCTGTAATCCCAGCTTGTCAGGAGGCTGAAGTGGGAGGATCAC
CTTGAGCCCAGGGANGGTCANGGATGCAGTGAGCCATGGGTCTCACCACTGCACTCTAGC
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TTTTACNAGATGGTGAAAATTGAGGGTTCANAAGAAGTAAAAGTCTATTGCTCAAGGTCA
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CCANTTTTTTTTTTAAAGCACCTATGNNTTGGGNGTTTTATCANGCATTAATNTTGNATT
GGCTTTTGGAAAANACCGNGTNTCNTNTNGGGGAAAGGGAAAAAAAAANTTTTTTTTCCA
ACTTGGCCCTTCGGNCCAANTTGGGAAAAA
Sequence 1383
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTGTGTTGTTGGTATCCAAAATTAGGACTCT
GAGATTCTTGTGTATTCAGAGAATTTTTAGTAGGAAACAAGGACAAATTTGCATATGAAA
TGAAAATAGTTATTACATGACAAAATATGTAGATCTGATTTCTAGAAACTGAATTAGTCC
AAAACAAGTAAGAGTGGGAAAAGCAGTAAAAAGTTCTTCTTGAATATTGCTGTTGTCATC
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CCCGNGNAAAAAAAAAAAAAAAAAAAA
Sequence 1384
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CTGATCTGGCTTGTCATTTTTCAGTAATAAAAAAAGTTACTGAATTTAATTGTTGAATAT
GATGCATATCTCATTCATTACGATTTATCAGAAACCAAAGATTTAAATTGCCTAGATTTG
TGGTTCTTTCTCTTCCTAAGTTCCCAGCGACTGCTTTCAAATACTATTTTTCTAAATTTCA
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CAAAAAGGTCAGGTAGCACCAACNTATTGNATGGTCAAATCAATAAAAGGTTACTTTCAA
AAAAAAAAAAAAAAA
Sequence 1385
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GNNTTTTAAAANNTNAAAAAAAAATTTTTTTTTTTTNTNGGNCCCCCCCCCAANCATNNTAAA
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TNAAAAAAAAAANGTTTTTTTTTTNCCNNAGGAGATTTTAAAAAAGACTNTTTTTTTTTTTTN
NCAGTTTTTATTTAAAAAAAAAAAA
Sequence 1386
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GTGCAGNTGTGTTCCAATAAACCTTTATTTACAAAAACCGGCAATGAGATGGATTTGGCC

Table 1

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GCTTGAAAACAGGAAGCAAAATACAAAAAGTACCTCGGCCGNGACCACGCTAAGGG
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Sequence 1387
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TNNAAAAAAAAANTNCNCCCCCCNNANANANAATAATTTNANCTTTTTTTTTTTTTTNGGGGNAA
AAAAATNTTTANAAAAAAAATTTTTTNTTAGAAAAGAANAANATATATGANAATTCTCTCAA
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GGGGNGGGAANNAAATTNTTTTTTTAAAAACATANATNTTCTATAAAAAAAACCCC
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Sequence 1388
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AAAGTCATGAAGAGAATTTAAATTAAGGTTTTGGTTCCACTTTGTCTCAACTTTAACTTT
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TTTTTCTATGTTGAAACAGTATTTGAAAATTCTAACTTATACTGGCAGATAAAATGATAA
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GGCGGG
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Sequence 1389
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CAGGCANTGANCCCACCATGCCTNGGCCGCATGTGGTCAATTTCTTGGGGGGGTAAAACCG
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Sequence 1390
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GACTGNACAAGAGACCCTTCTGNTGANTACCCTTGCCAAGNTGTCTGCAAATGCTTNGCC
GANTTTTCTACTGAGTT
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Sequence 1391
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GNANAAAAAAAANAAGNTTTTTTNTTTGTTTTGNNTTNGCAAAAACTTTTTTGAAGGAATGGC
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TTTACAAGTTNGCNAAAAAATTAAAANAAAAACTTAANCCTTTCCTACCCAANAACCCCA
TTTTTTNGAAAANTNGGANAAGGTTTTAAAAAAAATTCNAAAAAAAA
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Sequence 1392
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GTTTGTTTTTTTAATAAACTGTTATCACTTAAAAAAAAAAAAAAAAAAAAAAGTCCTCGGCCGC
GACCACGCTAAGGG
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Sequence 1393
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CCCTTAGCGTGGTCGCGGCCGAGGTACAACTGCCCTACATTTCTGCCTAAAGGCAATTTC
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Table 1

CAGACTACACANACNGAGANGAAATGCAAATAGAGCCCANCTGTCTCTGAAAAGAGACAA
GAGAAATCTAATTTCT
Sequence 1394
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TAGGAGTGCACCACCACGCCAAGCTGGCATTCTCTGTTTTCTTATTTCCTGATTCTACTT
TTAGCTTTCTTAATATGCTGATATGTTTTGTTTGGTATATCATATATTAAAAAAACAGTT
CATCTCATCCCCATCATTNTATCTTTAAGAAGCCCCCCAAACCATTTTACACATTTAGGN
AAACAATGGGCAGGCAATAAGGNTAGNGAACATTCCATAGCCCTCTTTTGATAAACCACA
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AAATTCAAAACCTTAACTTTTTTTTTGGGAGGGAGTTGGGNGGATNCCAATAAAANGCCNA
TNNTTTTTTTGAAAATCNTTGAATGGAATTGACCTGGATTGAATTCCCATTTAAAGTCTT
TTACTTTATTANGGTTTTTNAANACTTTATTTTAAAAATTTTTCCTTAAGAACTTNAAAAA
CNNCTTGGGGTTCTTAAAANNTTAAGAAAACNNAAAATTTTNTCCAAAATTTTAAAAAAA
Sequence 1395
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GNAAGATGTTCTACCATATCTCCCTAGAGCACGAAATCCTGCTGCACCCGCGCTACTTCG
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Sequence 1396
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Sequence 1397
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GATGCAGCTCCTTACTTTAAGTCTGGCAAGGAAGATGCATTTTTTACNTAACTTCCACAG
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ATTCCAGCACACTGGCCGGC
Sequence 1398
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GAGTGNTTAACCTACAA
Sequence 1399
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ATGGCTATTTCCTAAGTTGTAAAGTNCTGCATTTATAANTGCCANTGTTGNAAGGTGGTG
TTTCTANACCTTCCCTGATGCGATTTTA
Sequence 1400
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Table 1

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Sequence 1401
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TGGGCACAGTAGTTACACAATAAACGCTAAAAGCCTGATTTAACAACTGTATATAAACAA
ACTACTTTTATGTGACTACTATACCTCTGGGCATGGTATTAACCTATCCCAACCAGAGTA
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Sequence 1402
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Sequence 1403
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TAATANAAACNNCAAANAACCAAANAATTAAAATGCAAGCTNTTTAAAATCCCAACT
Sequence 1404
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GGAGGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1405
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CGACCACGCTAAGGG
Sequence 1406
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AACTTACTTT
Sequence 1407
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Table 1

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CACTGAGTGGGATGTGGGTGATGCTCACATGACTGGCTAGAGCTTTGGGGGTGGGGTGGG
GGNTNACTACTATTTTTTTTTGGNCANGATCTCTTTCCCCTTTTTTTTTTTTTTTTT
Sequence 1408
CCCTTAGCGTGGTCGCGGCCGAGGTACCCTTTATAGGAACCCTCAAATTAAAAAAAAATG
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Sequence 1409
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CTGTG
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TACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1411
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Sequence 1412
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Sequence 1413
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Sequence 1414
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Table 1

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AAGGG
Sequence 1415
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CACGTGAGCAGTGAATAACTTGCAAGGATGCAGACTTTTTTATTTTGCGATGCTACTTTT
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ATTCTTAAAAGGGTTTAGAAAGAAAGAAAAGACAGCTGTTAGGTTATTTGATTTTCAAGT
TTATCAAATAAAATTCAAATAGAATTGGCAAATCTTTAATGGCATATGAATACTTCTATC
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CCTCCATCTTTATACAAAAAGAACATACAGAAATTTAACAAAGATATATGACTTACTCA
TATGTTTTATAAAAAGTATCACCTAGCANGTGTCTTNCATTTAAT
Sequence 1416
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Table 1

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Table 1

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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234
Table 2

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Page 13
(of 261 pages in Table 2)

Table 2

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Page 14
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Page 35
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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264
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Page 43
(of 261 pages in Table 2)

Table 2

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266
Table 2

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Page 45
(of 261 pages in Table 2)

267
Table 2

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270
Table 2

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Table 2

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273
Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Page 77
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Page 85
(of 261 pages in Table 2)

Table 2

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Table 2

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Page 87
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

>Sequence 815
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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

C
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Table 2

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Table 2

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Page 138
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Page 168
(of 261 pages in Table 2)

Table 2

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Page 169
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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>Sequence 575
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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Page 198
(of 261 pages in Table 2)

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

>Sequence 1117
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Table 2

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Table 2

>Sequence 1127
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Table 2

>Sequence 1135
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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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466

Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 3

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Table 3

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Table 3

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>21.1
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GGGTG
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

>69.1
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TCTTAGTATCAGGCTTGTGATAGAGAAAAGGCTGCTATGAATTCTACTCA
GTGTGCTTAGACCAAAGGAAACCACCACAGGGATTTCACAGGC
>72.1
ACATATATCATTTATTCAAGAGGCAGATTTTAAACGTTTTTGTAAAAAGC
TAAATAACACCCAGAGTGACTCAAAAAAATTTCTCAACTTTGCC
>73.1
CTGCCTTTAAAAGCTCATAACAGTAGAGATCAGTTGTCTCTGGTTGCAAA
TCTAACATATATTCATGCAA
>74.1
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AACTCTATGTCAGTGTCTGTCCCAGGTCCTAGAACTGGAATAGACCAACC
AAGCCCAACCCTTCTTAAAAGTAAGACTAGGTGCTTCCTGATTATATATT
CAACTGCCTGGAAGCATGCAAGTAAAATTTCCTTGATGGCATTTCTAAAG
TTCAAACATATTCTTCCTAAAAATGCATTTACAAAAAATATTAAGATTGT
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GGCCTACCCCAAAATGGAT
>75.1
TGGCGGCCGAGGTGCGCGGGGAGGCGTTGTGGGAGGAGGTGCGGGGAGAG
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GCGTCTCAATCTGCAGTAAAGAGGAAACTAATCTGAAAGGGAACGATAGG
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TCTTGAATCATGCCCAAAAGAATGAGCTGTCGGTGCTGCAGTCGTGACCC
AGGCTGA
>76.1
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Table 3

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GTGCAGTTTTCTTTTTCACATTAGGCTGGTTGGTTCAAACTTTTGGG
>77.1
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GCTAGCCTGGTTACCCGTAGTGAGAATGGAGAGGGCCACCTGCCCAGCTA
CACAAATGTTTCCCAGGACAACAGGAGGCTGTGTCCACTGACAGTTCAGA
CCGAAGTGGAACCACTGGACCGGAAGCTCTAGCAAGTGTTGCCCACCT
>78.1
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TTAGCCTGG
>79.1
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GGCAGTTCCAGATTTCAACTGGTTCATAGATGGGCGGGAGAATGAAAACA
GATGGTGCAGCCACAGTTCGTTTGATCTCCACCTTGGTCCCTCCGCCGAA
AGTGACCGATGTCCTTCCATATTGTTT
>79.2
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>80.1
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GGCCTCTCT
>81.1
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CAAGACAAAGCTCAGGCAAGTGGCTCAGTAGTTGGCCAGCCCAGCAGGGT
CCTCTGTATGAGTGTGCACCCAGCTGAAGAGAAGAAATGGAGAGCAGCAA
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>82.1
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G
>83.1
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CA
>85.1
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TCAATGGATCATTACAATTAATGTAGGTGCCGTGGGCAGGAAAGCTAACT
TTAGCTGAAAGCATCTGAAACGTGCTTATTTTTAATGGGCCCTCAAAGGA
AAGGGATGAGGCCAGCCATAAAGAAAGGCTTGGCCAAATATAGTTCTTGT
TTGTCAAGAACAACAAATCCCATTTCACAACAGAACTAACCTGGCATGCC
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Table 3

AAGATTTCATTCCTTTGTTCCAC
>86.1
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GCTCTCTTCTTGGATTTCAAATCCACCAGCTTTTACCAGGGCCAGGGCCA
GGCCTCCCCCATGCAGAAGATCTTCATTGGCTGCATTCACCACAGCATCA
ACAGCATGTGTGGTGAGGTCATCTTTCCACACTGATAACTCTATCCTAGG
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>87.1
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CTACTTAAAAATA
>88.1
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GAAGGGTTGGGCGGAAAACCCCCGACCAGGGAAC
>88.2
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GGCGCCTCTTCCTTGTTTTCCCCGAACCCC
>89.1
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AGTCACAAGGCACTGTTATATCAATTCAGTGTGACACAAGCCCTGATTAT
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CATTTCCAGCAGCTGTATATTTAATTCACAGTTAGGGGCTGAACAAACTA
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>91.1
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GGTTCAGCCACCCGTATCTGTAATCTCTCCATTCTGCCCTCTTGATTTTA
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CATTTCCAGCAGCTGTATATTTAATTCACAGTTAGGGGCTGAACAAACTA
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>94.1
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GAGCACTGTGCAATTGAGTCAACAAGGTCTCAACTACTGACTGGCTAAGA

Table 3

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>95.1
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CTGTGTGAGCTGTGCGCTCCCGACTGGGAAATGTCTAACTCCATCGAAAA
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>96.1
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CCCCGCGT
>97.1
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>98.1
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ACAGA
>99.1
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>100.1
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·CTGTGCCACTGGGAGTTGGGAGGCGGCCTGCTGGGGTTCCCTGGGTGGCA
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CTCTGAAGATACTGCTCTTCACCCCTCTGAAGGGGGTCTCCTCAGGGGAA
·GGT·
>102.1
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Table 3

GCTGAAGATTTTAGATTTCTACCTATTAGAAATGAATATTCACTGAGGTT
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CAAAA
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>108.1
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TTGCAAAGGGCACTTTTATCCATCTCAGTTATTCCCAGAGGTGACAGAAT
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>109.1
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Table 3

GGTCCTAAAGAGAGAGCTAGGGGAGGTTCAGCTGGCCACAGAGATGCTAA
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>114.1
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Table 3

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ACAATTTTAACCCCAAATTGTGACAAACAAAACTATATGGAAAAGGTC
>123.1
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Table 3

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>123.3
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>124.1
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>127.1
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TTCCCAAGTGCTGTATGTGAACAATAAATCTGAGACATACCTCTAAGGCT
TTTCCAGAGACAAGAAAGCTCTCAACCTGTAAAGAATTCCTGGGACATGA
CTGAGAGCAATGAGAACTCCAGGCAGAAGGTTAGCAGATATAGTGTAGAG
CATACACAGATATACTATAGTTCATAACACTGGTGGCTTAGCTGTAAATC
ACAAAATAGCACTGGAATTATACTAGTGATCATAGCACATAGTCCAAGAA
GAAAAAATTTTGATCTTGTTCTTAAACTTTGTGGAGCCAGTGGTGAAATG
AGTCACACAAAGATGCAACAATG
>127.2
ATGAACCCAGCCCTCTTTAGACTAACATATTCTTGCCCATCACCACCAAT
ATTACAATAAAAATCAAGACACATGAAGGAGCATACCT
>128.1
TTGGAGCTCCCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTT
GAAACGACAGCGATGTTTCCGTAACGGCATCTTAGCACGAAAAAGCTCCA
CGGTCTCATTCCACAGCCTGGTAGCTCGGT
>129.1
GTGGCGGCCGCCCGGCAGGTACAGTCAAGGCCGAAAACCACTGAGCTTTT
CCCTCTGCCTGGCACATATCCACTGCCCTGCCTTCCTTCAGCTGATGAAC
TCTTCATATGCCTCCTTTTGGGTGTCAGTGGAAATGTCACTTCTTTCTAG
AAGCTTCTCTGGCTCTCCCAGCCTGGCCCAGGGCTCCAGCTATGAGCTTC
CATAACACCCCTAGTTTTCCTCACATTGCCCTCATAGTATATGGAATTTG
TTCATTCAATTGCCTGGCTTCCAACAGATGCCAGCTCCAAGAAGGCAGGA
GCTGCTTCTGGGTATTGCTTGCCATCAAGGCCCTCACACCCAACCTAATG
CCTGGGCCAGAGTAGGTGC
>131.1
TGAGCTCACCGCGGTGGCGGCCGCCCGGCAGGTACCTATCTGCAGAACGG

Table 3

TCATTAGCAGTTTTTCCAAACAAGCGACTTTTAGCAAATTAACCGTTAAT
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AGCTGTTATATAATTAGAGCTGGACACCCACATGGAGAAACTAATTTGAC
TGTGCTGCATTTGACTTCACTTTGGTAACAGGAAGCACTTTTTAGTCTGT
AGACCCTTGGGAGTTGTAGGGAGTTAAAGCTGATCATTATATACTATTAT
ATACTTAGGGATACAACCCAAGGGCAACCCCTGGCCTTTATGAAAACCTG
GAGTGAGTTATTATTTCCTGGTAATACAATTCTCTGCCAGCCAGTTGCTG
CATCAAAACAGTTCTGATACACACACCTAAAGTCACCACTTCCTCATTCT
GGTCCCCAATAACCCTATAAGCCTCTCTCCTTGTAGGTGACCTCTGCCCT
GTGAAGGGTTGGCTCACCCCAAGA
>132.1
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CATTGTTGGCCTTCAGCCCGTCAATATCGCCCTTGATGTCGATGTTCTGG
CTCTCCTCATCATGGCTCAGCGCAATGGCGGCGTTCGCCTTGCCGGTCGC
CTCCACGAGGAACAGGGCTGCGGCCGTCGACACATCGCTGGACGCGAGGG
TCAGGTTGCCCTGAAGCAGCCCCTTCTTGTCCTGGGTGACATCACCGCGC
AGCCGCGTGCCGCCGGCAATGAACTGGATATTGCTCAGGCGTTTTTCGTC
CTTGTGCAGGGCAAGTTCCGTGGCAAGATCGGCCCGCACGCCGTCGAGGA
ACGCCAGACCGGATACCTTGCCGTCCGCGCGTCCTTGACAGAAGTCCGTT
GAAGGAGAACGCGCCTTCCTGAGCTTGCCCCGGAAAGTTTGCCATCC
>133.1
GTGGCGGCCGAGGTACGATAATTCATGCCAATTTCTTTGGGAATACTTGT
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ATGCAGTTATTTTTTCTGAATAACATAAATTTTAAACAGAGACCTGAAAA
AAACCCCAAAAGTATTAACCTTTAAATACATAAACTCAATAGAAATAATT
TAACTGCCTTCTCTTCACAAGAGGCAATCAGAAGGCAGGACTATAGTTTT
CTGTGTTTCTTTTCCACAGGAGAGATAATTACATTTCTAGAGACCCATAG
AAACAATTCCATAGTTTTAATTTCATCTCTCTATCTCT
>134.1
GGATGCAGCCAATTTCTTTGTCAAGATTGGCTCCATGCTGTTATTTAATC
AGGTGTTTCCTACTGTGTAGACAAACCTAACAGCTCTCCATCTTAAAAAAA
GGAGTGAGGAATTGAGCTGGACAGAGATGTGCATTCCAAATTTTTCTTTC
CCTTTCATAAAGACTTGATCGTCTTATTTATCTGGATTGGCCATACACAG
TAATCTCACTAGCTGACAGTTGCTTCCCGCGT
>135.1
AGCTCCCCGCGGTGGCGGCCGAGGTACCTCTCCTGCAGGGCCCTCCATTC
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GTCCATGTAGTCATCATCTCTTTGACCTCTGCATTTTCCCCCAGAAAGGC
GAGCATGTTACTTGTCATCTTGGGATCCGAATGACAAACTCCACCAGATG
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TTCTTAGCATTTCTATAGCTGAACTTCTTTAAGT
>136.1
CGCGGTGGCGGCCGAGGTACTTAAAAGTATATCAGGGCAGTTTCATGCCA
GGGAGCCAGGGAAGGCACCCAAGGAAGTGATGGAAGAGTAGAAGTTCACC
AGGTGCAGCTCAGGAAAGGGCTCAGCAAATTTCTCTGTAACAGGATGCAG
ACCCCGCGT
>137.1
GCGGCCGAGGTACTAAATTTAGCAACTTTATTCATGAGGAACACCAGTCC
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GTCTCCAATGGAGATGGAGAGATTTTCTGAGGAGTTTCTTGCTTTGACAT
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CCCCAACACTCCAGT
>138.1

Table 3

CAGTTTGCATACATGCTAAACAGAGAAATGTCCTCAAAATTCAGTTACTA
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ATTACAAATAAATATTCCACAAATTTGGAAAGTTATTAGAGGAAGAATTT
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TTACATGGAGGAAAGAAAATAGGAAAATAAGTCACAGAAAAAGAAAATCA
AAACAAA
>139.1
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GCTAAAACTTGGATGGCCTCTGAAGATACTGCTCTTCACCCCTCTGAAGG
GGGCTCCTCAAGGGAAGGT
>140.1
TCACCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTTGAAACGA
CAGCGATGTTTCCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTC
ATTCCACAGCCTGGTAGCTCGGT
>141.1
TGGCGGCCGAGCCCAATTCTTGATTTCTTTCCATCCCAAACTCTTTAAAC
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CCCCTTCTCTGCATTCTCTTTCCCCCCTTGTTATGCTAAAACTTGGATGG
CCTCTGAAGATACTGCTCTTCACCCCTCTGAAGGGGGCTCCTCAGGGGAA
GGT
>144.1
CTCCCCGCGGTGGCGGCCGTTGCCCTTACATCTCTCATTTGGAAGTGACA
GGTATTAAATAACGGCATATGAAAGCTTAAAAGTCATCAAATACAATCAC
TGGGTACTTTCGATTACCCAAACCAGGCACTTTCCTAAACTCCCCACTTC
TTTACTTCTGCGGTCTCCTTTCTTTTATTCCCCCGCGT
>145.1
ACCGAGCTACCAGGCTGTGGAATGAGACCGTGGAGCTTTTTCGTGCTAAG
ATGCCGTTACGGAAACATCGCTGTCGTTTCAAGAGCTATGAGCATTGTTT
CACA
>146.1
CCCGCGGTGGCGGCCGTTCTGCTTAGCCAGTTTATTCTTTATTTTTTTAC
TGGAGTCATTGCCAGTGATGGAAACGGTGTTTGCTTCTCTTTCAGTCAAG
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TCTACATTCATCTTTCCAGCACTCTGAAGTTATCAGCAAGTTCTCAGTCA
GTTCAAGGCATTGGATTCTGCTTGATTTCTTTTTAATTCATTGTTTTTGA
CCCCTTTGAGAGTTTTAATAGAGAGGAGTCTGGAAGGCAGAGATCTCCAC
CACCTAACCGTGAGAAATTTGGAACTAAGGACTTGCACTGGTCCCCAAGT
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>147.1
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TAAAGGATTGGTAGCTATTTCCCCATCTACAAATACATGACAATTAACTA
AGCCCAATTCTTTAAAACTATCTGGAATTAGGTCAAAATTATCTAATTTT
TTTCTGATTTAATTATGGATTACGTAATCCAATAGTTGGCAACATTATAA
AACCCTAACTTTACCTCATTGTTTGGCTATACCAGGTCTCATGACTCTGG
ACATAACCACCA
>148.1
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GGTGCAGACTGCGGAGCGGGCCCTACCGTGTGCGCAGAAAGAGGAGGCGC
TGGACTTATCCTACCTTAAGTTGAAGCAGACCAGCAATTGTTGTGACCTA
CAATCTCCACACCCATCTTTACTCTGAGCCAAGGAAGTGTCTGTTCTTGT
GCTGAGTTTCAGGGGCCTTCAGCTTGCGGGAAATCCCGAAGATGGCCAAA

Table 3

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>149.1
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ATGTTCACAACTTGAATTGCAGAGGTCAAGAGTTTAAAGAGTTTGGGATG
GAAAGAAATCAAGAATTGGG
>150.1
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AGCCTGGTAGCTCGGT
>151.1
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TGAATTCTTATTCCTGAAAGAATGGATAATGAATCAGGAGATGAGCAAAA
ACGTATCTTTTACAAAGCTCTAGTCTTCCAAAAGCCTCTAAACTCAAACG
AAACCTTTTTAAAGTAGTTTTGTAAAAGCTCAAGGTATGCCATTTCCAGA
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GCAATGAAATTCAGGAATTGGACAATGACCTCTTGGCATATGAAAGAATT
AAAAGAGGGC
>152.1
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GGAGTTTGCTTCACGACAGAAAGGCTTTATGGAAACTGCAATGGATGTTG
ATTCTCCTGAGAATGATATTCCTATGGAGATCACCACGGCAGAACCACAG
GTTTCCGAGGCAGTATATGACTGTGTTATTTGTGGACAGAGTGGCCCCTC
CTCTGAAGATCGACCTACTGGATTAGTTGT
>153.1
GGTGGCGGCCGAGGTACACCTGCAACTGTGCGAATGGTCCTGTTGCCTCC
TGCATTTTGGCCTCTGTTCTATAAAGGAAGAGTAAAGATGGAGCTCCTCC
TGCCTCCATCACGAAAGCACATATCATCTGTCCCTTTGGATTTTACTTCC
AGGACGCGTGTCGTCCCCAGCGTGTGTTGCCTTATGGTGCCGGCAGAGCC
TCAGCTATCTGCCTGGGAAGTCGGATGTCCTTGGAGAGAATTTGGAATGC
AGATAATTTTTCTTATTTCTTGAGAGCTTACTTTAATCAGCATGACACTA
CCTAAACACTGAAGATGGCCTTATATTAGTAAGATTTGCACAAAATTAAG
TATACCTATGCAAACTATTACTTTGGTTTTTAGGAGTTTGGTCAGATGAA
GAAGTAATGGGATCACATATATATGTAAG
>154.1
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GCGGAAATGCGTGGTGCTGGCCGGGTGGATCACCAGGCTGCGGCAATCGC
CCACGTTGGCCAGGTGGCTGAAGACCTTGAGGGTTTCAATGAACTTCTTG
CCCTGCTCGCGGTTGCCCTTGAGGTCAAAGCT
>155.1
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CTAGAAAGTATGAAATGGCAGTCTACCTGGGCAACCTACAAAAAATTTAG
CTTGAAAAGACTTCAGTCTCCGCTCCCCTGTTGATCTCATGGAGTGGGGA
ATGGGAATTGAACCAGAACTGGAAAATTATTTAGGAAAGTTTGTTAACTA
CTCTTTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAGAACTGGA
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ATGTGTTCTGGACATTGTTGAGGTCTAGAATTGTCTATACAATGCCCTGT
ACC
>156.1

Table 3

ACCGGGCTGGCGGTCGCCCGCTCTGGTGCTTGCATCTTGGCTTCCTATAG
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ACAATGTTCTTGTTGTTCCTTGGGTTTCTTAATGATTTCTGAATCATCAT
TATTAATTATGGAATTCTCTGGTCGAAAAGTCACATTTGGTTTTCTCCTC
AGTTTCTCACATCTTTTTTTCTTGCAGCTCTTTCTCAGCTCTTCTTCCTTG
CCTTTTTTTACTGTCCTTTCCTTGTCTTACTTCAGGT
>157.1
CGGGGGCGGCCGAGAAATGTCGCCAACTGCCGTCTTCCCTCCTCGGCCGC
TGCGACAAACACCCCACAAAATGGCGGCAGCGCCGTCGCCCTAGAATCCC
CCGAGTCGCCTCTCCCCGCGT
>158.1
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AGAACAGCCAATGGATTGGAACGTCCTAGGACAGATGCCACGGCTTTGAC
CCAGGCTGGGGGTGCACGGATCTCACTGGGGCTAGTTGGTCGGATGGGAA
AGCCCCATGGGTCCACCAGGATGAGGTGTTTAACTCTATCAGGGT
>159.1
ACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAACATTCTACAG
CGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCT
GTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTT
ACACCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGG
AAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTTTATTCGTGG
TCCAAGTGTAGAACCAGGATCAATAGTCCCACAGATCGTTCTCAACATTG
ACTTGGCCCCCACGATCCTGGATATTGCTGGGCTCGACACACCTCCTGAT
GTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAA
CAGGTTTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCCTA
>160.1
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CGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCT
GTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTT
ACACCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGG
AAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTTTATTCGTGG
TCCAAGTGTAGAACCAGGATCAATAGTCCCACAGATCGTTCTCAACATTG
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GTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAA
CAGGTTTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCCTAG
TGGAAAGAGGCAAATTTCTACGT
>161.1
GGCCGAGGTACCATCCTATTAATACTAACTTCTGCTTCTACATACTGTAG
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TGAGAAAATCCTGACTCTTGCAAGTATCTATATACCAAGAAGTTGACCTC
ATCACTGCTTATACTCATCTTTATTCCCACTTAAACCATGAGGTCACACC
ACAGGATATAACCCATTGGCAGTGCATTGATGTGGGGATGTGCAACTGAA
TATCCGGGCACCGCCAATCACAAGTTGCTGTTGTTGATGCTGGAAACGGT
GGCCTTCAACGCCGCTTCCCCCCTTCCGGGAATCCCCGCG
>162.1
GGCGGCCGAGGTACCTGGCCTGCTGGCATAGTTCTTTGACCCGTTCATAT
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ACGTAGAAATTTGCCTCTTTCCACTAGGAATGTATCACGCCAAATTTTGG
CCTTCTTGTTTGTTCGAAACCTGTTACCTGGCTTTTCTGGGTCCAGAAGT
TTGAGGACAGACTTGCCGTCCACATCAGGAGGTGTGTCGAGCCCAGCAAT
ATCCAGGATCGTGGGGGCCAAGTCAATGTTGAGAACGATCTGTGGGACTA
TTGATCCTGGTTCTACACTTGGACCACGAATAAAAAAAGGCACACGAATA
TCAAAGTCATATGGCATGGATTTCCCCTTGACCAGTCCAAACTGCCCAAT
ATGGTAACCATGGTCGGCGGTGTAAATGATGT

Table 3

>163.1
TGTACATTGTCTTAAAATCTGTGGCTTGCCTGTTCAATTCATTAGTGGTG
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ATCACAAACATTATCCTATGTTTTCCTTCAAAAATTATATG
>163.2
TACTAAAGAAATTTGAGGGATTTGCTATAATGTTAGGGATTTTTCTAGAT
>164.1
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AGTATTTAGCCCAGAGGGTTGTGGTGAAGTGT
>165.1
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CTGCAAGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAG
AAGGGTGAGAAGAGATGTCTGAATCCAGAATCGAAGGCCGTCAAGAATTT
ACTGAAAGCAGTTAGCAAGGAAAGGTCTAAAAGATCTCCTTAAAACCAGA
GGGGAGCAAAATCGATGCAGTGCTTCCAAGGATGGACCACACAGAGGCTG
CCTCTCCCATCACTTCCCTACATGGAGTATATGTCAAGCCATAATTGTTC
TTAGTTTGCAGTTACCCCTAAAGGTGACCAATGAT
>166.1
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CATGTCAGCCTAGGGCTGGGAACAGTTTGTGAGGACTTATCTGTTGTACC
T
>167.1
AGCGCAAGTAGGTCTACAAGACGCTACTTCCCCTATCATAGAAGAGCTTA
TCACCTTTCATGATCACGCCCT
>167.2
CCCCTACCGCCAATCCCTTTTTACAATAAAACAGGACCGAAGGGTCCAAA
C
>167.3
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CTAAGG
>168.1
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TCCTAGGACAGTTCGCGGAAGAAGTGGCTCACGCCTTCCAGAGCCACATC
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GGTACCTCGGCCGCTCTAGAAC
>169.1
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GGGTGAGCCAGTGTCTTTTTCACTCTATTTCAGTGCCCTGCACATTTTCT
GGCACATAGTAAGCAT
>169.2
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>170.1
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TCCAGGGAGAAAACAAGCCATGACCATTGTTGGTTGGGAGACTGAAGGTG
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ACCCTTTGGTGGAGCCTGAAAAAAATCTGGGCAGAATGTAGGACTTCTTT
ATTTTGTTTAAAGGGGTAACACAGAGTGCCCTTATGAAGGAGTTGGAGAT
CCTGCAAGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAAACAATG
AGGAACATTTCATTTGACCCAACATCCTTTAGGAGCATAAATGTTGACAC
TAAGTTATCCCTTTTGTGCTAAAATGGACAGTATTGGCAAAATGATACCA

Table 3

CAACTTCTTATTCTCTGGCTCTATATTGCTTTGGAAACACTTAAACATCA
>171.1
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GTAGTCCAGTTGGCTTAGCAGTAGTTTCGTTGGGGGGGGAGCCGAGGTTCC
GGCAAGGGGCTAGGCCGGCTTGAAAAGAGATTATGACTGTACCTCGGCCG
TCGAGCGGCCGCCCGGGCAGGTACAACTTTTATACAACTCAGGAGATTAA
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ATTTCCCAGAATAAACAGATATGCATTGCATTAAAGGTAATTTTCAAATA
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GCAACTAATTCATTGCTAATACTGGGGCATGAATTTTTGGCAAATGTTTA
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GAAA
>172.1
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CTCTGTTTTCATTGTGACACACTGAGTTAATAAAGCACTTACTGAGGGAG
CCAGAGCCCAAACTCTAAATGTGCTGTAGAAAAAGGGCCAAGTCATTGAC
TGCACCACTCCTTCAGCCAGAGGTAGAAAGGATTTACTCTTCAGCCATCT
GGTAGAGCCCCAAGAACAAGTTACATGTGGACAAAGGGAGGGAGAGGTAT
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AAGCAGGTCAAGGAAGATACAC
>173.1
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CACCAAGATGTGGGTAAATGAAAATTATTAGTTCAC
>174.1
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TTAAATCCATGAGGTCACAATGATACTTAATTTTTTCATTATTCTGAAAAC
CAGTAAATAAAGGCTAAGATTCAACAAGCATTTATCCAGCCTTTCCTCAA
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>175.1
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AGCGTGTGTGGGAAAGTCTTCCTCCGTCATTCATTCCTGGACAGGGACAT
GAGAGCTCATGCTGGACACAAACGATCTGAGTGTGGTGGGGAATGGAGAG
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CAA
>176.1
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TAAGGCAGGAAGATGGCGGCCGCACAGAAGACGAAAAAGTCGCTGGAGTC
GATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGGAAGTG
>177.1
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Table 3

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>178.1
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AACCACTTTTCCTCTTTCCTCTGAAATATCAGAAGTTAAAAATCTACTCT
GAGTTATATGTGCATCAATTTTAGACATATTGCTGATTTTATTATGAAAA
TGAAGTGCTAAAGACAAAGGATATTTCCATTCCTCTGGACAGGCAGCCAC
AGACCAGCACTGCTTGACCCATGTGTATACACATGTGTGCTTTGT
>179.1
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CCTTGGGCTTCATGGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGC
TCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAGAACAAGGACAC
ACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTT
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CTGAGACAGTCTGATCAGTTT
>180.1
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TATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGAC
CTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAGCCGTGCACGCAGAC
TGTGAATTTGCGTGACTGTGAGT
>181.1
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GAGCGCTTTGTGAACTTCTCCAAATAAGAACAAGGACACACATTGTGTCA
GGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCACTATTC
ACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCACCCAATC
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TGATCAGTTT
>182.1
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CGCAGGAAAAAAACAAAAACTGGCTGGCGATCTGGAGTAAAGGATCCTC
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>183.1
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AGCAGTGTGAATCTTGACAAACTTATAAATGACTTCTCACAGATAGAAAA
GAAAATGGTAGAAACCAATGGAAAGAACAATATACTGGATATTCAGTTGG
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AAAGAAGAATGTGCTACTCTTCATAATATAATAAAAGGGCTACAACAGAC
CATTGAATATCAACAGAATTTGAAAGGTGAAAATGAACAACTAAAAATAA
GTGCTGATCTTATAAAAGAGAAGTTAAAGTCTCATGAACAGGAATATAAG
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Table 3

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>184.1
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>186.1
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TTCACCCATAATTAAGACCTTCTGAGGATGATCGATAGATAAACACACCT
CCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGGATCCCTACG
ACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAA
GAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATA
TGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAAT
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CTTTTCCTTGATCTGAGACAGTCTGATCAGTTT
>187.1
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AATATTTCCCGTAAATACTGCCAAATCGCTACACAGACTTAGTGGCCATC
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CTCCTACTACTGGATTGGGATCCGAAAGAACAATAAGACATGGACATGGG
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>188.1
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>188.2
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>188.3
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>189.1
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ATCAACAAGACTCAGCCCACCTGCACCCAGGTGATTAAAAAGCTTTATTG
CTCACACAAAGCCTGTTTGGTGGTCTCTTCACATGGACGCGCGCGACATT
TGGTGCCCTGACTTGGATCAGGGGACCTCCCTTGGGAGATCAATCCCCTG
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Table 3

TCTGTGAAAAAGACTAAGATATCAGAGAAATTATTAGTGCACATTATTAG
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ATTGGGGAAACTTTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGT
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TTCCGATGTGATTGATAGTCAGGAACTT
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CGTATAAGGTCCTTTTTGAGGTTTATTATTTCCTTGTCCATATACTTGAT
GCTCTTCATTGGCTTGTCTGGGACCTGCCTTAGGTTCTCCGAGGCATAAA
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GACAAGGATTTTTCCAGAATCTTCTACTTCAGTAGTTACTGGTATGAGAA
GTTTCGGCAACTTCTCCCTGATCCCCAAGTCCCAATTACA
>192.1
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>193.1
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>194.1
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AAAAAAAAAAAAGT
>196.1
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TGAAGATTTAGATTTATTTGAAAACACTTAGTCTAATTTATATTAGTGCA
GAAAAATCACATTCAATAAACCACAATTGTAGAAGAGACAGATAAGTGTG
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>197.1
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GGAGCGCCTCACTAACTCCATGATGATGCA
>198.1

Table 3

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>199.1
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CAGTTTGTGAGGACTTATCTGTTGT
>200.1
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>201.1
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CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCA
>201.2
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>202.1
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>203.1
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ACCT
>204.1
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TGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
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>205.1
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TGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
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GTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGC
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Table 3

>206.1
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GTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCA
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CCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGAG
ACAGTCTGATCAGTTT
>207.1
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CCAATCATTATTGGGAAGAAAGTCAATTATATTAGAAATGGTTAAGAGCT
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>208.1
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GGATTAAAACAAAGGTCATCTGATCTCCAATCATTATTGGGAAGAAAGTC
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TGATTTAAAAAGAT
>209.1
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GGATAGTCAATAGAACATGAGAATCAGAACAATCTGGGCAAATGGGTATG
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>210.1
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GGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCACTATTC
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TGATCAGTTT
>211.1
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ACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTT
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Table 3

>212.1
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>213.1
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>214.1
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AGAAGTAATACCTGATTAATTAGAATTCCCAACCCTCATCAAGTGTGTGC
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>215.1
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CGGACTTGAGCAGGTCACTGGGTCCTTTACACTTGTGAATTCGAAGCTTG
CCAGATGTATCCTCAATGCATTGCCACTTCTGCCCCGGTTGTTCACAGGC
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GCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCTACTCCAAAGAG
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CGGCCTGCGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCT
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GA
>217.1
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Table 3

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>219.1
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CCGCGTACCTCGGCCGCTCTAGAACTAAGTGGGATCCCCCGGGCT
>220.1
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>221.1
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CCCCAAATGCTCTTCAGGATTTAAATAACAATTTTTAAAAAGACACTTAA
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GAGCAGTTTTTC
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GTCTCTCATGTCTCTCAAGCGAAAGGAAAAGGAGTGATATTTGGGTCCC
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Table 3

>224.1
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GCAGCCCACAAAAAAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTA
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TGTATCCTACTGCATCAGGACATTTGTGTCAATGTCAGGTGACGAGGGGA
AATGAAAGTGATGAGACGATGAGAGGAGTGAAATACCAAGGACGCCATAC
TAGGAAACCCAGGTCTATTTGTTATCAGAGTAAGGATCAAGCCAGATAGC
CTGTTATGTAATTTCTCCGATAAAAGATTTTGAAAGCAGGTGCTGTGGGC
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CAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGT
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>226.1
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>227.1
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CTT

Table 3

>229.2
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GCTCGATTCAGTTTTAGCTAAATTTATAGTCTAGGTAGTATGTTACATTT
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>237.1

Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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>274.1
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>276.1
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Table 3

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>283.1
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Table 3

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>291.1

Table 3

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Table 3

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524

Table 3

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Table 3

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Table 3

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Table 3

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>336.1
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TCAGGCTCCCAGGAACCTGCCTCAAAACACAGGTCTCCACGACCAGGAGA
CAGGTGCTGTGGTCTGGACAGCTGGGCCCCAGGGACCAGCCATGCGTGAC
AACAGAGCTGTATCCCTCTGTCAGCAAGAATGGATGTGCCCAGGCCCTGC
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GGCTA
>337.1
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>338.1
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>339.1
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>340.1

Table 3

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CTGATGGGAGTGTATC
>341.1
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TGTAATTGTTCCCAATTATTAGAAACTTTTTTCCATTTTTCAAAATGTTT
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TCTCCTGCTCTATCCGCTGCTGTGGCAAATCCTCTAAAAACAGCGTTTTG
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Table 3

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>346.1
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CCTGAATCTTTGGAGTACCCATTCCCTTGATGTCTACAATATCACCTTTC
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>348.1
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>349.1
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>352.1
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Table 3

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>353.1
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>354.1
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>358.1

Table 3

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>359.1
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>364.1
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>365.1
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Table 3

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>366.2
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>367.1
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>369.1
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Table 3

>372.1
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GGAGT

>373.1
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>374.1
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>375.1
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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554

Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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>735.1

Table 3

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Table 3

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Table 3

>748.1
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 4

>1

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Table 4

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Table 4

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˙NNN
·>9

Table 4

>10

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>36
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Table 4

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Table 4

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Table 4

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Table 4

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>49

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607

Table 4

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Table 4

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>52
>53

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

>123

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

>207
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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781

Table 4

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782

Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

>708

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

>949

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>950

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>951

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>952

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>958

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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